Winter 2014

DEVELOPMENT OF GENOMIC RESOURCES AND IDENTIFICATION OF MARKER-TRAIT ASSOCIATIONS IN STRAWBERRY

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DEVELOPMENT OF GENOMIC RESOURCES

AND

IDENTIFICATION OF MARKER-TRAIT ASSOCIATIONS

IN STRAWBERRY

BY

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DISSERTATION

Submitted to the University of New Hampshire
in Partial Fulfillment of the
Requirements for the Degree of

Doctoral of Philosophy
in
Plant Biology

December, 2014

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On October 10, 2014

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DEDICATION

I dedicate my dissertation to my husband, Peter Myles Mahoney, family and friends who encouraged me every step of the way and which have made it possible for me to successfully complete this project.

ACKNOWLEDGEMENTS

This investigation was made possible through the financial support of the following: the UNH Department of Biological Sciences, the New Hampshire Agricultural Experiment Station, the UNH Graduate School Summer TA Fellowship program, the USDA Specialty Crop Research Initiative Grant 2009-51181-05808, "*RosBREED: Enabling Marker-Assisted Breeding in Rosaceae*"; and the Anna and Raymond Tuttle Environmental Horticulture Fund. In addition, *Fragaria iinumae* genomic resource development and genotyping was funded in part by a consortium consisting of: Thomas M. Davis, UNH; James Hancock, Michigan State University, Kevin Folta, University of Florida; Judson Ward, Driscoll Strawberry Associates; and Dan Sargent, Fondazione Edmund Mach, Research and Innovation Centre, San Michele all'Adige, Italy. Finally, research reported in the verticillium wilt chapter (Scientific Contribution Number 2530 from the New Hampshire Agricultural Experiment Station) was in part funded by a grant from the USDA National Germplasm System (Small Fruits) award #358-2100-038-01S, *Screening for Verticillium Wilt Resistance in Wild Diploid and Octoploid Strawberry Germplasm.*

I wish to thank my advisor and committee for their support and valuable critics in the course of this project. Particularly, I want to thank my advisor Thomas M. Davis for his thorough edit of my dissertation. I want to thank Brent Loy for his encouragement and ideas towards development and release of new strawberry hybrids. I want to thank Joanne Curran-Celentano for her generosity in the use of her lab and equipment. I want to thank Becky Sideman for her insights on cultural practices related to strawberry. And finally, I want to thank Jim Pollard for his encouragements and belief in my abilities.

In addition, I want to thank John McLean and the staff at the Woodman Farm for their continual maintenance of the strawberry fields and David Goudreault and staff at the McFarlane Greenhouses for their continual maintenance of the strawberry plants.

I wish to thank my family and friends, who have patiently encouraged me during this project. And, finally, I wish to acknowledge my husband, Peter Myles Mahoney, who has held up the home front and without whose support I would not have been able to complete my dissertation.

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LIST OF ABBREVIATIONS AND UNITS

Array	Affymetrix Axiom® platform IStraw90 (International Strawberry 90K) Array
B	Cultivar ‘Bountiful’
PP	Cultivar ‘Pink Panda’
B-PP	Accessions of an F_1 population of ‘Bountiful’ (B) x ‘Pink Panda’ (PP)
DW	Dave Wood F1D F. iinumae reference-guided pipeline (internally developed)
ERS	Economic Research Service
F.	*Fragaria*
f.	forma
FRA=CFRA	NCGR Inventory ID number prefix
FV×FB	*F. vesca* ‘815’ × *F. bucharica* ‘601’
FvH4	F. vesca ‘Hawaii4’
GBS	Genotyping-by-sequencing
GTC	Affymetrix Genotyping Console
F1D	*F. iinumae* F1 plant, parent of F2D population
F2D	*F. iinumae* F2 population
J17	*F. iinumae* female parent of F1D
J4	*F. iinumae* male parent of F1D
LG	Linkage group of *F. iinumae* F1D
LOD	Logarithm odds score
MAB	Marker-assisted breeding
NCGR	National Clonal Germplasm Repository
NH	New Hampshire
NPGS PI	National Plant Germplasm System Plant Introduction number
NW	Non-white flowers
QTL	Quantitative Trait Locus
RF	Recombination Frequency
PC	Pseudochromosome of *F. vesca* FvH4 reference genome
PCR	Polymerase Chain Reaction
ssp.	subspecies
SNP	Single Nucleotide Polymorphism
UN	Buckler Lab TASSEL 3.0 non-reference based UNEAK pipeline
UNH	University of New Hampshire

USDA	United States Department of Agriculture
W	White flowers

Affymetrix cluster classifications

PHR	Poly High Resolution Affymetrix Array genotyping cluster classification
CRBT	Call Rate Below Threshold Affymetrix Array genotyping cluster classification: SNP call rate is below threshold.
MHR	Mono High Resolution Affymetrix Array genotyping cluster classification: less than two examples of the minor allele
NMH	No Minor Homozygous Affymetrix Array genotyping cluster classification: Two clusters with no minor homozygous genotypes
OTV	Off-Target Variant Affymetrix Array genotyping cluster classification: Typified by a fourth cluster
Other	Affymetrix Array genotyping cluster classification: One or more cluster properties are below quality threshold.
NoCls	Not classed used as a place-holder for the mSnps whose qualities were not classified.

IStraw90 Array marker types

F1Dsnp	*Fragaria iinumae* discovery-based SNP
Snp	Octoploid discovery-based SNP with two alternate alleles
mSnp	Octoploid discovery-based SNP with four alternate alleles
ins	Octoploid discovery-based insertion relative to *F. vesca* 'Hawaii4'
del	Octoploid discovery-based deletion relative to *F. vesca* 'Hawaii4'
SnpSnp	Octoploid discovery-based subgenome-specific SNP adjacent to a marker SNP
indelSnp	Octoploid discovery-based subgenome-specific indel adjacent to a marker SNP
SnpinIns	Octoploid discovery-based SNP inside a subgenome-specific insertion
SnpinDel	Octoploid discovery-based SNP inside a subgenome-specific deletion

Verticillium disease classifications

VR	Very resistance to verticillium wilt
MR	Moderate resistance to verticillium wilt
I	Intermediate resistance to verticillium wilt
MS	Moderate susceptibility to verticillium wilt
VS	Very susceptible to verticillium wilt

Units

aq.	aqueous
ml	milli (10^{-3}) liter
µl	micro (10^{-6}) liters
µg	micro (10^{-6}) gram
µM	micro (10^{-6}) molar
Mbps	Million base pairs
g	gram
N	Normality, equivalents of solute per liter of solution: i.e. for HCl, 1N =1M
cM	centi-Morgan (1 cM = 1% recombination frequency)

Chemical, enzymes, and processes

COA	Certificate of analysis
FDW	Freeze Dry Weight
HPLC	High Performance Liquid Chromatography
ORAC	Oxygen radical absorbance capacity, µM Trolox equivalent
[ ]	concentration
Cyn	Cyanidin
Plr	Pelargonidin
Anth	Anthocyanidin = Cyn and Plr
HCl	Hydrochloric Acid
CHS	Chalcone synthase
CHI	Chalcone isomerase
FS	Flavone synthase
FLS	Flavonol synthase
F3H	Flavonone 3-hydroxylase
F3'H	Flavonoid 3'-hydroxylase
F3'5'H	Flavonoid 3', 5'-hydroxylase
DFR	Dihydroflavonol 4-reductase
ANS	Leucoanthocyanidin oxygenase
ANR	Anthocyanidin reductase
3GT	Anthocyanidin 3-*O*-glucosyltransferase
GST	Glutathione S-transferase
LAR	Leuco-anthocyanidin 4-reductase

ABSTRACT

DEVELOPMENT OF GENOMIC RESOURCES AND IDENTIFICATION OF MARKER-TRAIT ASSOCIATIONS IN STRAWBERRY

BY

LISE L. (BOUCHARD) MAHONEY

University of New Hampshire, December, 2014

Crosses were performed and progeny populations were developed in diploid and octoploid strawberry *(Fragaria)* species for the purposes of genetic analysis and breeding. A high throughput genotyping platform – the Affymetrix IStraw90® Axiom® strawberry SNP array – was evaluated and employed for these purposes. Phenotyping was conducted with respect to several traits of interest, including flower color, flower and fruit pigment compositions, and verticillium wilt resistance, for the ultimate purpose of identifying marker-trait associations useful in breeding.

In the ancestral diploid species *Fragaria iinumae*, an F2 mapping population was developed from a cross between two accessions previously collected in Hokkaido, Japan. High-throughput genotyping platforms, the IStraw90 SNP Array and Genotyping-by-Sequencing (GBS), were utilized to develop high density linkage maps for *F. iinumae*. A linkage map based on 21 of the F2 generation plants genotyped on both platforms consists of 4,110 markers, while the second map based 85 F2 plants genotyped on only GBS consists of 895 markers. The linkage

maps will used in a parallel research project to anchor an *F. iinumae* genomic sequence assembly, with the aim of providing an additional reference genome for *Fragaria.*

A 455 member Closed Pedigree Set of octoploid strawberry plants was developed with diverse flower colors and progress was made on improvement of fruit quality through selection. The range of floral cyanidin and pelargonidin contents determined by HPLC in the progeny exceeded the range of contents of the founding parents, and thus exhibited transgressive segregation. The non-white (NW) flower trait was found to be a completely dominant to white, and no true-breeding, non-white flowered plants were found. The IStraw90 SNP Array was utilized to genotype 41 members of the Closed Pedigree Set and among a total of 5,674 segregating markers, 35 markers predictive of NW flower color were identified on chromosome 5. Additional genotyping will be required to further characterize the marker-trait association for color and to identify quantitative trait loci for hue.

Fragaria diploid and polyploid species were phenotyped for verticillium wilt resistance, and disease resistance ratings of the octoploid cultivars were compared to the results of previous published studies and presented in a pedigree format to help identify sources of resistance. The results will be used to identify germplasm for developing populations for high throughput genotyping on the IStraw90 Array for the ultimate goal of identifying marker-trait associations for the purpose of marker-assisted breeding for resistance.

INTRODUCTION

Strawberry is an important crop

Strawberry is an important crop in the United States valued at over $2.9 billion per year. Annual production has increased steadily to the current level of 3.0 billion pounds from a mere 500 million pounds in 1970 (ERS-USDA 2012). New Hampshire produces slightly over one million pounds of strawberries per year, valued at $2 million (Schloemann 2006). Assuming NH residents are typical consumers of strawberry, at the current nationwide strawberry per capita consumption of 9.0 pounds a year (ERS-USDA 2012), and a NH population of 1.3 million people (Gallager 2011), NH consumes an estimated 11.7 million pounds of strawberries annually. In sharp contrast, NH is only producing 1 million pounds (Schloemann 2006) of strawberries a year, indicating that demand far exceeds local production. The presence of a strong ornamental industry, which is the single largest agricultural sector in NH, also highlights an opportunity for developing locally adapted ornamental cultivars targeting homeowners and landscapers, and a broader extended season for consumption of locally grown strawberries.

Public strawberry breeding programs in the USA

In the United States, public strawberry breeding programs exist at six locations: University of California, Davis; University of Florida; NC State University; USDA Beltsville Maryland; Cornell University; and Oregon State University. In the northeastern U.S. and Canada, the only strawberry breeding programs are those at Cornell University and the Nova Scotia Kentville Research Station. The strong genotype × environment interaction observed in

strawberry cultivars points to the need for locally developed varieties (Hokanson et al. 2000). A breeding program in New Hampshire will provide specialty growers, small farms, and a strong ornamental industry with cultivars selected in and suited for our environment. These locally adapted cultivars should also be well-suited for other New England states including Maine, Vermont, and Massachusetts, which have similar agricultural settings and climates.

Strawberry germplasm

Fragaria is part of the economically important Rosaceae family. This family includes fruit- or nut-bearing members such as *Malus* Mill. (apple), *Prunus* L. (almond, apricot), and *Rubus* L. (raspberry), and ornamentals such as *Potentilla* L. (cinquefoil) (Judd et al. 2002). The *Fragaria* genus has a basic chromosomes number of x=7, and is represented by twelve diploid species, five tetraploid species, one hexaploid species, three decaploid species, and three octoploid species (Hummer et al. 2011, Hummer 2012).

Diploid strawberry - There are currently twelve recognized diploid strawberry species (Hummer et al. 2011), including *F. vesca, F. bucharica, F. chinensis, F. viridis, F. iinumae, F. nilgerrensis, F. daltoniana, F. nubicola, F. mandshurica, F. nipponica, F. pentaphylla,* and *F. ×bifera* (Hancock et al. 1993, Hummer et al. 2011). *Fragaria vesca* is found from the northern part of British Columbia, across North America, and south to Central America in San Salvador (Staudt 1999), on the island of Hawaii (Hancock et al. 1993), and in Europe (Hancock et al. 1993). *Fragaria vesca* is represented in the Americas by subspecies *americana, bracteata,* and *californica* (Darrow 1966), and by *subspecies vesca* from Europe to Siberia (Folta et al. 2006). *F. ×bifera* is found in France and Germany. *F. viridis* ranges from Europe to western Eurasia. The remaining nine species are found in the Far East. Most of the diploid species are

red-fruited, but there are a number of exceptions including white-fruited forms of *F. nilgerrensis* ssp. *nilgerrensis*, white-to-pink *F. daltoniana*, white-fruited *F. pentaphylla* (Hummer et al. 2011) and a few *F. vesca* ssp. *semperflorens* varieties *that* have yellow fruit (Darrow 1966).

Diploid ancestors of *F. vesca* and *F. iinumae*, and possibly a third as-yet-to-be-identified diploid are considered to be ancestral to the octoploid strawberry (Hancock 1999, Folta et al. 2006, Davis et al. 2007, DiMeglio et al. 2014). The only current reference sequence for strawberry is based on yellow-fruited *F. vesca* ssp. *semperflorens* 'Hawaii 4' (Shulaev et al. 2011).

Tetraploid strawberry - There are currently five recognized tetraploid strawberry species. All are found in the Far East and include *F. corymbosa*, *F. gracilis*, *F. moupinensis*, *F. orientalis*, and *F. tibetica* (Hummer et al. 2011). The tetraploids are typically red-fruited, but *F. tibetica* f. *alba* is white-fruited (Hummer et al. 2011).

Hexaploid strawberry - There is only one recognized hexaploid strawberry, *F. moschata*, indigenous to Europe and Siberia (Hummer et al. 2011), and it has red fruit.

Decaploid strawberry – There are three recognized decaploid strawberry species, *F. iturupensis* found on the Iturup Island, *F. cascadensis* found in the North American cascades, and *F. ×vescana* cultivated in Europe (Hummer et al. 2011, Hummer 2012). All three of these decaploid species are red-fruited.

Octoploid strawberry - There are three recognized octoploid species, *F. chiloensis*, *F. virginiana*, and *F. ×ananassa* (Hummer et al. 2011).

F. chiloensis is found on the west coast of North America (Alaska to California) and South America (Ecuador, Peru, and Chile), and in Hawaii. *F. chiloensis* also grows at high altitudes in South America in areas where it has been under cultivation for many years, as early

as 1,500 (Darrow 1966). *Fragaria chiloensis* is represented by four subspecies: *lucida* and *pacifica*, which are red-fruited and found in North America, and *F. chiloensis* f. *chiloensis* (white fruited) and f. *patagonica* (red-fruited) found in Central and South America (Staudt 1999).

Fragaria virginiana grows wild throughout North America including Canada and the United States from Alaska to Mississippi (Staudt 1999). *F. virginiana* is represented by four subspecies *virginiana*, *glauca*, *grayana*, and *platypetala* (Staudt 1999). All of the subspecies have red fruit with white to red internal color (Staudt 1999).

F. ×*ananassa* arose in a French garden from an accidental hybridization in the 1700's between a white-fruited Chilean strawberry *F. chiloensis* ssp. *chiloensis* and a wild North American species, *F. virginiana.* (Darrow 1966). The considerable diversity exists within both *F. chiloensis* and *F. virginiana* wild species (Hancock et al. 2000) offer a rich germplasm pool for breeding (Hancock et al. 1993, Hancock et al. 1993, Hancock et al. 2010, Stegmeir et al. 2010). Both the white- and red-fruited forms of the South American *F. chiloensis* have been used in breeding, and cultigens of the white-fruited *F. chiloensis* are grown and marketed in Chile (Hancock et al. 2001, Carrasco et al. 2007). The white-fruited forms of *F. chiloensis* contain only trace levels of anthocyanins (Saud et al. 2009), although the achenes are red, while the red-fruited form lacks the high cyanidin trait of particular interest to my research. In contrast, I have identified in a certain North American *F. chiloensis* germplasm accession exceptionally high fruit cyanidin content (Mahoney, 2007; Mahoney et al., 2009a).

The genome of strawberry

The *F.* ×*ananassa* genome (2n=8*x*=56) has a 1C genome size of 780-800 million base pairs (Mbp) (Davis et al. 2007). The complexities of octoploidy provide a challenge for genetic analysis, thereby drawing attention to the ancestral diploid species, *F. vesca* and *F. iinumae* (Davis et al. 2009, Mahoney et al. 2009) as research models. Diploid, *F. vesca* 'Hawaii 4' (2n=2x=14), the reference genome for strawberry (Shulaev et al. 2011) has a 1C genome size of ~240 Mbp. 'Hawaii 4' shares a high degree of microsynteny with *F.* ×*ananassa* (Sargent et al. 2009).

The majority of strawberry cultivars on the market are *Fragaria* × *ananassa.* The few exceptions are European diploid *F. vesca* 'Alpine' varieties, including 'Yellow Wonder', and 'Baron Solemacher'. Most *F.* × *ananassa* cultivars have been derived from continual breeding and hybridizations of the original cross of *F. chiloensis* and *F. virginiana* (Darrow 1966) with some introgression from wild octoploid species. For example, the day-neutrality of the cultivars 'Seascape' and 'Tribute', and 'Tristar' are the result of introducing *F. virginiana* ssp. *glauca* into their pedigree (Bringhurst 1991). *Fragaria* × *ananassa* cultivars are described as either short-day cultivars, which form flower buds during photoperiods of short days (long nights), or day-neutral cultivars, which do not require short photoperiods to form buds. There is also a growing interest in developing cultivars with increased nutritional value, with a focus on secondary metabolites and anthocyanins (Just 2004, Crosby et al. 2007, Khanizadeh et al. 2007, Scalzo et al. 2007, Yoo et al. 2007), the success of which may be increased by gene introgression from wild species.

Development of new cultivars is not limited to intra- and inter-specific breeding within *Fragaria*. For example, 'Pink Panda' is the result of intergeneric hybridization of *F.* × *ananassa* with *Potentilla palustris* (Ellis 1962, Ellis 1991), now classified as *Comarum palustre* L. (Crow et al. 2000, Lundberg et al. 2009). *Potentilla palustris* differs from all the other *Potentilla* species in that it has "a large fruit with a large but non-succulent spongy receptacle" (Ellis 1962).

Marker-assisted breeding

The mission of the USDA-SCRI funded RosBREED project has been to develop high-throughput genotyping platforms to facilitate marker-assisted breeding in peach, apple, cherry and strawberry. The development and commercialization of the IStraw90 (International Strawberry 90K) SNP Array based on the Affymetrix Axiom ® platform is such a tool for strawberry (Bassil et al. manuscript submitted). The Array for genotyping strawberry contains 95,062 marker sites distributed in mostly genic sites across the genome.

Overview of Dissertation

The body of my Dissertation consists of three chapters. As detailed below, the first two chapters employ a new tool for genotyping in strawberry, called the IStraw90 Array, which I will refer to simply as the Array. The third chapter looks at verticillium resistance in strawberry and employs pedigree-based tools to identify sources of resistance.

Chapter I - *A high density linkage map of the ancestral diploid strawberry, F. iinumae using SNP markers from the IStraw90 Array and GBS,* includes a thorough review of all of the results from the Array genotyping of a subset of the *F. iinumae* mapping population that included the two founders, the F1 parent, and 21 F2 individuals. Also included in the first chapter, is the

application of genotyping-by-sequencing (GBS) to a larger subset of the *F. iinumae* mapping population. *Fragaria iinumae,* an ancestral diploid of strawberry provided a model to: 1) understand and utilize the results from the Array; 2) evaluate the performance of the Array; 3) construct the first high density map for *F. iinumae*; and 4) to inform the analysis of octoploid data. The study of *F. iinumae* as reported in Chapter I validated the Array as a very useful tool and GBS as a complementary tool and informed the decision for a concerted focus on the use of the Array for genotyping of the octoploid breeding population. The bioinformatics methods employed for the diploid data in Chapter I guided the analysis of the octoploid data in Chapter II.

Chapter II - *Pedigree-based analysis of flower color variation using SNP markers from the IStraw90 Array* describes the development of a Closed Pedigree Set. The Closed Pedigree Set is based on three founders, two with white (W) flower color, and one with non-white (NW) flower color. The NW flowers varied in hue from light pinks and corals to orange and scarlet reds. The objectives were to develop hybrids with red flower color and to advance the potential for marker-assisted breeding by identifying marker-trait associations.

Chapter III – *Germplasm resources for verticillium wilt resistance breeding and genetics in strawberry (Fragaria)* describes the results of trials conducted in the greenhouse involving diploid and octoploid germplasm. A pedigree of the tested cultivars was developed and overlaid with results of detailed research of previous studies published on cultivar resistance to verticillium wilt. Resistance × susceptible hybrids were developed for the purposes of conducting genetic studies in the future. Cultigens were identified as resistant and susceptible as an information resource relevant to breeding for resistance, which may inform choice of germplasm for additional screening and parent selection as well as future efforts to identify associations between markers and resistance traits.

In association with my Dissertation project, I am a co-author on a recently submitted manuscript on the design and evaluation of the IStraw90 Array (Bassil et al. manuscript submitted). The Array contains a total of 138,099 probe sets including replicated probe sets. The Array can detect up to 95,062 unique SNP probe sets for each plant sample. The Array includes 3,751 SNP probe sets that were especially based on *F. iinumae*, 85,663 probe sets based on discovery in an octoploid germplasm panel, and 5,648 speculative "codon-based" probe sets. The data included in Chapter I and II are outcomes from the first use of the Array. I am also a co-author on a RosBREED publication about strawberry phenotyping protocols (Mathey et al. 2013) and co-author on *F. iinumae* mitochondrial (Mahoney et al. 2009) and chloroplast (Davis et al. 2009) publications.

CHAPTER I

A HIGH DENSITY LINKAGE MAP OF THE ANCESTRAL DIPLOID STRAWBERRY, *F. IINUMAE*, USING SNP MARKERS FROM THE ISTRAW90 ARRAY AND GBS

Abstract

An ancestral form of diploid *Fragaria iinumae* is recognized as a subgenome donor to the octoploid strawberry species, including the cultivated strawberry, *Fragaria ×ananassa*. Here I report the construction of the first high density linkage maps of *F. iinumae*. These maps will serve as the basis for comparisons of genome structure among *Fragaria* species, for analyzing trait variation in *F. iinumae*, and for anchoring the assembly of an *F. iinumae* reference genome sequence. The segregation data sets used for construction of the linkage maps were generated by genotyping an F2 population derived from a cross between two divergent *F. iinumae* accessions that were collected from the wild in Japan. SNP (single nucleotide polymorphism) genotyping was based on two high-throughput platforms, the newly released Affymetrix IStraw90® Strawberry SNP Array, and Genotyping-by-Sequencing (GBS). The maps are based on Array and/or GBS segregation data from two subsets of an F2 mapping population (F2D): the 21F2D map is based on Array and GBS data from 21 F2D progeny; while the 85F2D map is based on GBS data from 85 F2D progeny, including the 21 from the 21F2D subset. The mapped markers are well-distributed across the expected 7 linkage groups. The 21F2D map has a length of 486.7 cM, and has 4,110 (3,215 Array and 895 GBS) markers at 158 loci. The 85F2D map has a length of 447.3 cM, with 895 GBS markers at 217 loci.

Introduction

The octoploid (2*n* = 8*x* = 56) cultivated strawberry, *Fragaria* ×*ananassa*, and its immediate octoploid ancestors *F. chiloensis* and *F. virginiana* are recognized as having an allopolyploid genome composition (Rousseau-Gueutin et al. 2009, DiMeglio et al. 2014), which means that they have arisen from multiple diploid ancestors via processes of hybridization and chromosome number doubling (polyploidization). The most widely cited subgenome composition model for the octoploid genome is that of Bringhurst (1960). In this AAA'A'BBB'B' model (Bringhurst 1990), the letters A, A', B, and B' represent subgenomes, each of which is present in two copies within the overall octoploid genome. The A-type (A and A') subgenomes are considered to be highly differentiated from the B-type (B and B') subgenomes, while less differentiation exists between A and A', and between B and B'. Diploid *Fragaria vesca* is widely considered to be the source of an A-type genome (Senanayake et al. 1967, Potter et al. 2000, Folta et al. 2006). In the past decade, phylogenetic and other evidence has accumulated implicating an ancestral form of diploid (2*n* = 2*x* = 14), *F. iinumae,* as a second diploid progenitor and B-type subgenome contributor to the octoploid *Fragaria* species (Folta et al. 2006, Davis et al. 2009, Mahoney et al. 2009, Rousseau-Gueutin et al. 2009, Staudt 2009, Isobe et al. 2013, Njuguna et al. 2013, DiMeglio et al. 2014). At present, the *F. vesca* 'Hawaii4' (FvH4) reference assembly (Shulaev et al. 2011) is the only sequenced reference genome for strawberry. A goal of the Davis group is to assemble a reference genome for *F. iinumae*. The Davis research group is also engaged in developing germplasm resources for *F. iinumae*, including various *F. iinumae* hybrids. The assembly of plant reference genomes is reliant upon a process of "anchoring" assembled sequence scaffolds to a genetic linkage map. As a step toward

assembling the *F. iinumae* genome, a mapping population was developed, and the first genetic linkage maps of *F. iinumae* was constructed, as reported here.

The construction of a linkage map relies upon marker segregation data from an appropriate progeny population, such as the F2 generation of a cross between genetically distinct parents. A linkage map establishes the linear order of marker loci along each chromosome, and defines the recombination frequencies between markers, where recombination frequency (RF) is expressed in units of centi-Morgans (cM), and 1% RF = 1 cM. Thus, the lower the recombination frequency between markers, the shorter the map distance between markers. For anchoring the assembly of the published *F. vesca* FvH4 reference genome (Shulaev et al. 2011), a linkage map was employed that was based on an F2 mapping population derived from a cross of *F. vesca* '815' × *F. bucharica* '601' (FV×FB) (Sargent et al. 2011). The respective FV×FB F2 mapping population consisted of 76 seedlings, and was genotyped with Single Sequence Repeat (SSR) markers (Sargent et al. 2011). The SSR marker segregation data were used to construct a genetic linkage map of seven linkage groups (LGs). The FV×FB map has a length of 444.8 cM, with 411 markers distributed over the seven linkage groups, corresponding to the seven chromosomes in the basic ($x = 7$) diploid strawberry genome.

Fragaria iinumae is distributed in the Russian Far East (Sakhalin) and in Japan (Staudt 2005, Hummer et al. 2006, Iketani et al. 2010). During a collection trip in 2004 to Hokkaido, Japan, among numerous accessions collected (Hummer et al. 2006, Davis et al. 2009), Tom Davis and Kim Hummer collected two *F. iinumae* accessions, J17 and J4, which are now maintained by the National Clonal Germplasm Repository (NCGR) in Corvallis, Oregon, under the accession numbers FRA1855 (PI637969) and FRA1849 (PI637963), respectively (Figure 1.1). These two accessions were crossed by Davis to generate an F1 hybrid (F1D), which was

then allowed to self-pollinate to generate an F2 generation mapping population referred to as the F2D population (Figure 1.2). This population is maintained at the UNH McFarlane greenhouses and the Woodman Farm (Figure 1.3). The F2D population was expected to segregate with respect to numerous molecular markers based on a previous genetic diversity study that included J4 and J17 (Njuguna et al. 2011). The F2D population provides a necessary resource for linkage analysis and construction of the first high density linkage map for *F. iinumae*.

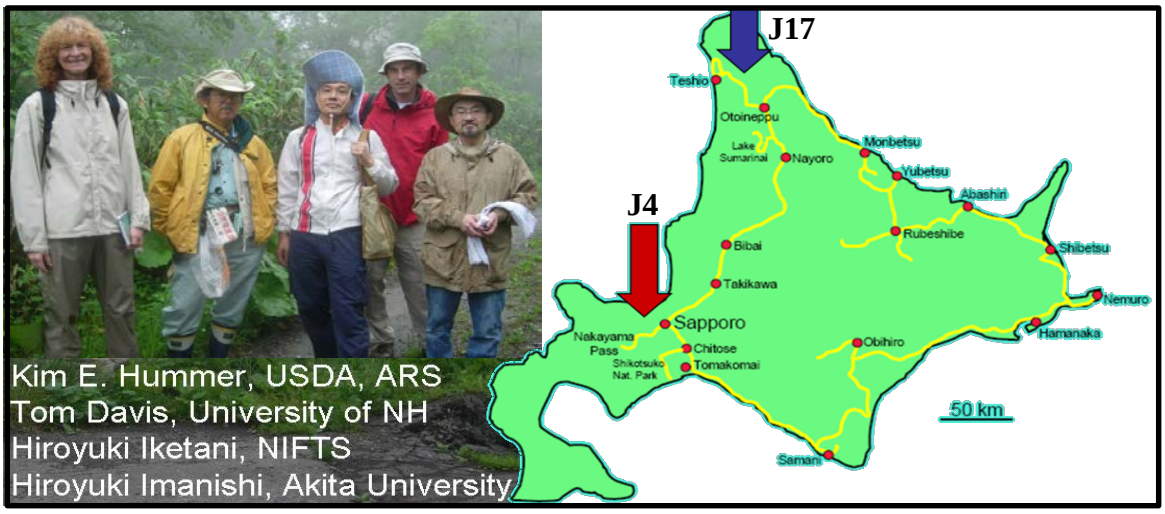


Figure 1.1: Hokkaido, Japan – 2004 fruit germplasm expedition team and collection route. The collection route is traced with a yellow line on the map. Arrows indicate collection sites for the J17 and J4 accessions used for development of the mapping population.

The segregating genetic markers for linkage map construction were obtained by employing two molecular marker methodologies: array based SNP genotyping and GBS. While both the Array and GBS approaches generate information in the form of SNP genotype calls, the two approaches utilize very different mechanisms to generate these calls. The principles and practical aspects of these two approaches are briefly reviewed below.

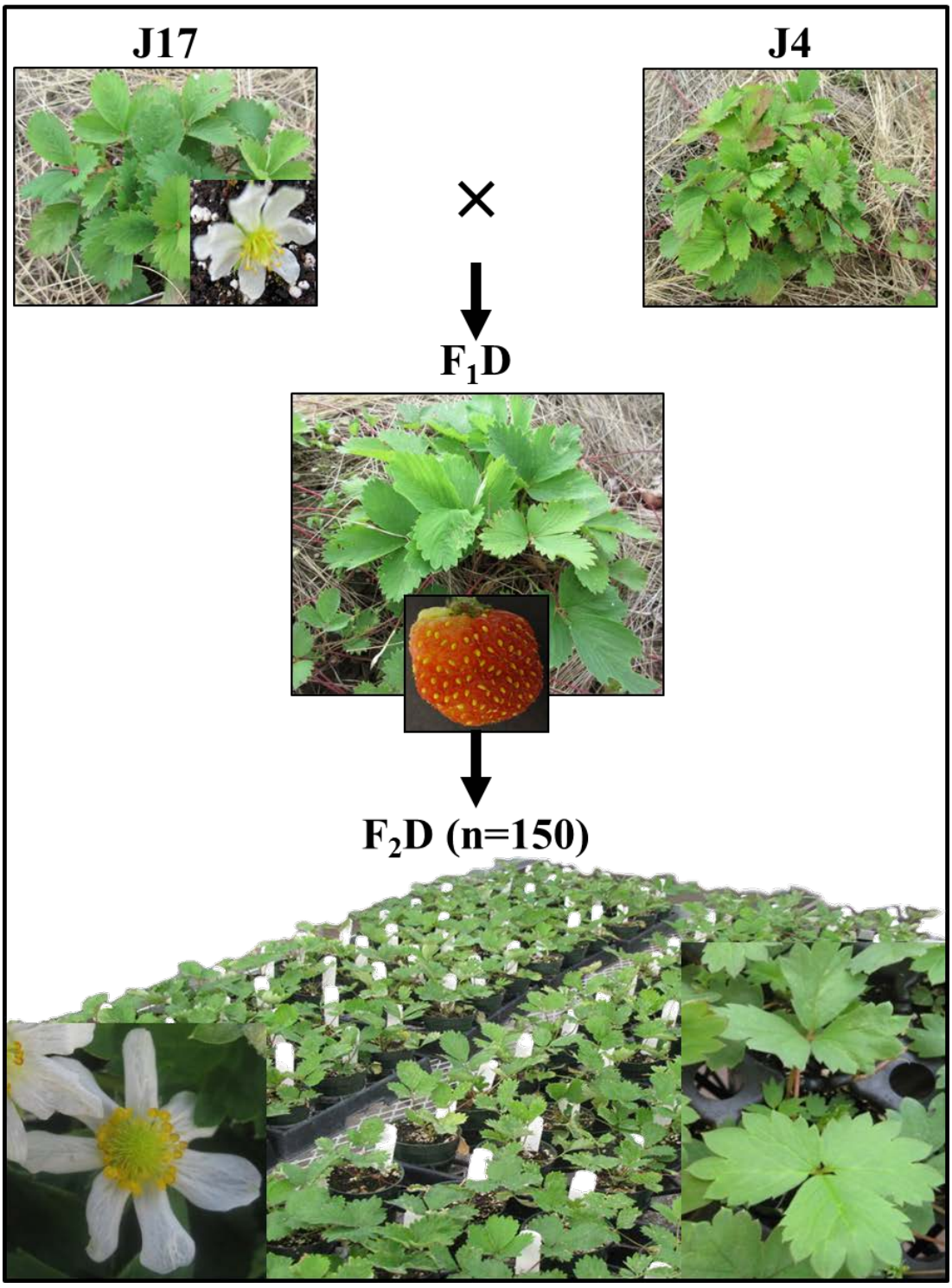


Figure 1.2: *F. iinumae* mapping population. The F2 mapping population derived from F1D, an F1 hybrid derived from a cross of J17 × J4. A subset of the population was genotyped for linkage map construction.

Figure 1.3: *F. iinumae* mapping population maintenance. As pictured from top to bottom, plants were grown at the UNH Horticultural Woodman Farm in matted rows mulched with saltmarsh hay, or in plasticulture, and at the UNH MacFarlane Greenhouses in 6" pots.

Array-based SNP genotyping

A SNP genotyping array is a kind of microarray (Gresham et al. 2006), in which tens or hundreds of thousands of short DNA molecules, which serve as probes or primers, are anchored to a surface within a small (5.5 mm in diameter) chamber (Figure 1.4). The chambers are arranged on a grid that mirrors the structure and dimensions of a 96 or 384 well microtiter plate, thus 96 or 384 genomic DNA samples can be processed at one time. Fragmented genomic DNA from each individual of interest is introduced into its own chamber, followed by instrumentally controlled annealing processes that result in the generation of fluorescent signals at the sites where genomic fragments have annealed to complementary probes. The colors and intensities of the fluorescent signals are then digitally recorded. The fidelity of the annealing process is so high that single nucleotide polymorphisms (i.e., SNPs) in otherwise identical DNA molecules can be differentiated, thereby allowing the genotype of the tested individual to be determined (or "called") at each of several thousand genetic loci.

The design of a genotyping array probes depends on prior discovery of SNP loci on the basis of sequence alignments and variant calling in comparison to a reference sequence. Conserved 24 to 33 bp of sequence on either the 5' or the 3' end of the SNP are needed for the design of primers, which are anchored onto the array, and are designed to complement the genomic sequences of interest (Figure 1.4). Generally two colors of 'hapten' labeled solution probes are utilized to pair to a specific base for detection of SNPs; one color for G or C and second color for A or T bases. As such, the detection process cannot differentiate A from T or C from G; therefore G/C and A/T SNPs are generally excluded in the array design process.

In a diploid species, true SNPs are di-allelic (i.e., no more than two alleles of a marker can exist in an individual), and their detection on the array results in clear genotyping cluster

plots which display and differentiate the genotypic classes in the studied population (Figure 1.5). Tri-allelic and tetra-allelic levels of polymorphism can occur in polyploid species, where they add to the complexity of genotype calling (Bassil et al. manuscript submitted); however, the occurrence of polyploid-like cluster patterns in a diploid species (Figure 1.5) are indicative of a problem with the marker, such as paralogy (occurrence of the marker locus in more than one genomic site), or of incorrect reference sequence assembly.

As part of the USDA Specialty Crop Research Initiative RosBREED project (http://www.rosbreed.org), a strawberry 'IStraw90' Array was designed, built and evaluated on an Affymetrix® Axiom platform (Bassil et al. manuscript submitted)**.** I made significant contributions to this project and am a co-author of the submitted paper (Bassil et al. manuscript submitted). The design of the IStraw90 Array was based primarily on prior SNP discovery in an octoploid germplasm panel. The SNP discovery process relied primarily on separate sequence alignments and variant calling for the octoploid panel members in comparison to the FvH4 reference sequence. However, SNP discovery was also performed on the *F. iinumae* hybrid F1D, and 3,751 of these "F1Dsnp" markers were incorporated into the Array. Thus, to the benefit of this project, the Array could be used to genotype the members of the *F. iinumae* F2D mapping population. A speculative, non-discovery-based "codon based" approach was also explored (Bassil et al. manuscript submitted).

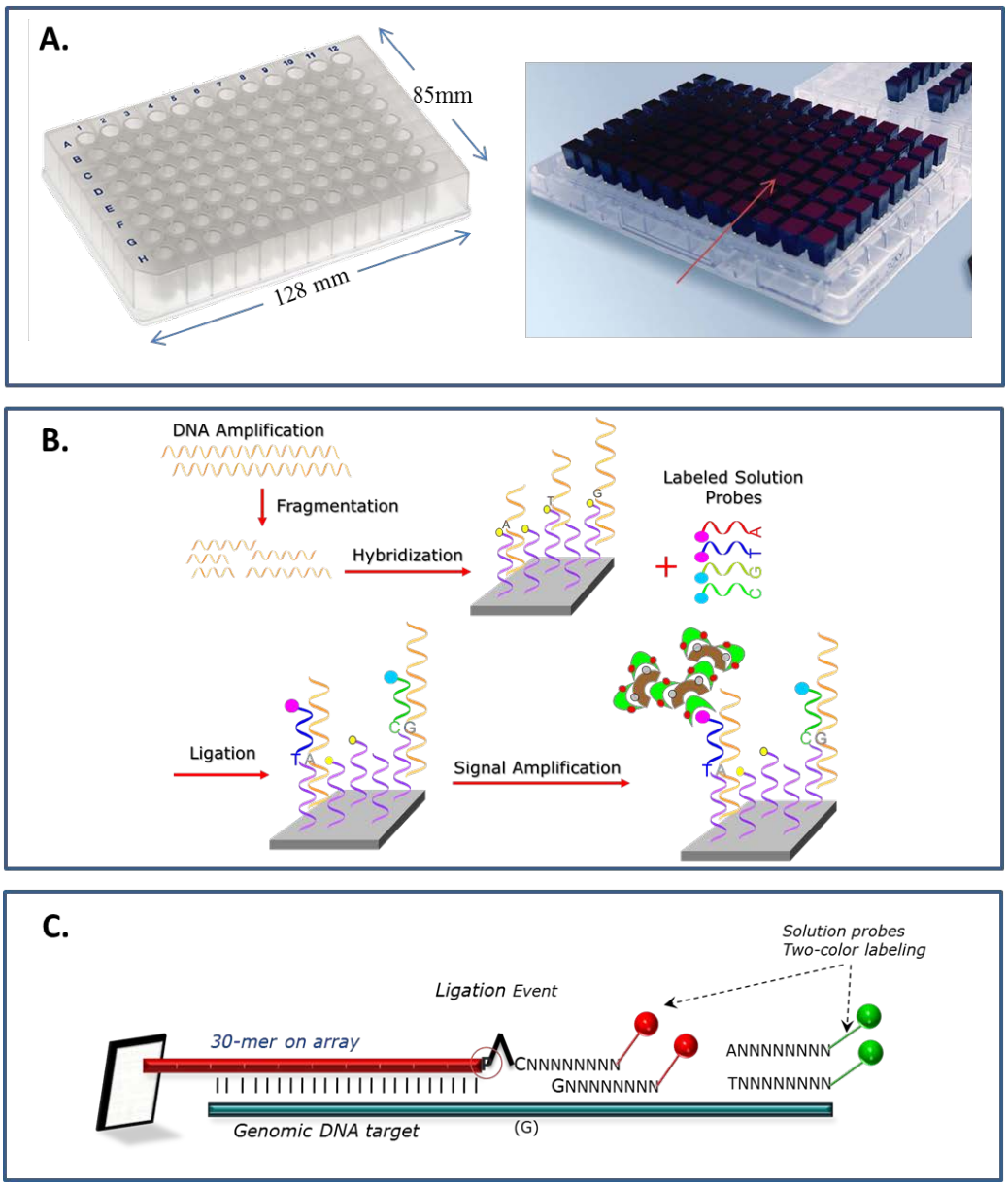
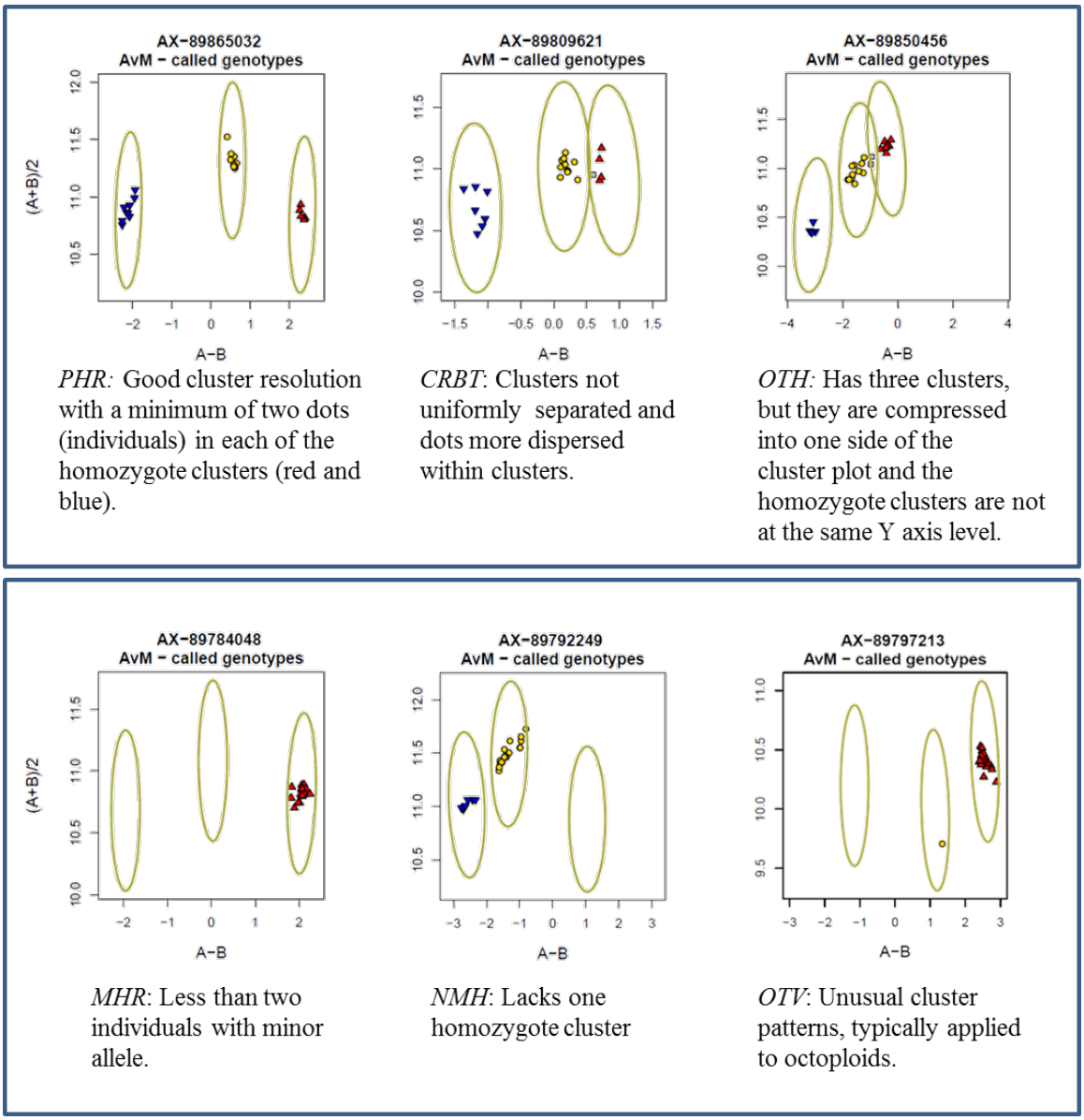


Figure 1.4: Affymetrix Axiom® Array process and genotyping. A. The sample plate (left) holds fragmented genomic DNA samples from 96 individuals. Each sample is loaded into its own array chamber on the Array plate (right). **B.** Within each array chamber, genomic DNA fragments anneal to complementary probes that are anchored to the array. **C.** Allele-specific ligation event result in an allele-specific fluorescent signal.



PHR: Good cluster resolution with a minimum of two dots (individuals) in each of the homozygote clusters (red and blue).

CRBT: Clusters not uniformly separated and dots more dispersed within clusters.

OTH: Has three clusters, but they are compressed into one side of the cluster plot and the homozygote clusters are not at the same Y axis level.

MHR: Less than two individuals with minor allele.

NMH: Lacks one homozygote cluster

OTV: Unusual cluster patterns, typically applied to octoploids.

Figure 1.5: Examples of cluster diagrams with different cluster quality classes. Within each diagram, each colored dot corresponds to an individual, and the dot location is indicative of a SNP genotype. Based upon the dot locations and cluster resolutions, the Affymetrix GTC and SNPolisher software programs "calls" the genotype of each individual, and assigns a dot color corresponding to that genotype. The *PHR* class is the highest quality class, because it discerns and clearly distinguishes among the three expected genotypic classes: homozygous AA (red dots), heterozygous AB (yellow dots), and homozygous BB (blue dots).

Unlike the SNP arrays recently published for other Roseaceae crops; apple (Chagne et al. 2012), peach (Verde et al. 2012), and cherry (Peace et al. 2012), which contain up to 9,000 SNPs on an Illumina ® Infinium ® genotyping platform, the strawberry Array comprises over 90K (90,000) SNPs on an Affymetrix Axiom platform (Bassil et al. manuscript submitted).

Genotyping-by-sequencing (GBS)

GBS is a non-discovery based approach for reduced representation of the genome. GBS relies on selected restriction endonuclease enzymes for fragmenting, followed by ligation of linker molecules to the cut ends of the genomic DNA fragments, and PCR amplification and size selection processes that result in a reproducible subset of genomic DNA fragments, thereby achieving reduced genomic representation. The reduced representation fragment pool is then subjected to high throughput sequencing. The GBS methodology has been successfully applied to wheat, barley, and switchgrass (Poland et al. 2012, Lu et al. 2013). One enzyme approaches using *ApeK*I have been successful (Elshire et al. 2011), and seem most appropriate for small genomes. A GBS approach with two methylation sensitive enzymes *Msp*I and *Pst*I has been utilized to enhance representation of genic regions and minimize the representation of repetitive regions, and to enhance the read depth as outlined by (Poland et al. 2012). An additional increment of complexity reduction is achieved with the two enzymes as compared with the one enzyme approach, which translates to increased read depth for the remaining represented segments of the genome. Thus, the two-enzyme approach is well suited to large genomes, including those of polyploid plants.

Array and GBS comparison

The design of a SNP array is based on prior SNP discovery, and provides genotype calls only for the SNP loci that have been programmed onto the array. In contrast GBS requires no prior discovery, and in fact results in the de novo discovery of the very SNP loci that are genotyped. Both platforms utilize sequence data, but in different ways. An array utilizes sequence data for SNP discovery and probe design, while producing data in the form of cluster plots (Figure 1.5) and genotyping calls. In contrast, GBS produces new sequence data for each of the genomic samples, and these sequences must then be aligned to each other and/or to a reference sequence to discover the SNP loci, if present, and to generate their respective genotyping calls. An array is limited to genotyping of SNPs discovered within the discovery germplasm panel, when compared to sequence provided in a reference genome. GBS requires no prior discovery and is not thus constrained.

Both the Array and GBS (when using methylation sensitive enzymes) were intended to survey genes and avoid repetitive regions. It was expected that the two platforms would sample similar portions of the *F. iinumae* genome, but that GBS would also sample regions not evident or present in the *F. vesca* FvH4 reference genome sequence and therefore not discoverable in the Array SNP discovery process. Thus, the genotyping platforms were selected to complement each other to provide comprehensive coverage of the gene-rich regions of the genome.

Materials and Methods

Plant material

The plant material consisted of *F. iinumae* accessions J17, J4, F1D (an F1 derived from a cross between J17 and J4), and subsets of an F2 mapping population (F2D) of 150 siblings derived from a self-pollination of F1D (Figure 1.2). The population and parents were maintained in pots at the UNH McFarlane greenhouses and in matted rows at the UNH Woodman Farm (Figure 1.3). Of the 150 F2Ds, 88 were genotyped by GBS, of which 21 were also genotyped on the Array.

DNA isolation

Young, furled leaf tissue was collected into 1.5 ml microfuge tubes on ice, and stored frozen at -80C. The tissue was lyophilized to minimize degradation during the isolation process. Just prior to freeze drying, leaf samples were taken out of the -80^{o}C freezer, the caps were quickly opened and the tissue was pre-conditioned at -20^{o}C for 1 to 2 hours. The samples were then freeze dried (Labconco, Kansas City, MO) under vacuum at 0.20 to 0.25 mbars with a condenser temperature of -60^{o}C to -80^{o}C for 48 hours and without the use of a heat plate. Immediately upon completion of freeze drying, the microfuge tubes were quickly closed and the lyophilized tissue was stored at -80^{o}C until ready for the DNA isolation. For the Array, the lyophilized leaf tissue was shipped to Nahla Bassil and the DNA was isolated by her group. The DNA for both genotyping platforms was isolated using the E-Z® 96 Plant DNA kit (Omega bio-tek, Inc) following (Gilmore et al. 2011), with modifications. Here described in detail, is the procedure executed at UNH. In preparation for the DNA isolation, the lyophilized leaf tissue

was pulverized. A 10-15 mg weight of each lyophilized sample was placed into a individual cluster tubes (Corning 4413/4418) containing a 3 mm tungsten carbide bead, capped and the tube rack was floated on liquid nitrogen briefly (until the nitrogen bubbling calmed). The tube rack was then secured in the Mixer Mill MM100 (Retsch GmbH) for three sessions of 30 second pulverizing at frequency of 30 cycles/sec with intermediate cooling with liquid nitrogen. The pulverized leaf tissue was equilibrated to -20^{o}C in preparation for isolation using the E-Z® 96 Plant DNA kit, including the use of Proteinase K as required by Affymetrix.

The DNA for the Array was quantified with Quant-IT™ PicoGreen® dsDNA at 485nm/535nm for 1.0 second using a Tecan infinite® 200 (Tecan Austria GmbH) microplate reader. The DNA for GBS was quantified with Qubit™ fluoremeter (Invitrogen Corp) and as an indication of the DNA quality, the absorbance ratios of 260/280 and 260/230 were determined on a NanoDrop ND-1000 (NanoDrop Technologies, USA). Aliquots of 2 µl of a random selection of the DNA samples were run on 1.0% standard agarose gel electrophoresis to access the integrity of the DNA (lack of degradation). For the Array, a minimum of 750 ng of DNA was provided, the DNA samples were diluted with TE (10 mM Tri-HCl, 0.1 mM Na2-EDTA) to a 15ηg/µl concentration. For GBS, a DNA quantity of 1 µg was provided in sample concentrations ranging from 28 to122 ηg/µl.

SNP discovery

Genomic DNA from F1D was sequenced at the University of Illinois on one lane of Illumina HiSeq 2000 100 x 100 bp paired end reads (300 bp fragment size) from which 17,518 SNPs were discovered using an internally developed bioinformatics pipeline, and 3,751 of these SNPs were incorporated into the Array (Bassil et al. manuscript submitted).

Genotyping Array marker data

The Array data set was generated on the IStraw90 Array designed by the RosBREED *Fragaria* SNP consortium (Bassil et al. manuscript submitted). The Array includes 3,751 SNPs based on discovery in the F1D genomic sequence (F1Dsnps), 85,663 SNPs based on an octoploid strawberry discovery panel (octoploid-based SNPs), and 5,648 codon-based SNPs. The octoploid-based SNPs are further subdivided by discovery categories (Bassil et al. manuscript submitted), as described in Table 1.1. The two founding parents J17 and J4, the F1D parent, and 21 of the F2 population chosen at random were genotyped on the Array.

Table 1.1: Counts of IStraw90 Array SNPs by category. The primary categories are the *F. iinumae* diploid-based F1Dsnps, octoploid-based, and codon-based SNPs.

Marker name	Count	Description
F1Dsnp	**3,751**	Discovered in F1D
Octoploid-based		
Snp	63,263	SNP with two alternate alleles
mSnp	1,761	SNP with four alternate alleles
ins	4,615	An insertion
del	4,913	A deletion
SnpSnp	7,092	Subgenome-specific SNP adjacent to a marker SNP
indelSnp	1,176	Subgenome-specific indel adjacent to a SNP
SnpinIns	2,007	SNP inside a subgenome-specific insertion (insertion relative to *F. vesca* reference)
SnpinDel	836	SNP inside a subgenome-specific insertion (deletion relative to *F. vesca* reference)
Octoploid-based total	**85,663**	Discovered in octoploid germplasm panel
Codon-based	**5,648**	Non-discovery based SNP candidates
Array Total	**95,062**	All SNPs on the Array

Marker Type	Count	
Octoploid-based total	**85,663**	
F1Dsnp	**3,751**	
Codon-based	**5,648**	
Array Total	**95,062**	

GBS marker data

A two enzyme GBS approach as outlined by (Poland et al. 2012) was executed by the Hubbard Center for Genome Studies (HCGS). A two enzyme system with the use of

methylation sensitive enzymes *Msp*I and *Pst*I was chosen to enhance the read depth by reducing genomic representation, and to secure gene regions and minimize the representation of repetitive regions. A library preparation of the DNA from 95 genotypes and one negative control was sequenced on one lane of Illumina HiSeq 2500 100 x 100 bp paired end reads (300 bp fragment size) Single Flow Cell High Output Run Mode. The 95 genotypes included duplicates of J17, J4, and F1D, the 21 F2Ds plants genotyped on the SNP array, and an additional 68 F2D plants chosen at random.

Genotyping bioinformatics

The SNPs from the Array were genotyped using the Affymetrix Genotyping Console (GTC) and SNPolisher, with the standard default settings for diploid organisms. According to the Affymetrix rating system, the genotyped SNPs were classified into 6 cluster classes (Figure 1.5), of which the *Poly High Resolution* (*PHR*) class comprises the markers that meet the strictest quality criteria. The six cluster classes and their characteristics are as follows. 1) In the *PHR class,* cluster diagrams must contain highly distinct clusters, including both of the expected homozygous genotyping clusters. 2) The *Call Rate Below Threshold* (*CRBT*) class is exemplified by dispersed clustering and contains both of the expected homozygous genotyping clusters. 3) In the *Mono High Resolution* (*MHR*) class, there are less than two occurrences of the minor allele. 4) The *No Minor Homozygous* (*NMH*) class displays only two clusters and lacks one of the expected homozygous clusters. 5) The *Other* (*Oth*) class has distinct clusters but they are shifted off center and/or dispersed. 6) In the *Off-Target Variant* (*OTV*) class, the cluster plot displays indicative of aberrant annealing of probes. In addition, a seventh group of genotyping results for

mSNPs (designed to reduce complexity in the octoploid germplasm) were provided but these were not classified, and these are grouped as *Not Classified* (*NOCLS*).

Markers suitable for linkage mapping using an F2 population were required to display three clusters in a cluster diagram. These three clusters represent the three expected genotypic classes: homozygous (AA), heterozygous (AB), and homozygous (BB), where A and B represent the alternate alleles of the marker locus. For convenience in the management and analysis of the marker data spreadsheet, the genotype clusters AA, AB, and BB are designated as 0, 1, or 2 respectively in the Array data output, while -1 indicates missing data. Thus, the 0 and 2 genotypes represent homozygosity for the alternate alleles, while the 1 genotype represents a heterozygous genotype.

The SNPs from the GBS dataset were identified using two pipelines, the Tassel 3.0 UNEAK (UN) non-reference based pipeline found at http://www.maizegenetics.net, and the referenced-based DW pipeline developed in the Davis lab by graduate student David Wood (unpublished). Implementation of the latter pipeline required a preliminary assembly of F1D sequence (D. Wood, unpublished) to serve as the reference genome.

Selection of Array and GBS markers for mapping

Markers of potential use for mapping were required to be heterozygous in F1D, and concordant in the parental trio (F1D and its parents J17, J4). Concordance exists when no trio member displays a genotype that could not exist given the genotypes of the other two trio members. Additional criteria for selection of GBS markers suitable for mapping were: 1) consistent genotype calls for replicates of J17, J4, and F1D, allowing no missing data; and a minimum sequence alignment read depth of six at each SNP. At a mean read depth of 6x (number of reads/SNP/individual), the error calling rate is expected to be minimized (Lu et al.

2013). One lane of Illumina HiSeq 2500/1500 sequencing generally provides about 200,000,000 reads, which based on the genome and reduced representation for 95 of *F*. iinumae individuals (J4, J17, F1D, all in duplicate; and 88 F2Ds) was estimated to result in a read depth exceeding 6x per allele, and expected to provide sufficient allelic representation to enable confident genotyping.

For linkage analysis using the JoinMap4.1 program (Kyazma B.V.) the marker genotypes were coded for an 'F2 population', according to the founding parent genotypes as described in Table 1.2. When the maternal parent was 0 or 2, it was replaced with an 'a'. When the paternal parent was 0 or 2, it was replaced with a 'b'. When either parent was a 1, it was replaced with an 'h'. Missing data as indicated by '-1' was replaced with '-'. Where the founding parents were both heterozygous, the replacements were made in both coupling and repulsion phases. In addition, the GBS data were sorted by quantity of missing data in the progeny, and initially any marker with two or more missing genotypes in the progeny was excluded.

Table 1.2: Recoding of Array data for JoinMap. The replacement codes for F2D progeny genotypes are based on J17 and J4 parental genotypes, which occurred in the eight permutations indicated in the "Parents" column.

Parents (Array codes)			Code replacements for JoinMap				Parents (JoinMap codes)		
J17	J4	F1D	0	2	1	-1	J17	J4	F1D
0	2	1	a	b	h	-	a	b	h
1	2	1	a	b	h	-	h	b	h
0	1	1	a	b	h	-	a	h	h
2	0	1	b	a	h	-	a	b	h
1	0	1	b	a	h	-	h	b	h
2	1	1	b	a	h	-	a	h	h
1	1	1	a	b	h	-	h	h	h
1	1	1	b	a	h	-	h	h	h

The Array markers with identical segregation patterns were grouped into genotypic bins and given a unique hundred-series bin name. Then, the GBS markers were added to the Array marker bins or into GBS-specific bins, as they were grouped by segregation pattern during the mapping process.

Linkage map construction

Two linkage maps were constructed using JoinMap 4.1(Van Ooijen 2006) with the Maximum Likelihood algorithm and the Kosambi mapping function. A minimum LOD (logarithm odds score) of 3.0 to group was specified and default settings were in effect for the remaining parameters. The correct phase of markers with heterozygous parental genotypes was determined during the mapping process as correct if mapped and incorrect if unmapped.

Markers that caused excess fit-stress of greater than $\pm$ 1 cM were excluded. The construction of the linkage maps was completed iteratively. A linkage map was initially constructed with only Array data for the 21 F2Ds. The GBS data were later incorporated. Plants with excessive missing data were excluded for the map construction. The resulting linkage map, the 21F2D map, including both the Array and GBS datasets for the 21 F2Ds, provided a framework for developing a GBS map for the 85 F2Ds: the 85F2D map.

Following construction of the two *F. iinumae* maps, the correspondences between the *F. iinumae* linkages groups (LGs) and the *F. vesca* pseudomolecules (PCs) were examined, to define the chromosomal patterns of homology between *F. iinumae* and *F. vesca*. This was done by using DNA sequence information to determine the locations of the mapped Array and GBS marker sites (in *F. iinumae*) within the *F. vesca* PCs. Sets of markers located on the same chromosome in two species are said to be syntenic (chromosomes from two different species

having common markers considered to be homologous). The linkage groups (LGs) of the F2D maps were then renumbered to correspond to the PCs of FvH4 with which they had the most synteny; F2D LGs were renamed LG1 through LG7 to correspond to PC1 through PC7 of FvH4.

Results

Array genotyping

The results of genotyping of J4, J17, F1D and 21 F2D individuals are summarized in Tables 1 through 4. In summary, of the 95,062 SNP markers on the Array, the number of SNPs that fell into each of the six cluster classes were as follows: 3,380 *PHR*, 2,605 *CRBT*, 71,682 *MHR*; 900 *NMH*; 12,827 *Oth*, 1,907 *OTV*, and 1,761 *NOCLS* markers (Table 1.3). Of the critically important *PHR* class, which was expected to provide the majority of the markers amenable to mapping, 3,171 were F1Dsnps (i.e., discovered in *F. iinumae* F1D), while 199 were octoploid-based (i.e., discovered in the octoploid germplasm discovery panel) SNPs, and 10 were codon-based SNPs (Table 1.3).

Selection of Array markers suitable for mapping

Although the Array provided genotype data for 95,062 SNP sites, only a minority of these SNPs sites was expected to be suitable candidates for map construction, and even fewer were expected to be successfully incorporated into the final linkage map. To be considered suitable for use in map construction, marker heterozygosity in F1D was required, because markers that were genotyped as homozygous in F1D would not be expected to segregate in the F2D population. Implementation of this criterion narrowed the marker candidate list to 13,245 (Table 1.4), in part by eliminating the entire *MHR* cluster class of 71,682 Array SNPs (Table 1.3), as would be expected because by definition the *MHR* markers are not heterozygous in any

population member, including F1D. Some markers from other categories were also eliminated by the F1D heterozygosity requirement.

Additionally, genotypic concordance with no missing data was required among the parental trio members (J17, J4, F1D): on this basis, 1,103 markers were eliminated (Table 1.5). Among the remaining 12,142 marker candidates, all of which exhibited heterozygosity in F1D and trio concordance, J17 and J4 did not share the same homozygous genotype with respect to 3,068 F1Dsnps, 554 octoploid-based, and 55 codon-based SNPs, while both J17 and J4 were called as heterozygous for 238 F1Dsnps, 7,264 octoploid and 963 codon SNPs (Table 1.5). The final list of F1Dsnps deemed suitable for map construction totaled 3,306, of which 3,022 were *PHR* class markers (Table 1.6a). In contrast, the final list of octoploid-based SNPs selected for map construction totaled 7,818, out of which only 168 were *PHR* markers (Table 1.6b). Finally, 1,011 codon-based SNP candidates were deemed suitable for mapping, of which only 7 were classified as *PHR* (Table 1.6c).

Table 1.3: Summary of Array genotyping results for all SNPs. The columns are subdivided for the SNPs types for the F1Dsnps, and the octoploid-based and codon-based SNPs.

SNPs genotyped	Number of SNPs in SNP category											SNPS on Array
	F1Dsnps	Octoploid based SNPs									Codon-	
SNP Class	total	snp	mSnps	Ins	Del	SnpSnp	IndelSnp	SnpinIn	SnpinDel	Total	based	
Poly High Resolution (PHR)	**3,171**	158	-	10	11	14	-	6	-	**199**	**10**	**3,380**
Call Rate Below Threshold (CRBT)	64	1,406	-	185	172	401	61	99	28	2,352	189	**2,605**
MonoHighResolution (MHR)	199	54,629	-	3,051	3,626	3,964	671	1,316	581	67,838	3,645	**71,682**
NoMinorHom (NMH)	36	518	-	72	62	112	14	34	11	823	41	**900**
Other (Oth)	274	5,417	-	1,165	910	2,379	396	501	198	10,966	1,587	**12,827**
Off-Target Variance (OTV)	7	1,135	-	132	132	222	34	51	18	1,724	176	**1,907**
Not Classified (NOCLS)	-	-	1,761	-	-	-	-	-	-	1,761	-	**1,761**
Total Markers	**3,751**	**63,263**	**1,761**	**4,615**	**4,913**	**7,092**	**1,176**	**2,007**	**836**	**85,663**	**5,648**	**95,062**

Table 1.4: Distribution of Array markers in F1D.

F1D genotype	F1Dsnps	Octoploid	Codon	Total
-1	14	1,141	179	1,334
0	236	30,253	3,164	33,653
2	23	45,632	1,175	46,830
1	3,478	8,637	1,130	13,245
Total	3,751	85,663	5,648	95,062

Table 1.5: Evaluation of markers suitable for mapping by genotypes of parents. The criteria that determined the suitability of markers for mapping are indicated in the column 'Marker disposition for mapping'. The groups are sorted by genotype of F1D (homozygosity, heterozygosity, missing data) and by trio concordance.

Marker disposition for mapping	F1D genotype	F1Dsnps	Octoploid-based	Codon-based	Total
Not heterozygous in F1D (= homozygous)					
Segregation not possible: Homozygous J17 = J4 = F1D = 0	**0**	221	29,515	3,058	32,794
Segregation not possible: Homozygous J17 = J4 = F1D = 2	**2**	15	44,148	1,083	45,246
Segregation not possible, from cross aa x ab	**0**	7	512	66	585
Segregation not possible, from cross ab x bb	**2**	2	851	46	899
Lack of concordance and segregation not possible	**0**	1	17	5	23
Lack of concordance and segregation not possible	**2**	1	18	1	20
Missing Data in J4 or J17 or both	**0**	7	209	35	251
Missing Data in J4 or J17 or both	**2**	5	615	45	665
Subtotal F1D not heterozygous	**0 or 2**	**259**	**75,885**	**4,339**	**80,483**
Missing Data in F1D and possibly J4 and J17	**-1**	**14**	**1,141**	**179**	**1,334**
Missing Data in J4 or J17 or both	**1**	**21**	**661**	**93**	**775**
Lack of concordance	**1**	**151**	**158**	**19**	**328**
Heterozygous in F1D and concordant					
Concordance, segregation possible, J17 = J4 = F1D = 1	**1**	238	7,264	963	8,465
Concordance, F1D heterozygous and segregation likely	**1**	3,068	554	55	3,677
Subtotal F1D heterozygous and concordant	**1**	**3,306**	**7,818**	**1,018**	**12,142**
Grand-total		**3,751**	**85,663**	**5,648**	**95,062**

Table 1.6: Distribution by cluster class and parental genotypes of SNPs considered suitable for mapping and of SNPs actually mapped. The SNPs considered suitable are heterozygous in F1D and concordant with J17 and J4.

6a. Distribution of F1Dsnps.

F1Dsnps suitable for mapping	**J17:**	0	2	1	1	0	2	J17 ≠ J4 and	J17 ≠ J4	J17 ≠ J4	Total	Total	Grand total
genotyped by class -	**J4:**	2	0	0	2	1	1	homozygous	J17 = 1, J4 = 0, 2	J4 = 1, J17 = 0,2	J17 ≠ J4	J17 = J4 = F1D = 1	
Poly High Resolution (PHR)		**1,084**	**1,067**	**44**	**62**	**363**	**384**	**2,151**	**106**	**747**	3,004	**18**	**3,022**
Call Rate Below Threshold (CRBT)		5	8	-	-	4	3	13	-	7	20	6	26
MonoHighResolution (MHR)		-	-	-	-	-	-	-	-	-	-	-	-
NoMinorHom (NMH)		-	-	13	5	6	2	-	18	8	26	3	29
Other (Oth)		7	4	1	1	4	1	11	2	5	18	211	229
OTV		-	-	-	-	-	-	-	-	-	-	-	-
Not Classified (NOCLS).		-	-	-	-	-	-	-	-	-	-	-	-
Total Markers		1,096	1,079	58	68	377	390	2,175	126	767	3,068	**238**	**3,306**
Mapped F1Dsnps													
Poly High Resolution (PHR)		**1,083**	**1,066**	**40**	**55**	**363**	**383**	**2,149**	**95**	**746**	2,990	18	**3,008**
Call Rate Below Threshold (CRBT)		5	5	-	-	3	1	10	-	4	14	-	14
MonoHighResolution (MHR)		-	-	-	-	-	-	-	-	-	-	-	-
NoMinorHom (NMH)		-	-	-	-	-	-	-	-	-	-	-	-
Other (Oth)		3	4	-	-	1	1	7	-	2	9	-	9
OTV		-	-	-	-	-	-	-	-	-	-	-	-
Not Classified (NOCLS).		-	-	-	-	-	-	-	-	-	-	-	-
Total Mapped Markers		1,091	1,075	40	55	367	385	2,166	95	752	3,013	18	3,031

6b. Distribution of the octoploid-based SNPs.

Octoploid SNPs suitable for mapping/	**J17:**	0	2	1	1	0	2	J17 ≠ J4 and homozygous	J17 = 1, J4 = 0,2	J4 = 1, J17 = 0,2	Total	Total	Grand total
genotyped by class -	**J4:**	2	0	0	2	1	1				J17 ≠ J4	J17 = J4 = F1D = 1	
Poly High Resolution (PHR)		**67**	**47**	**2**	**2**	**23**	**25**	**114**	**4**	**48**	166	**2**	**168**
Call Rate Below Threshold (CRBT)		1	4	3	6	6	16	5	9	22	36	69	105
MonoHighResolution (MHR)		-	-	-	-	-	-	-	-	-	-	-	-
NoMinorHom (NMH)		-	-	11	20	10	26	-	31	36	67	67	134
Other (Oth)		3	8	11	59	48	83	11	70	131	212	6,310	6,522
OTV		-	1	23	21	5	9	1	44	14	59	245	304
Not Classified (NOCLS).		1	3	2	-	3	5	4	2	8	14	571	585
Total Markers		72	63	52	108	95	164	135	160	259	554	**7,264**	**7,818**
Mapped octoploid SNPs/													
Poly High Resolution (PHR)		**66**	**46**	**2**	**2**	**23**	**25**	**112**	**4**	**48**	164	2	**166**
Call Rate Below Threshold (CRBT)		-	-	-	-	-	-	-	-	-	-	-	-
MonoHighResolution (MHR)		-	-	-	-	-	-	-	-	-	-	-	-
NoMinorHom (NMH)		-	-	-	-	-	-	-	-	-	-	-	-
Other (Oth)		2	2	1	1	1	-	4	2	1	7	-	7
OTV		-	-	-	-	-	-	-	-	-	-	-	-
Not Classified (NOCLS).		1	2	-	-	1	-	3	-	1	4	-	4
Total Mapped Markers		69	50	3	3	25	25	119	6	50	175	2	177

6c. Distribution of codon-based SNPS. The only codon-based SNPs that mapped are PHR.

Codon-based SNPs suitable for mapping	**J17:**	0	2	1	1	0	2	J17 ≠ J4 and homozygous	J17 = 1, J4 = 0,2	J4 = 1, J17 = 0,2	Total	Total	Grand total
genotyped by class -	**J4:**	2	0	0	2	1	1				J17 ≠ J4	J17 = J4 = F1D = 1	
Poly High Resolution (PHR)		**2**	**4**	**-**	**-**	**1**	**-**	**6**	**-**	**1**	7	**-**	**7**
Call Rate Below Threshold (CRBT)		1	-	-	-	2	2	1	-	4	5	2	7
MonoHighResolution (MHR)		-	-	-	-	-	-	-	-	-	-		-
NoMinorHom (NMH)		-	-	2	3	1	1	-	5	2	7	1	8
Other (Oth)		-	-	3	3	15	4	-	6	19	25	946	971
OTV		-	-	8	1	-	2	-	9	2	11	14	25
Not Classified (NOCLS).								-	-	-	-		-
Total Markers		1	-	13	7	18	9	1	20	27	48	**963**	**1,011**
Mapped codon SNPs													
Poly High Resolution (PHR)		**2**	**4**	**-**	**-**	**1**	**-**	**6**	**-**	**1**	7	-	**7**

GBS results

A potential count of 5,281 SNPs resulted from the UN pipeline. The DW approach resulted in 2,213 candidate SNPs. After filtering the datasets for missing data, non-concordance, and homozygosity for F1D, the UN pipeline provided 579 SNPs, while the DW pipeline resulted in 690 SNPs suitable for mapping. Three of the 88 F2Ds were excluded from the mapping dataset, due to a large amount of missing data; therefore the 85F2D map was based on 85 of the 88 F2Ds.

Map construction

When the SNPs deemed suitable for mapping were entered into the map construction process using JoinMap (Van Ooijen 2006), variable percentages of the markers of different categories and classes were successfully incorporated into linkage maps, as summarized in Table 1.6. The criteria for successful marker incorporation were: 1) incorporation into one of the seven expected linkage groups, with a LOD score of 3 or better; and 2) linkage group incorporation without artifactually lengthening of the map. With regard to the latter, artifactual lengthening can occur when the placement of a marker at its most highly probable position within the map implies the presence of highly localized double recombinants (sometimes called "singletons"), which are generally regarded as indicators of genotype misclassification (van Os et al. 2006). In such cases, the marker can be tentatively discarded from the data set, or the offending genotype calls can be changed to "missing data".

Array markers - Of the 3,306 F1Dsnps deemed suitable for mapping, 3,031 were successfully mapped, of which 3,008 were *PHR* F1Dsnps (Table 1.6b). Of the 298 F1Dsnps that could not be placed in the 21F2D map, 14 were *PHR* class markers that caused the map to

artifactually lengthen, while the remaining 284 unmapped markers were not *PHR* class markers, and either caused the map to lengthen or did not show any linkage. Of the 7,818 octoploid-based SNPs rated as suitable for mapping, only 177 including 166 *PHR* class markers could be placed on the 21F2D map. The final list of codon based SNPS suitable for mapping totaled 1,011, of which only 7 (all *PHR*) could be mapped (Table 1.6c).

The 21F2D map contains 3,215 Array SNPs (Table 1.7), of which 3,181 were *PHR* class including 3,008 F1Dsnps, 166 octoploid SNPs, and 7 codon-based SNPs. The 34 mapped, non-*PHR* SNPs included 14 *CRBT* F1Dsnps, 16 *Oth* (9 F1Dsnps, and 7 octoploid-based SNPs), and the remaining four *NOCLS* (mSNPs). The numbers of SNP markers mapped relative to the total number of markers of each category on the Array were tabulated (Table 1.7). The category with the highest proportion of mapped markers was the diploid F1Dsnps with 80.8%, while of the octoploid classes, the percentage mapped markers were low and ranged from 0.12% to 0.23% (Table 1.7). Overall, including all Array markers, the mapped SNPs were 98.9% *PHR* quality (Table 1.7), as expected for the highest quality genotyping cluster classification as illustrated in Figure 1.5.

GBS markers - The GBS sequence dataset analyzed by the two bioinformatics pipelines, a Tassel non-reference based UNEAK (UN) pipeline and a F1D *F. iinumae* reference-guided, internally developed pipeline (DW), resulted in 895 mapped markers distributed across the linkage groups in both linkage maps (Table 1.9). The mapped markers include 300 unique markers for the UN and 399 for the DW pipelines, and a total of 195 markers in common between the UN and DW pipelines. Of the 895 GBS markers, 21 were found to be identical to Array markers (Table 1.9). The 895 GBS markers that could be mapped in 21F2D were used to make the 85F2D map.

Table 1.7: Comparison of genotyped and mapped SNPs by cluster class and discovery group. The mapped percentage by class is the total number mapped divided by the total number genotyped for each class.

Array class	Genotyped SNPs				Mapped SNPs				Mapped % by class
	F1Dsnps	Octoploid-based	Codon-based	Total	F1Dsnps	Octoploid-based	Codon-based	Total	
Poly High Resolution (PHR)	3,171	199	10	3,380	3,008	166	7	3,181	94.1%
Call Rate Below Threshold (CRBT)	64	2,352	189	2,605	14	-	-	14	0.5%
MonoHighResolution (MHR)	199	67,838	3,645	71,682	-	-	-	-	0.0%
NoMinorHom (NMH)	36	823	41	900	-	-	-	-	0.0%
Other (Oth)	274	10,966	1,587	12,827	9	7	-	16	0.1%
Off Target Varaint (OTV)	7	1,724	176	1,907	-	-	-	-	0.0%
Not Classified (NOCLS)	-	1,761	-	1,761	-	4	-	4	0.2%
Total Markers	**3,751**	**85,663**	**5,648**	**95,062**	**3,031**	**177**	**7**	**3,215**	3.4%

Linkage maps

The additional 895 GBS markers were added to the mapped Array markers for a total of 4,110 markers on the 21F2D map (Figure 1.6, Table 1.9 and Table A). In addition, the 895 GBS markers were used to construct the 85F2D map, which is based upon 85 F2D individuals and does not include any Array markers. The 21F2D and the 85F2D maps (Figure 1.6) contain 158 (Table 1.9 and Table B) and 217 (Table 1.9 and Table C) genotypic bins with map lengths of 486.7 and 447.3 cM, respectively. The number of markers per genotype bin was consistent across the linkage groups with an average of 26 for the 21F2D map and 4 for the 85F2D map (Table 1.9). A measure of map resolution is indicated by the recombination frequency; the lower the recombination frequency the higher the map resolution between any two loci. The minimum LOD on the 21F1D map was 1 for LG5. The additional genotypes in the 85F2D map resulted in greater resolution with the detection of additional recombination and increased the minimum LOD to 10 for each LG.

Representation of Array and GBS markers in the LGs – The mapped Array and GBS markers are uniformly distributed across the 7 LGs (Table 1.8). On the 21F1D linkage map (Figure 1.6), F1Dsnp-based SNPS are represented in 148 of the 158 loci. Of the remaining 10 loci, one locus includes only an octoploid-based marker and nine loci include only GBS markers. All of the loci in LG1 and LG7 are represented by F1Dsnp markers. All 19 loci of LG1 are represented by both F1Dsnp and GBS markers. LG2 has five loci represented by F1Dsnp markers, one locus represented by only GBS markers, and the remaining 15 loci are represented by both F1Dsnp markers and GBS markers. LG3 has seven loci represented by only F1Dsnps, four loci are represented by only GBS markers, while the remaining 19 loci are represented by both F1Dsnps and GBS markers. LG4 has two loci with only F1Dsnps, four loci with only GBS

markers, the remaining 11 loci are represented with both F1Dsnps and GBS markers. LG5 has five loci with only F1Dsnp markers, the remaining 18 loci are represented by both F1Dsnp and GBS markers. LG6 has six loci represented by only F1Dsnp markers, with 20 loci are represented by both F1Dsnp and GBS markers and one locus represented by an one octoploid-based del SNP, and this is the sole locus represented by only an octoploid-based SNP in all of the seven linkage groups. LG7 has 4 loci represented by F1Dsnps, and the remaining 17 loci are represented by both F1Dsnps and GBS markers.

Heterozygosity and segregation distortion - The founding parents, J4 and J17, were evaluated for heterozygosity in terms of the numbers and percentages of heterozygous markers. Among the SNPs deemed suitable for mapping, the 28.5% heterozygosity of J4 was more than three times that of 8.8% for J17, while among the SNPs that were actually incorporated into the maps, the relative level of heterozygosity of J4 is 25.6%, eight times higher than the 3.8% of J17 (Table 1.10). Overall there was little to no segregation distortion in the F2D map (Table 1.11, Figure 1.7 and Figure 1.8).

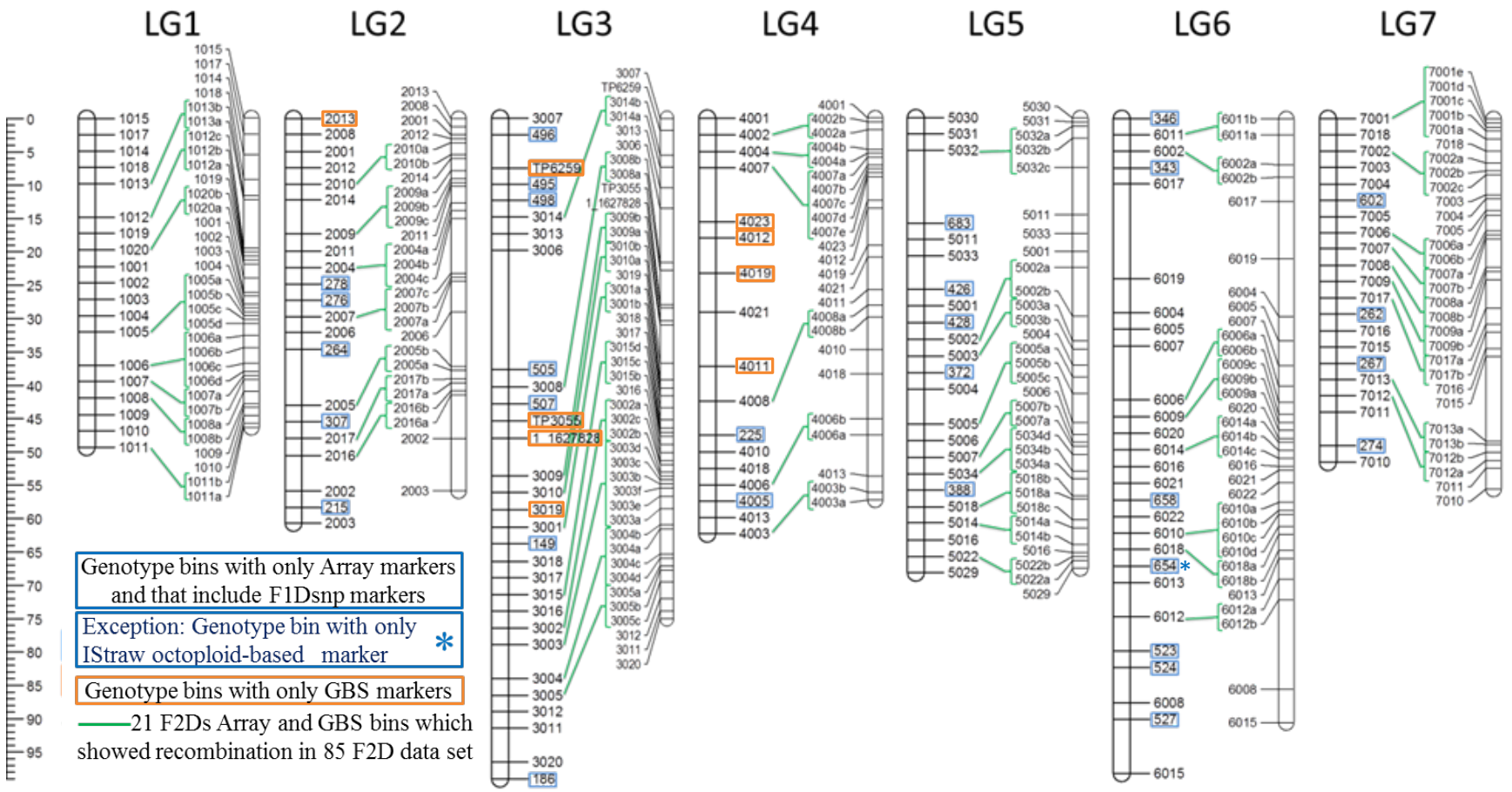


Figure 1.6: *F. iinumae* high density linkage map. The figure provides a comparison of mapping results for the 21F2D and the 85F2D linkage groups. For each linkage group, the 21F2D version is on the left and the 85F2D version is on the right. The linear orders of mapped loci within linkage groups are in agreement between the 21F2D and 85 F2D maps.

Table 1.8: Distribution of mapped markers by SNP type and F1D linkage group. 8a. The Array and GBS SNP marker distribution on the seven linkage groups and in total is provided. The last column provides the percentage conversion of the number of mapped SNPs to the total number of SNPs on the Array. **8b**. The table shows the distribution of markers from the two GBS bioinformatic pipelines, and itemizes unique and shared markers between the two pipelines and provides a tally of the number of mapped markers common between the Array and GBS. The two GBS pipelines were the UNEAK (UN) generated using non-reference based Tassel pipeline, and DWF1DRf (DW) generated by Dave Wood's developed *F. iinumae* reference based pipeline.

8a.

SNP Basis	LG1	LG2	LG3	LG4	LG5	LG6	LG7	SNP Type Totals	%Array
F1D Discovery SNPs	337	431	482	339	417	687	338	3,031	80.81%
Octoploid Discovery									
Snp	15	18	16	20	19	35	17	140	0.22%
mSnp	-	-	1	1	1	1	-	4	0.23%
ins	2	3	-	1	2	-	-	8	0.17%
del	1	1	-	2	1	2	2	9	0.18%
SnpSnp	-	-	-	-	3	4	5	12	0.17%
indelSnp	-	-	-	-	-	-	-	-	0.20%
SnpinIns	1	-	-	-	-	2	1	4	0.20%
SNPinDel	-	-	-	-	-	-	-	-	0.20%
total octoploid SNPs	**19**	**22**	**17**	**24**	**26**	**44**	**25**	**177**	**0.21%**
Codon-based SNPs	1	4	-	-	-	2	-	7	0.12%
total Array	**357**	**457**	**499**	**363**	**443**	**733**	**363**	**3,215**	**3.38%**
total GBS	**114**	**133**	**148**	**121**	**119**	**189**	**71**	**895**	NA
grand-total Array and GBS mapped	**471**	**590**	**647**	**484**	**562**	**922**	**434**	**4,110**	NA

8b.

GBS Markers	LG1	LG2	LG3	LG4	LG5	LG6	LG7	Total
UN	37	61	45	31	26	66	29	295
DW	50	54	66	57	60	80	23	390
Array & DW	-	1	1	1	4	2	-	9
Array & UN	-	1	2	-	1	-	1	5
Array & UN & DW	-	-	3	2	2	-	-	7
UN & DW	27	16	31	30	26	41	18	189
total common markers between UN&DW GBS	**27**	**16**	**34**	**32**	**28**	**41**	**18**	**196**
total unique UN GBS markers	**37**	**62**	**47**	**31**	**27**	**66**	**30**	**300**
total unique DW GBS markers	**50**	**55**	**67**	**58**	**64**	**82**	**23**	**399**
grandtotal mapped GBS markers	**114**	**133**	**148**	**121**	**119**	**189**	**71**	**895**
Total common markers between Array & GBS	**-**	**2**	**6**	**3**	**7**	**2**	**1**	**21**

Table 1.9: Summary of F1D map statistics. The number of loci (= number of genotype bins), the number of SNP markers, the average number of SNP markers, the lengths of the maps and the actual LODs are provided for both the 21F2D and 85F2D maps and for each linkage group.

F1D Map	# of Loci		# of SNPs		Avg #SNPs/Locus		Length (cM)		LOD	
	21F2D	85F2D	21F2D	85F2D	21F2D	85F2D	21F2D	85F2D	21F2D	85F2D
LG1	19	32	471	114	25	4	49.3	46.4	3	10
LG2	21	26	590	133	28	5	59.5.	54.5	4	10
LG3	30	42	647	148	22	4	99.0	75.0	2	10
LG4	17	24	484	121	28	5	60.4	58.0	3	10
LG5	23	31	562	119	24	4	68.2	67.4	1	10
LG6	27	32	922	189	34	6	98.2	90.5	3	10
LG7	21	30	434	71	21	2	51.5	55.5	3	10
Total	**158**	**217**	**4,110**	**895**	26	4	**426.6**	**447.3**		

Map Density	cM/locus
21 F2D Map	2.70
85 F2D Map	2.06

Table 1.10: Heterozygosity of J17 compared to J4 in suitable mapped and unmapped markers. The markers included were heterozygous in F1D and concordant in the trio. The total SNPs of each genotypic permutation is the sum of the SNPS from the three Array discovery groups. The total SNPs in each genotype group is the sum of the SNPs from the three Array discovery groups by genotypic groups of J17 and J4; homozygous for the alternate allele, J4 heterozygous, J17 heterozygous, and J17 and J4 both heterozygous. The last two columns indicate the relative heterozygosity of J17 and J4 in calculated at % number of markers heterozygous in J17 and J4 respectively, divided by the total number of markers in both 10a and 10b.

10a. Markers suitable for mapping.

Genotype			Array discovery markers			Total SNPS of each genotypic permutation	Total SNPS in genotypic group	% heterozygosity	
J17	J4	F1D	F1Dsnps	Octoploid	Codon			J17	J4
0	2	1	1,096	72	3	1,171			
2	0	1	1,079	63	4	1,146	2,317	0	0
2	1	1	390	164	9	563			
0	1	1	377	95	19	491	1,054	0	28.5%
1	2	1	68	108	7	183			
1	0	1	58	52	13	123	306	8.3%	0
Total J17 ≠ J4			**3,068**	**554**	**55**	**3,677**			
1	1	1	18	2	-	20	20	0.5%	0.5%
Total SNPS			**3,086**	**556**	**55**	**3,697**	**3,697**	**8.8%**	**29.1%**

10b. Mapped markers.

0	2	1	1,091	69	2	1,162			
2	0	1	1,075	50	4	1,129	2,291	0	0
2	1	1	385	25		410			
0	1	1	367	25	1	393	803	0	25.0%
1	2	1	55	3		58			
1	0	1	40	3		43	101	3.1%	0
Total J17 ≠ J4			**3,013**	**175**	**7**	**3,195**	**3,195**		
1	1	1	18	2	-	20	20	0.6%	0.6%
Total SNPS			**3,031**	**177**	**7**	**3,215**	**3,215**	**3.8%**	**25.6%**

Table 1.11: Segregation distortion and allelic frequencies in 85F2D map. In 11a, the numbers of loci with levels of significant segregation distortion are determined by Chi-square Goodness of Fit test to a 1:2:1 ratio in JoinMap. Significance (* = 0.1, ** = 0.05).

11a. Genotypic frequencies.

LG	Genotypic Frequencies			Ratios			Segregation distortion	
	a	h	b	a	h	b	*	**
1	618	1,414	685	0.23	0.52	0.25	0	0
2	611	1,149	790	0.24	0.45	0.31	4	0
3	762	1,975	833	0.21	0.55	0.23	1	0
4	460	865	630	0.24	0.44	0.32	4	1
5	565	1,356	713	0.21	0.51	0.27	1	0
6	752	1,183	785	0.28	0.43	0.29	1	1
7	552	1,176	737	0.22	0.48	0.30	3	0
Total	**4,320**	**9,118**	**5,173**	**0.23**	**0.49**	**0.28**	**14**	**2**

11b. Allelic frequencies.

LG	Allelic Frequencies		Total	Ratios	
	A	B		A	B
1	2,650	2,784	5,434	0.49	0.51
2	2,371	2,729	5,100	0.46	0.54
3	3,499	3,641	7,140	0.49	0.51
4	1,785	2,125	3,910	0.46	0.54
5	2,486	2,782	5,268	0.47	0.53
6	2,687	2,753	5,440	0.49	0.51
7	2,364	2,736	5,100	0.46	0.54
Total	**17,842**	**19,550**	**37,392**	0.48	0.52

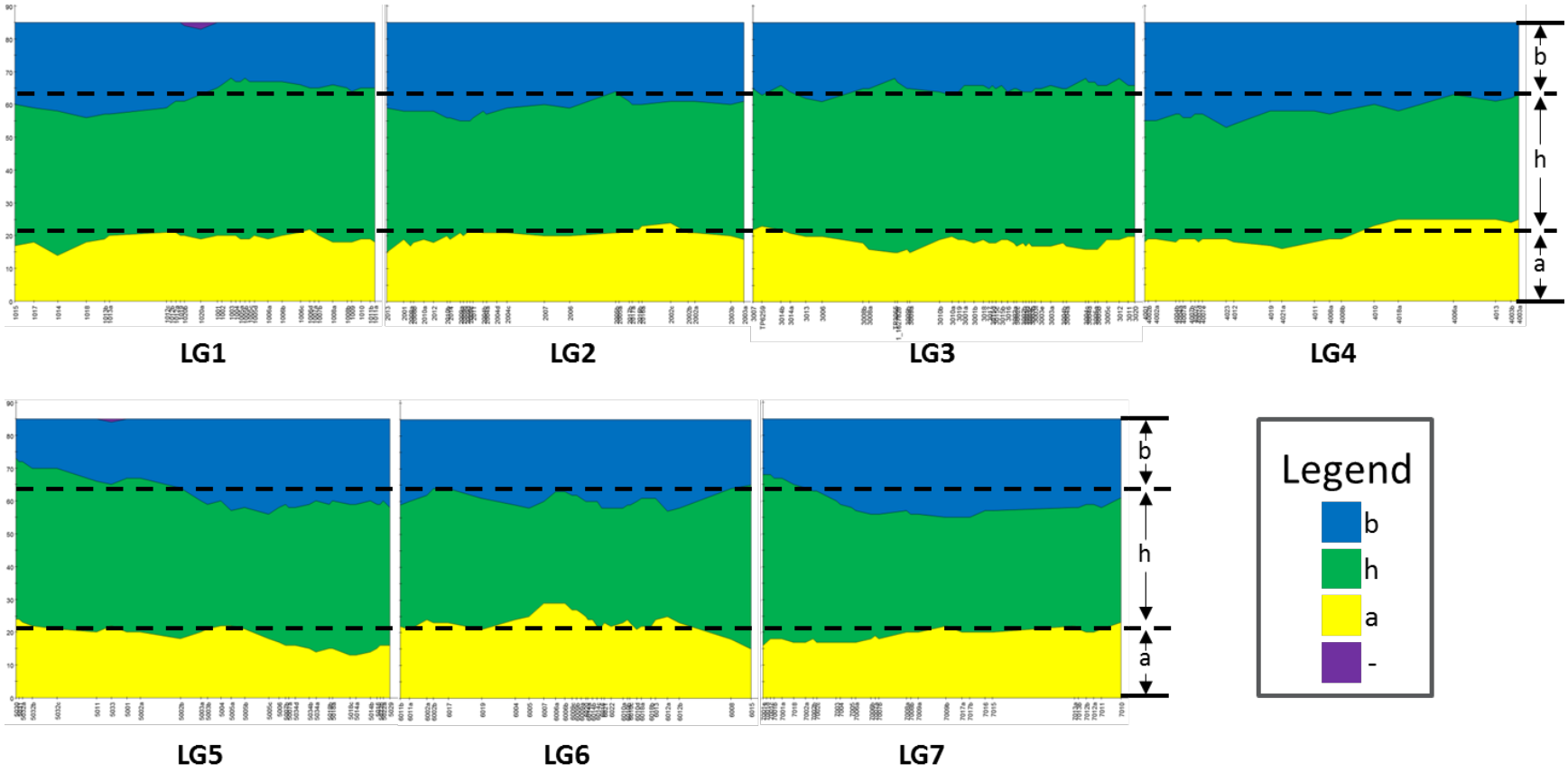


Figure 1.7: Genotypic frequencies across the seven LGs for 85F2D map. The expected frequencies of the three genotypes are shown with dotted lines. The Y axis represents the number of individuals from 0 to 85; the x axis represents the individual loci in each linkage group.

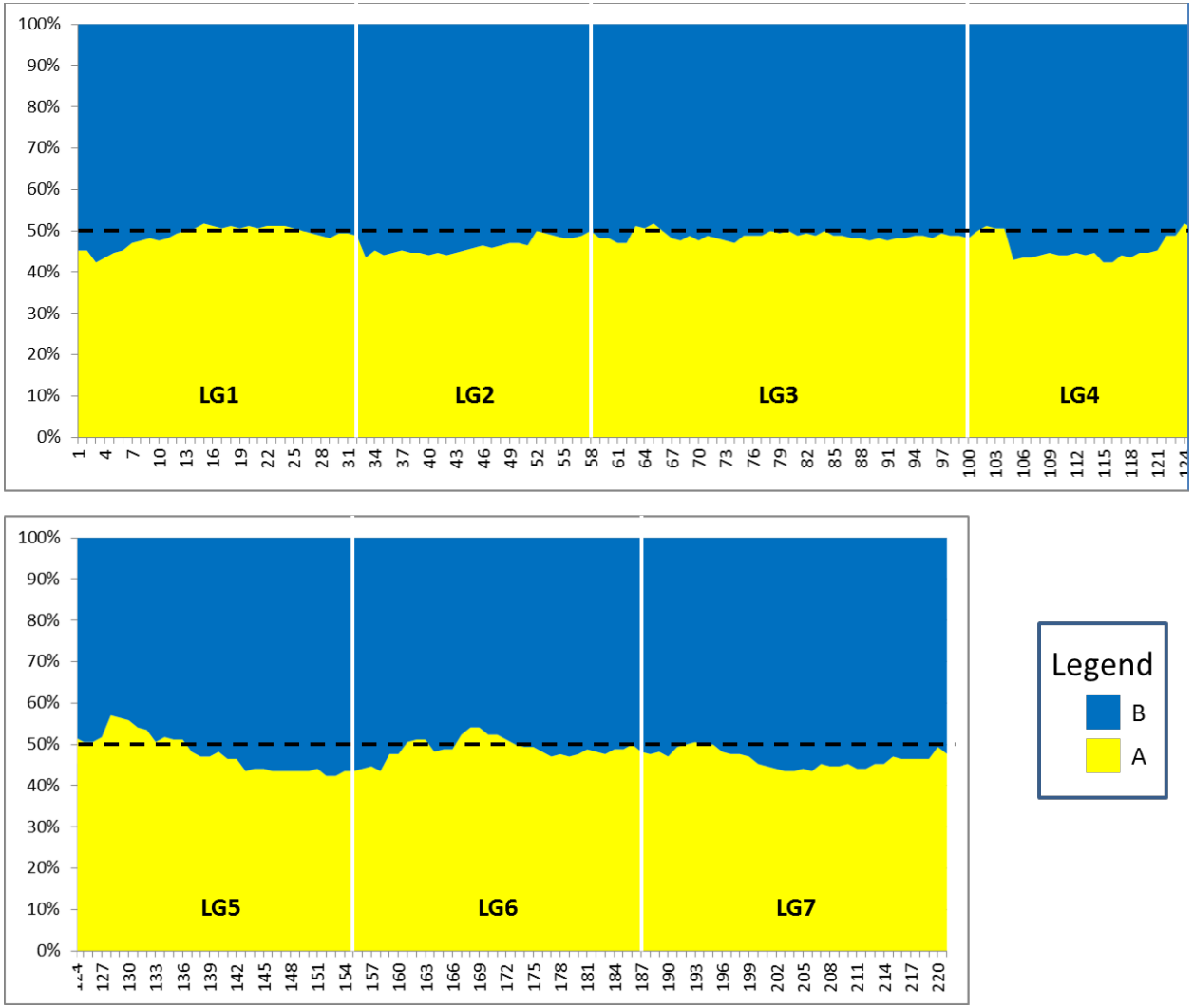


Figure 1.8: Allelic frequencies across the seven LGs for 85F2D map. The expected frequencies of A and B are 50% and are shown with a dotted line at 50%.

Comparison of *F. iinumae* F1D LGs to *F. vesca* FvH4 pseudochromosomes

A comparison of the F1D linkage groups to the *F. vesca* Hawaii4 v1.1 reference pseudochromosome (PC) physical map revealed high macrosynteny (Figure 1.9), but the degree of synteny varies for each LG (Figures 1.10 through 1.16 and Table 1.12), and within each of the LGs the degree of collinearity with FvH4 varies widely (Figure 1.17 to 1.23).

Overall an indication of synteny of F1D with FvH4 was calculated by dividing the number of markers syntenous with the homologous FvH4 relative to the total number of markers mapped for an overall value of 88.9%, ranging from a low of 85.9% for LG5 to a high of 95.2% for LG7 (Table 1.12). Correspondingly, 460 (11.2%) of the markers were identified with non-homologous LGs, with a high of 108 markers to PC4, followed by 63, 62, and 57 markers to PC6, PC1, and PC3 respectively. The lowest frequency of markers identifying with other PCs includes 35, 30, and 25 markers to PC7, PC5, and PC1, respectively (Table 1.12). In addition, 13 markers had homology to PC0, which consists of scaffolds that could not be mapped using the FV×FB linkage map. The remaining 67 markers in the Misc category include 33 GBS markers from LG4 that have homology with two scaffolds in *F. vesca* v.1.1 scaffold database. The general syntenic relationships and significant departures from synteny are illustrated in Figures 1.10 through 1.16. LG1 (Figure 1.10) and LG2 (Figure 1.11) had the highest number of markers identifying to non-homologous PC6 with 30 and 17 markers respectively, of which of 30 and 4 markers, respectively were to the lower end of PC6. For LG3, the highest number of markers identified to non-homologous PCs were 23 marker to PC2 (Figure 1.12). LG4 could not be assembled as one linkage group until the GBS data were incorporated with the Array data (Figure 1.13), the non-discovery based GBS approach discovered SNPs that were not part of the *F. vesca* FvH4 reference genome but were found later found to be homologous to unmapped

scaffolds of FvH4. For both LG5 (Figure 1.14) and LG6 (Figure 1.15), the highest number of markers to non-homologous groups were to PC4 with 41 and 51 markers respectively. LG6 (Figure 1.15) also had many (48) markers with homology to PC1 from 19.1 to 19.9 Mbps. LG7 (Figure 1.16) had the highest conservation of synteny with *F. vesca* of any of the linkage groups at 95.3% (Table 1.12), with the highest non-conservation to PC3 with only 13markers.

The LGs are individually compared to their homologous PCs for collinearity (Figures 1.17 to 1.23). The figure legends include observations about potential inversions and other rearrangements. Although there is a degree of collinearity, there is not one LG without some level of rearrangement with respect to its homologous PC. Analogous to the synteny comparison, LG4 appear to have the least collinearity to PC4, and LG7 appears to have the most collinearity with PC7.

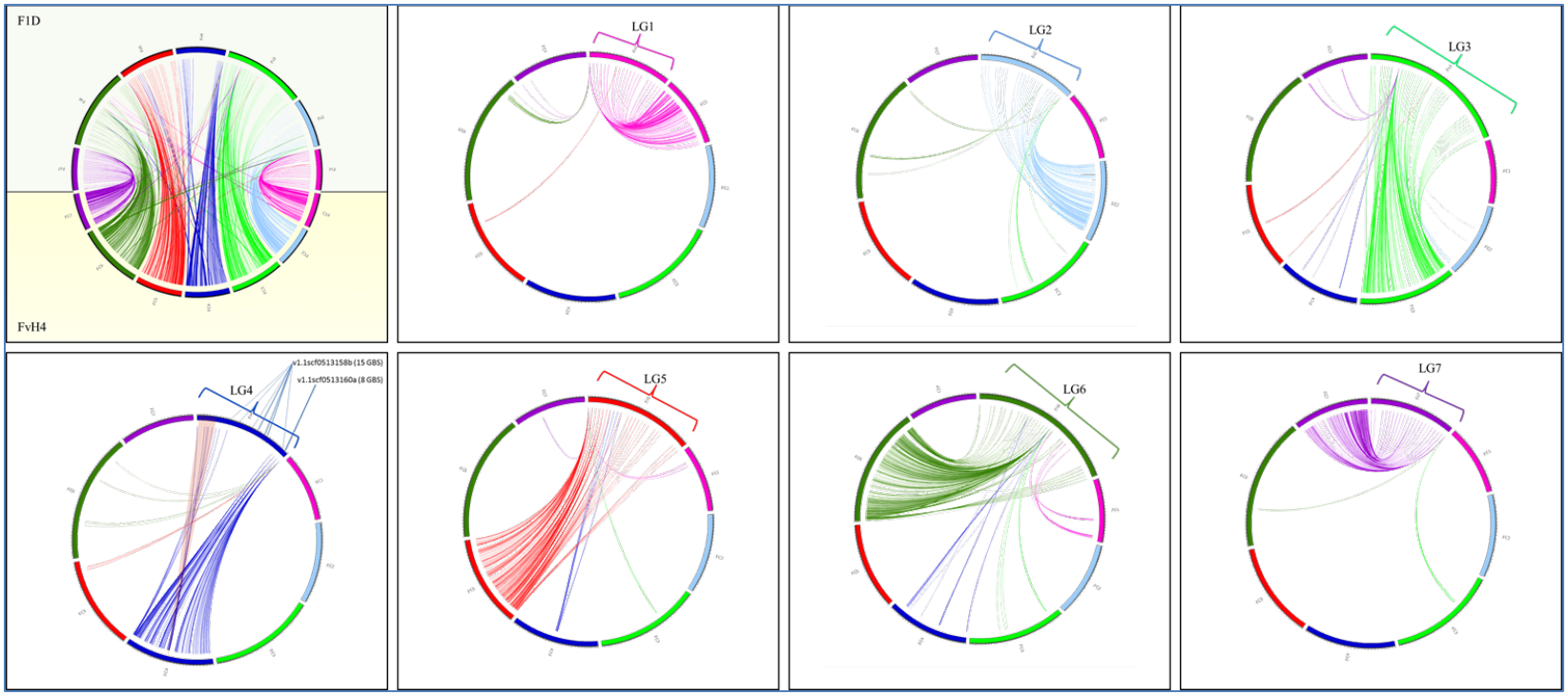


Figure 1.9: F1D synteny with FvH4. The top left figure provides an overview of synteny between the seven LGs of F1D and the PCs of FvH4. The remaining figures provide an overview of synteny and collinearity of each LG to FvH4.

Table 1.12: Synteny of *F. iinumae* F1D to *F. vesca* FvH4. The synteny is based on the percentage of markers on an LG that are syntenic with the corresponding F. vesca pseudochromosomes (PCs). For each LG, the LG with highest number of markers to a non-homologous PC are in bold.

F1D LG	21F2D map	Synteny with FvH4	% Synteny	# markers identified with non-homologous *F. vesca* PCs									
				PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC0*	Misc **	Total
LG1	471	419	89.0%		0	2	3	6	**30**	4	4	3	52
LG2	590	544	92.2%	1		13	2	3	**17**	3	4	7	50
LG3	647	567	87.6%	1	**23**		10	10	1	19	4	11	79
LG4	484	431	89.0%	2	1	3		7	7	0	0	**33**	53
LG5	562	487	86.7%	8	1	7	**41**		5	5	1	7	75
LG6	922	792	85.9%	**48**	0	19	**51**	3		4	0	5	**130**
LG7	434	413	95.2%	2	0	**13**	1	1	3		0	1	21
Total	**4,110**	**3653**	**88.9%**	62	25	57	**108**	30	63	35	13	67	460

* Markers with homology with FvH4 PC0, which includes scaffolds not mapped using the FV×FB linkage map.

** For LG4, Misc includes 23 markers with homology to FvH4 v1.0 scaffolds: 8 markers to scf0513160a, and 15 markers to scf0513158b, and 10 with discernable homology with FvH4.

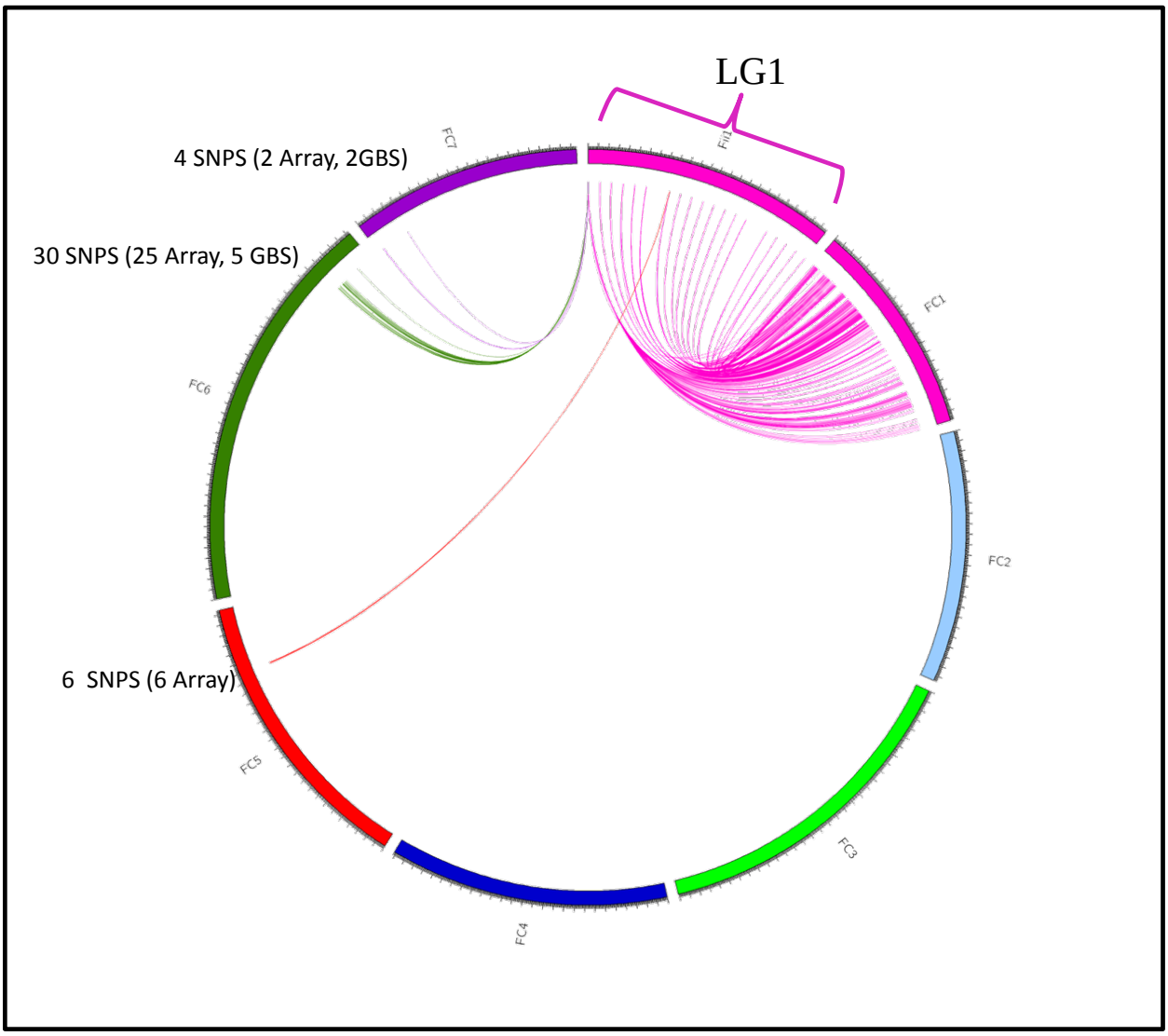


Figure 1.10: LG1 synteny with FvH4. Most (419 of 471, 89.0%) of the markers on LG1 are located on FvH4 PC1. Some LG1 markers are located elsewhere on the FvH4 genome. LG1 includes markers to non-homologous PCs including: 6 markers within the locus at 32.0 cM to PC5 from 21.8 to 21.9 Mbps; and 30 markers on the bottom 49.3 cM locus of LG1 to the lower end of PC6 from 35.3 to 37.7 Mbps.

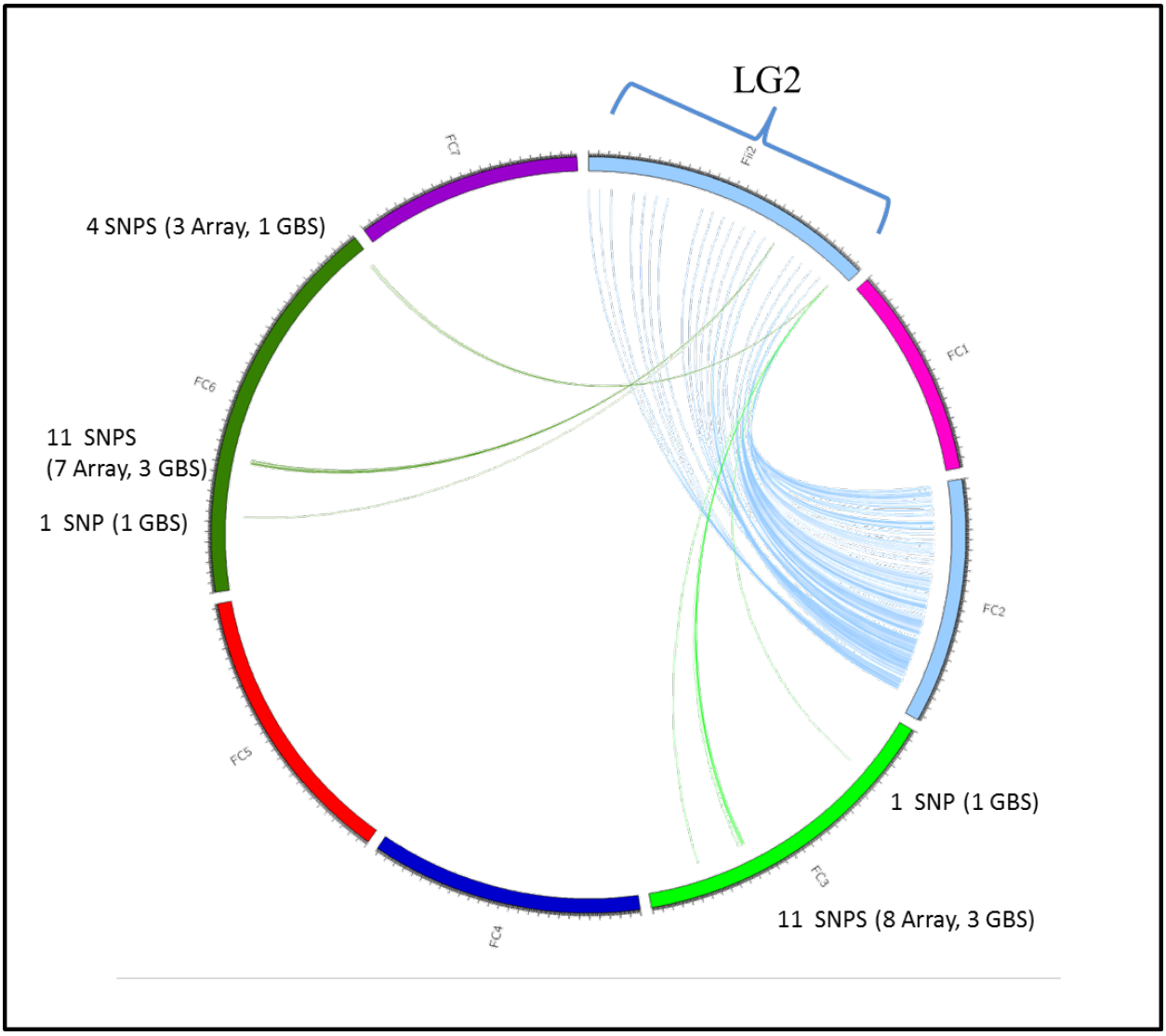


Figure 1.11: LG2 synteny with FvH4. Most (544 of 590, 92.2%) of the markers on LG2 are located on FvH4 PC2. Some LG2 markers are located elsewhere on the FvH4 genome. For instance, at the 2.5 cM locus, 10 markers correspond to PC3 from 20.9 to 21.6 Mbps and 4 markers correspond to PC6 from 38.7 to 39.1 Mbps; and at the 17.3 cM locus, 11 markers correspond to PC6 from 13.3 to 13.8 Mbps.

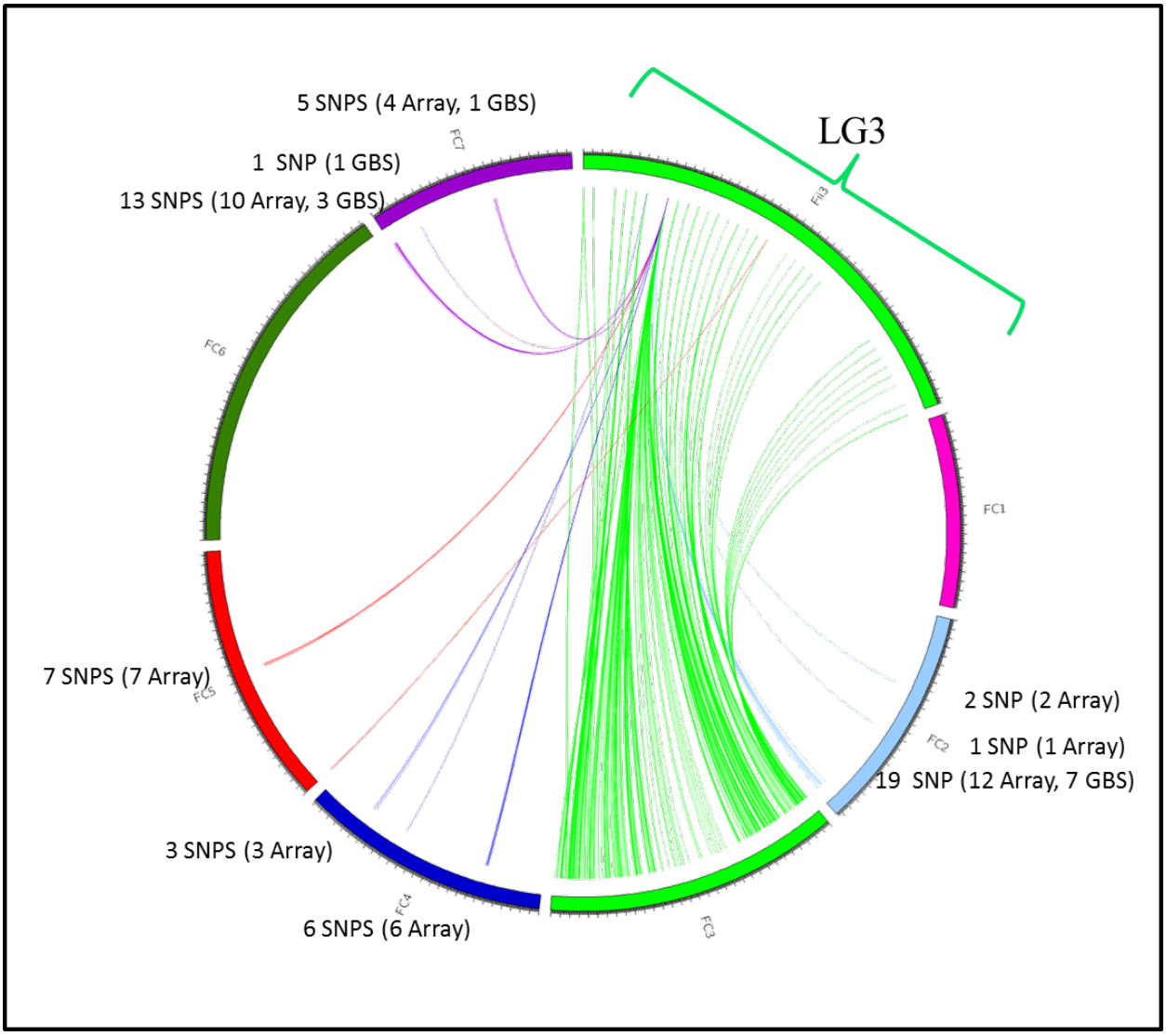


Figure 1.12: LG3 synteny with FvH4. Most (567 of 647, 87.6%) of the markers on LG3 are located on FvH4 PC3. Some LG3 markers are located elsewhere on the FvH4 genome including at locus 78.9 cM: 19 markers homologous to PC2 from 23 to 24.1 Mbps; 6 markers homologous to PC4 from 6.6 to 6.9 Mbps; 13 markers homologous to PC7 from 0.18 to 0.6 Mbps; and 5 markers homologous to PC7 from 13.1 to 13.4 Mbps.

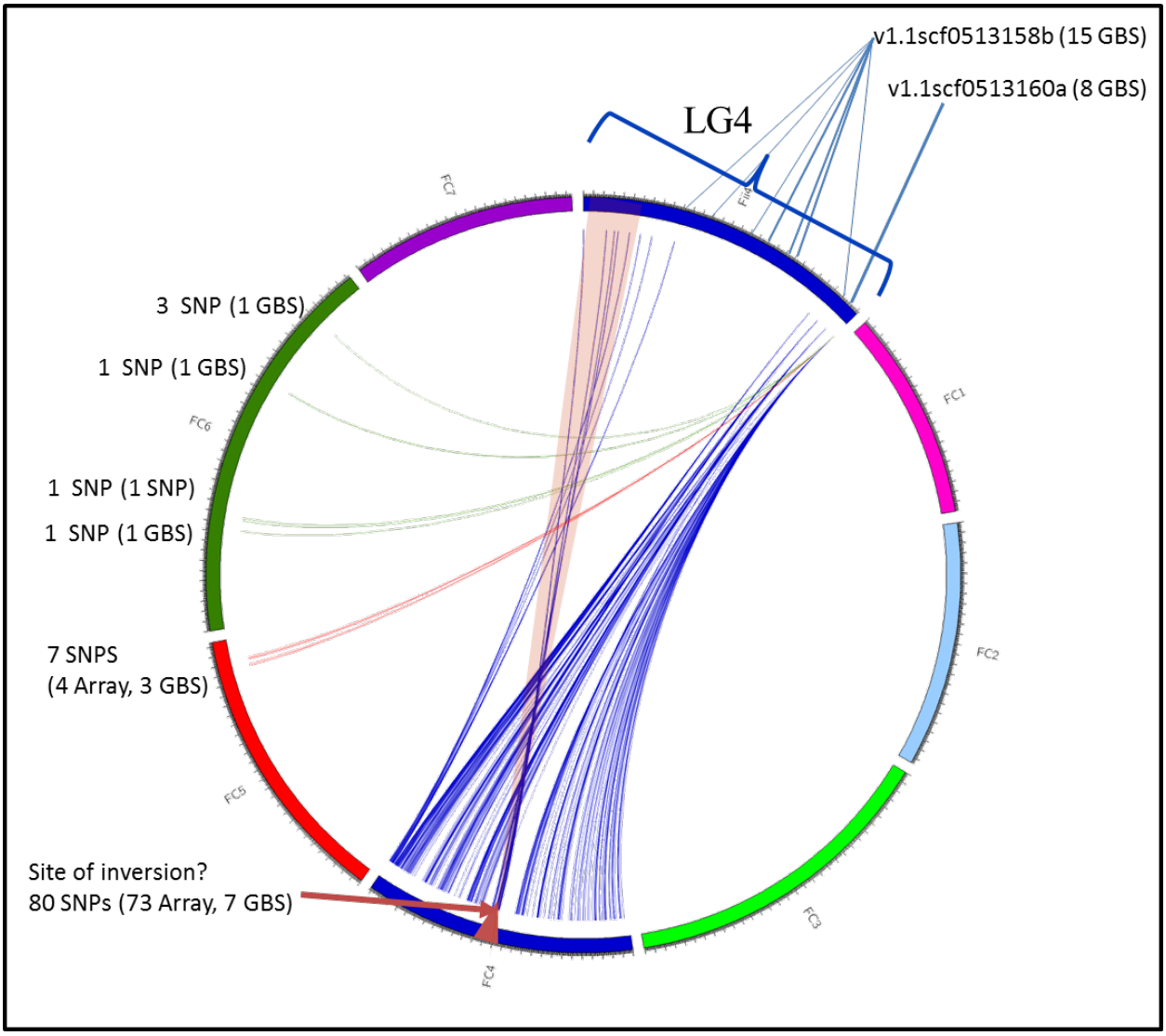


Figure 1.13: LG4 synteny with FvH4. Most (431 of 484, 89.0%) of the markers on LG4 are located on FvH4 PC3. Some LG4 markers are located elsewhere on the FvH4 genome; at the 0.0 cM locus, 6 markers have homology to PC5 from 25.2 to 26.2 Mbps and 3 markers have homology to PC6 from 10.3 to 11.7 Mbps. Nineteen of the markers on LG6 defining the loci from 4.8 to 40.8 cM do not have homology to any FvH4 PCs. However when these same 19 markers were compared to Hawaii4 v1.1 scaffolds, the seven markers at 4.8 cM shared high identity to scf0513160a, and the remaining twelve markers from 15.03 to 40.48 cM had high identity to the scaffold 0513158b and to FvH4 v1.0 PC4.

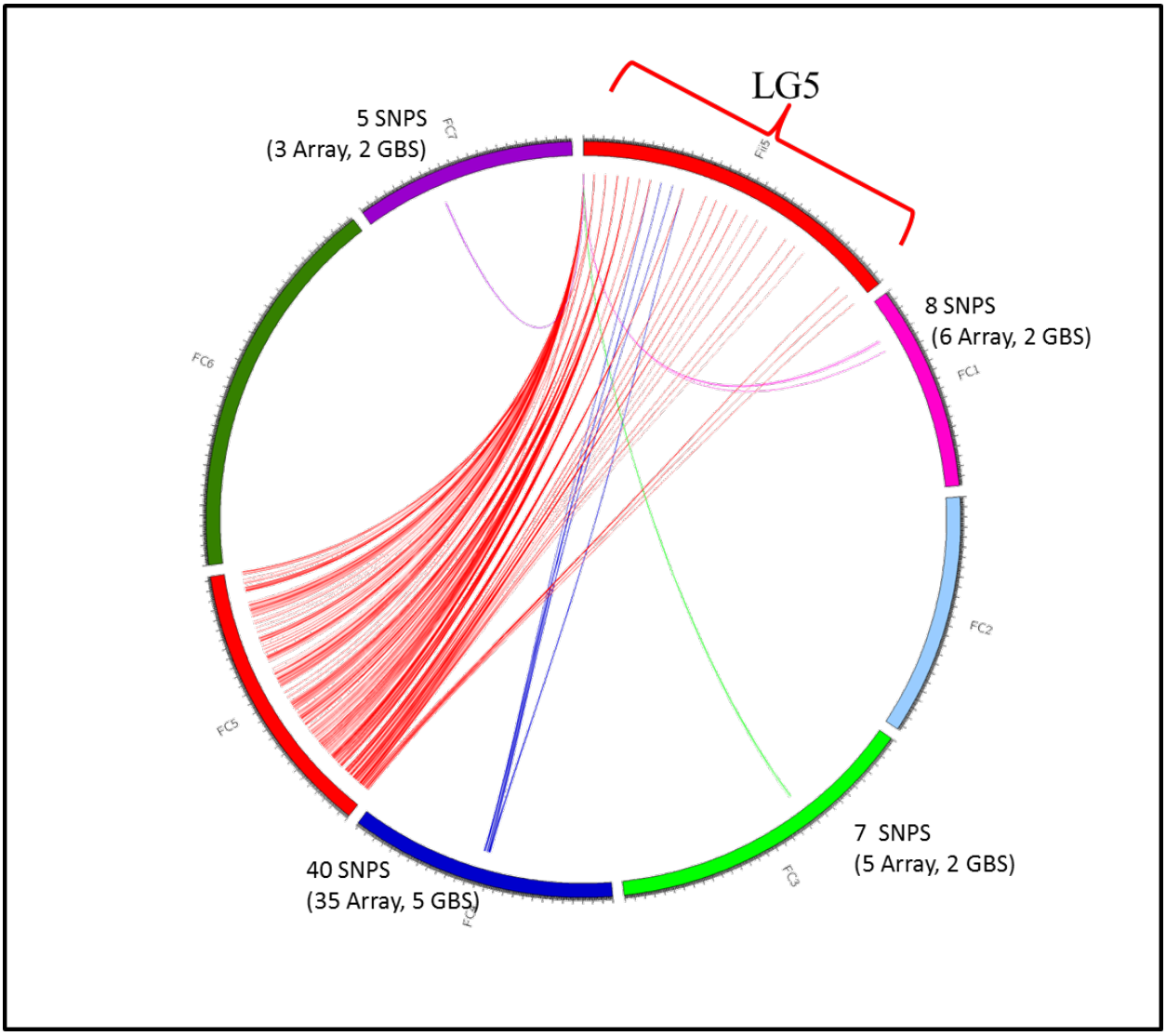


Figure 1.14: LG5 synteny with FvH4. Most (487 of 562, 86.7%) of the markers on LG5 are located on FvH4 PC4. Some LG5 markers are located elsewhere on FvH4 genome including: 39 markers within four loci from 46.0 to 53.4 cM have homology to PC4 from 13.2 M to 14.0 Mbps; and at the 68.2 cM locus, 7 markers with PC1 from 3.3 to 5.1 Mbps, 7 markers with PC3 from 11.6 to 11.9 Mbps, and 4 markers with PC7 from 8.1 to 8.2 Mbps.

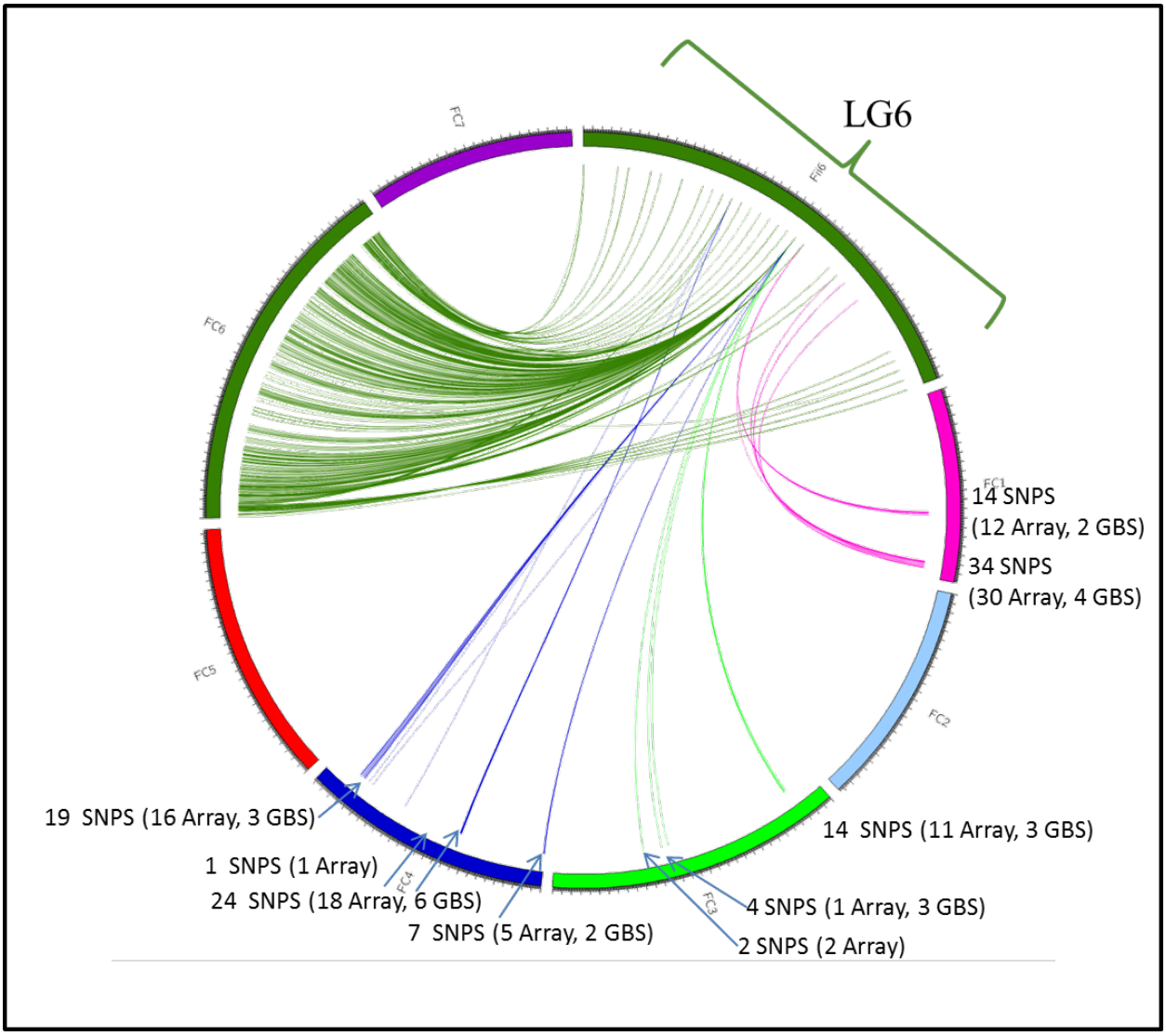


Figure 1.15: LG6 synteny with FvH4. Most (792 of 922, 85.9%) of the markers on LG6 are located on FvH4 PC6. Some LG6 markers are located elsewhere on the FvH4 genome including 31 markers within 3 sequential loci from 24.0 to 31.58 cM have homology with PC1 from 19.1 to 19.9 Mbps; and at one locus at 44.7 cM, 14 markers have homology with PC3 from 3.4 to 3.7 Mbps, 4 markers are homologous with PC3 from 18.7 to 21.7 Mbps, 7 markers to PC4 from 0.04 to 0.2 Mbps, and 19 markers have homology to PC4 from 21.9 to 23.9 Mbps. Additionally at 62.2 cM, 24 markers are located on PC4 from 10.0 to 10.3 Mbps.

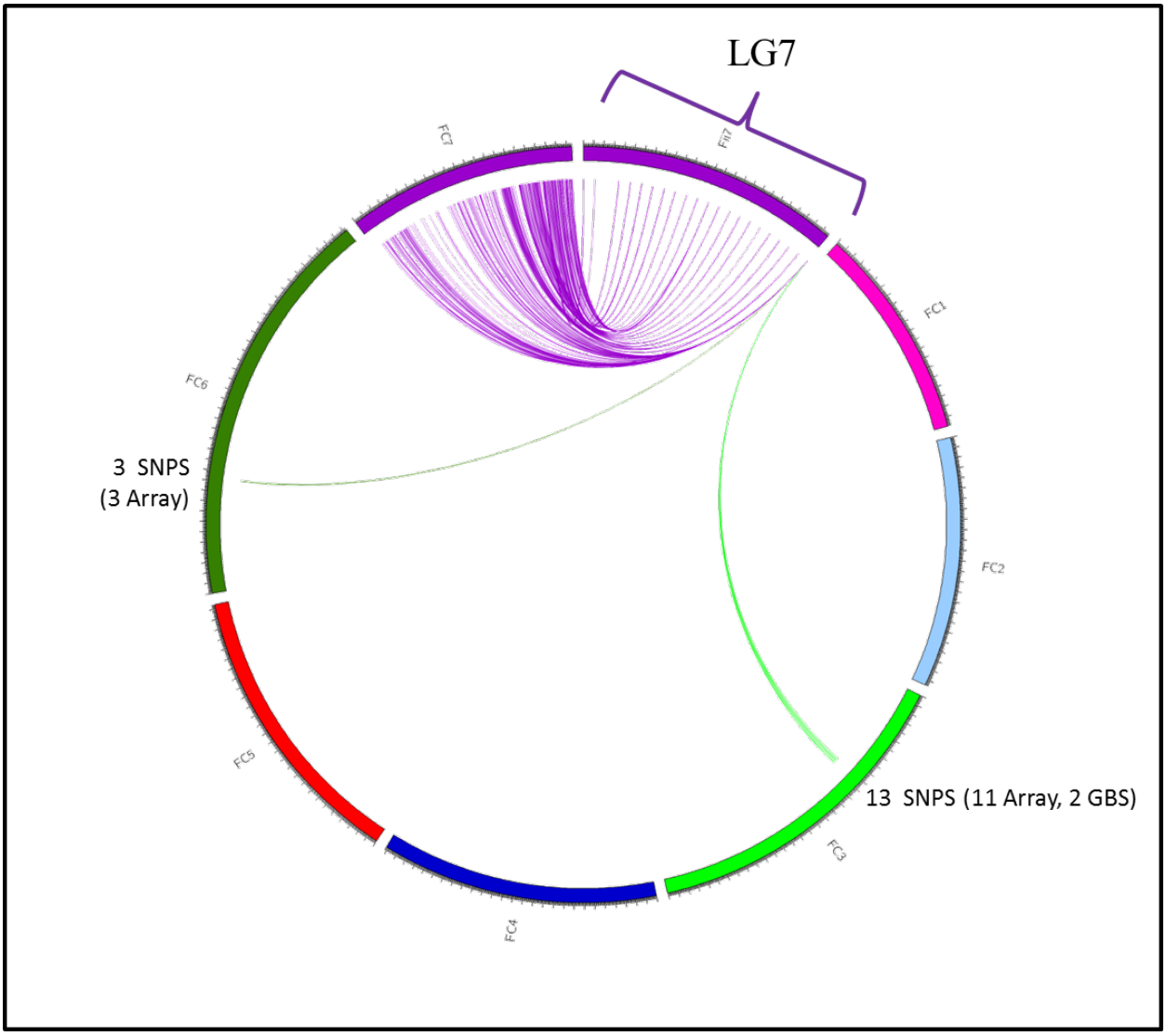


Figure 1.16: LG7 synteny with FvH4. Most (413 of 434, 95.2%) of the markers on LG7 are syntenic with PC7. Some LG7 markers are located elsewhere on FvH4 genome including 13 markers at locus 0.0 cM with homology with PC3 from 10.0 to 10.7 Mbps.

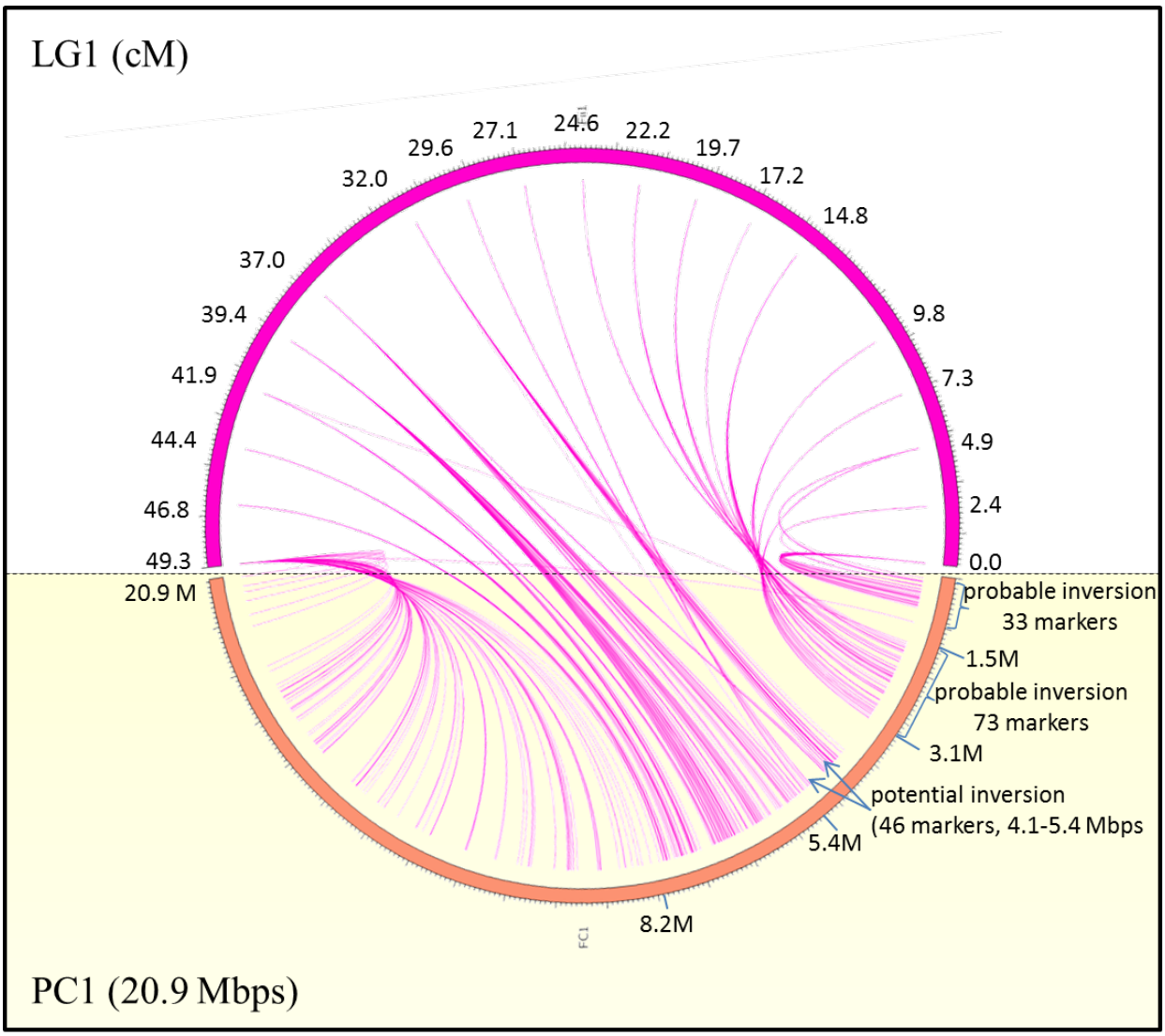


Figure 1.17: LG1 collinearity with PC1. The top end of LG1 from 0.0 to 27.1 cM shows signs of three separate inversions: 1) three loci and 33 markers to PC1 from 0.86 – 0.72 Mbps; 2) eight loci and 84 markers to PC1 from 1.5 – 3.1 Mbps; and 3) three loci and 46 markers to PC1 from 4.7-5.5 Mbps. LG1 with seven loci from 32.0 to 49.3cM (293 markers), appears collinear with PC1 from 5.4 to 20.9 Mbps. The locus at 49.3 cM with 111 markers has homology with PC1from 8.8 to 20.9 Mbps.

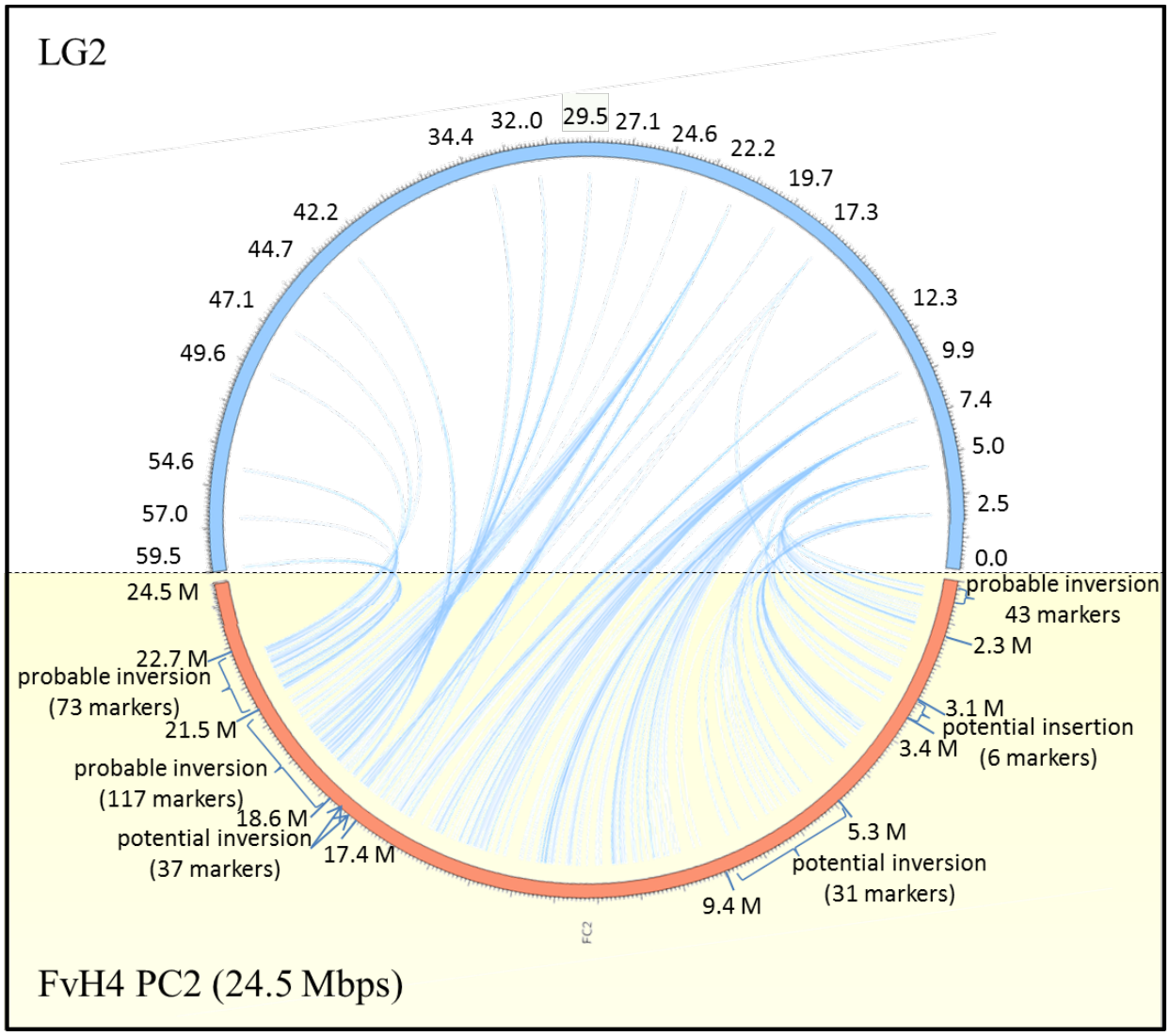


Figure 1.18: LG2 collinearity with PC2. LG2 is rearranged with respect to PC2. LG2 loci at 2.5 and 5.0 cM with 72 markers have an inverted homology to PC2 from 5.3 to 9.3 Mbps. At the current map resolution, it is unclear whether or not the markers at 5.0 cM are inverted with respect to PC2 from 0.2 to 2.3 Mbps. The locus at 7.42 cM includes 6 markers with homology to PC2 from 3.1 to 3.4 Mbps. The LG2 locus at 17.3 cM has homology to PC2 from 2.3-2.4 Mbps and also has homology to 17.4 to 18.5 Mbps while the preceding and following loci at 12.3 and 19.74 cM have homology to PC2 from 16.9 to 17.3 and 18.1 to 18.4 Mbps respectively. The loci from 19.7 to 22.2 cM (37 markers), 22.2 to 42.2 cM (117 markers), and from 44.7 to 59.5 cM(73 markers) have homology to FvH4 PC2 from 17.5 to 18.4 Mbps, 18.6 to 21.3 and 21.5 to 22.7 Mbps as three separate inverted regions.

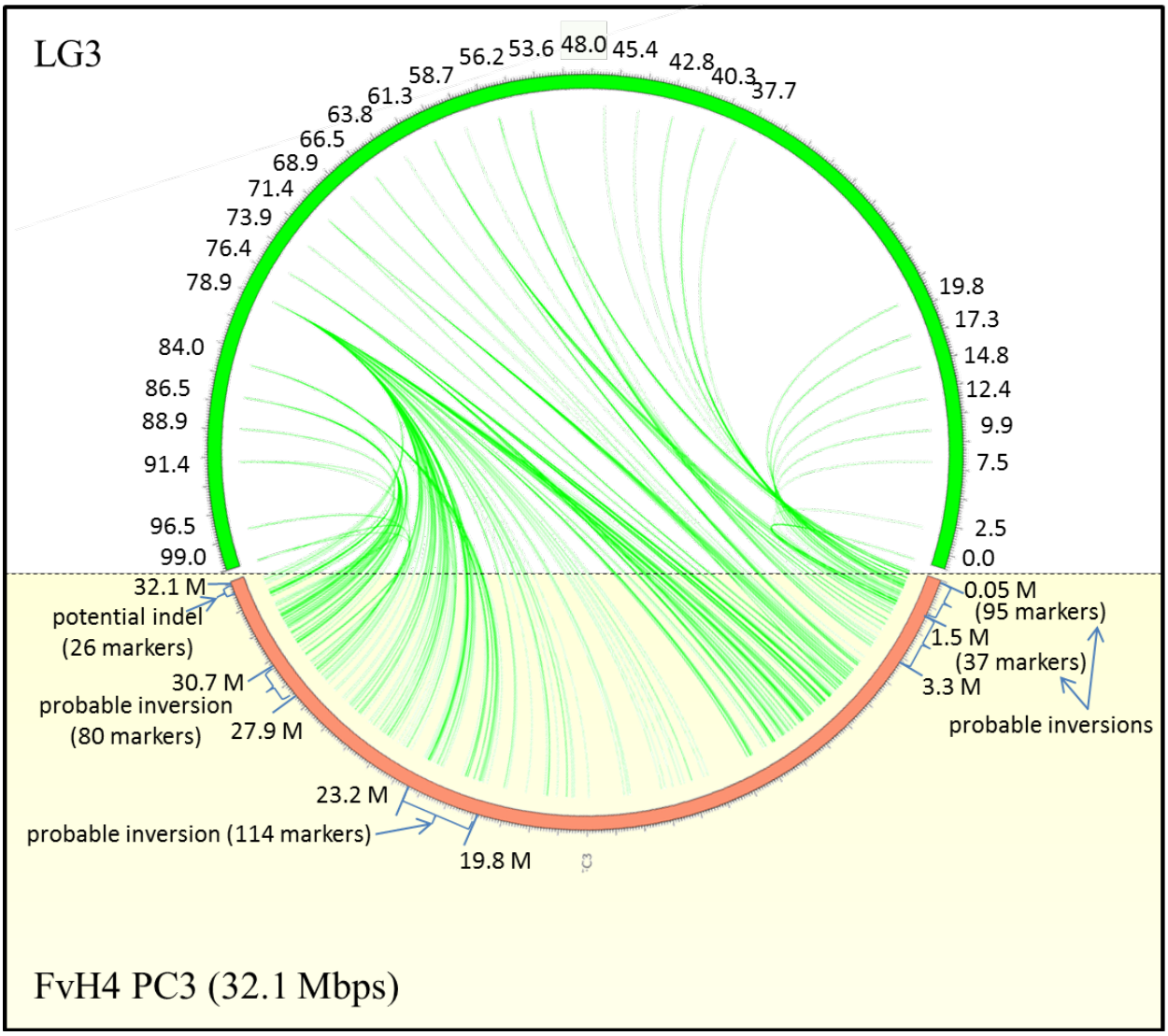


Figure 1.19: LG3 collinearity with PC3. LG3 has 14 loci from 0.0 to 53.6 cM (101 markers) with an inverted homology with respect to PC3 from 0.05 to 1.5 Mbps. Additionally, the four loci from 53.61 to 61.3 cM (38 markers) and the two loci from 61.3 to 63.8 cM (14 markers) have an inverted homology to PC3 from 1.5 to 3.3 and 3.7 to 4.0 Mbps, respectively. The 7 loci from 66.5 to 84.0 cM (378 markers) are collinear with PC3 from 4.3 to 23 Mbps. A rearrangement is indicated from 84.0 to 91.4 cM (81 markers) and from 91.4 to 99.0 cM (13 markers) with homology to PC3 from 28.7 to 31.0 and from 27.9 to 28.5 Mbps, respectively. Finally indel rearrangements are indicated at within two loci: at 78.9 cM (6 markers) and at 99.0 cM (10 markers) with homology to 31.5 to 31.8 and 30.6 to 30.7 Mbps, respectively.

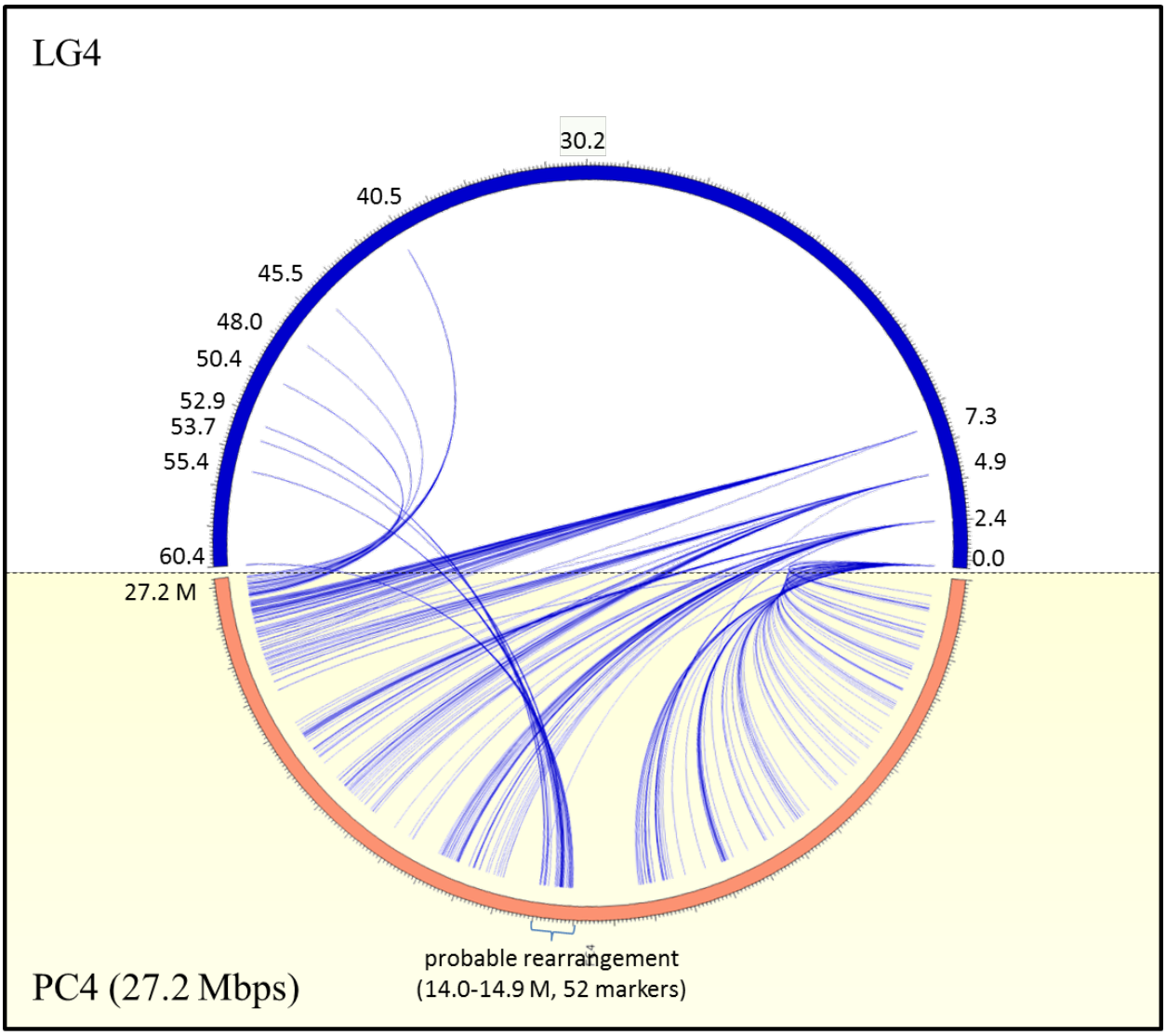


Figure 1.20: LG4 collinearity with PC4. LG4 at the locus at 0.0 cM (131 markers) is collinear with PC4 from 0.5 to 16.4 Mbps, while two of the markers at 0.0 cM locus and 88 markers at 2.4 cM locus have inverse homology to PC4 from 9.2 to 22.8 Mbps.

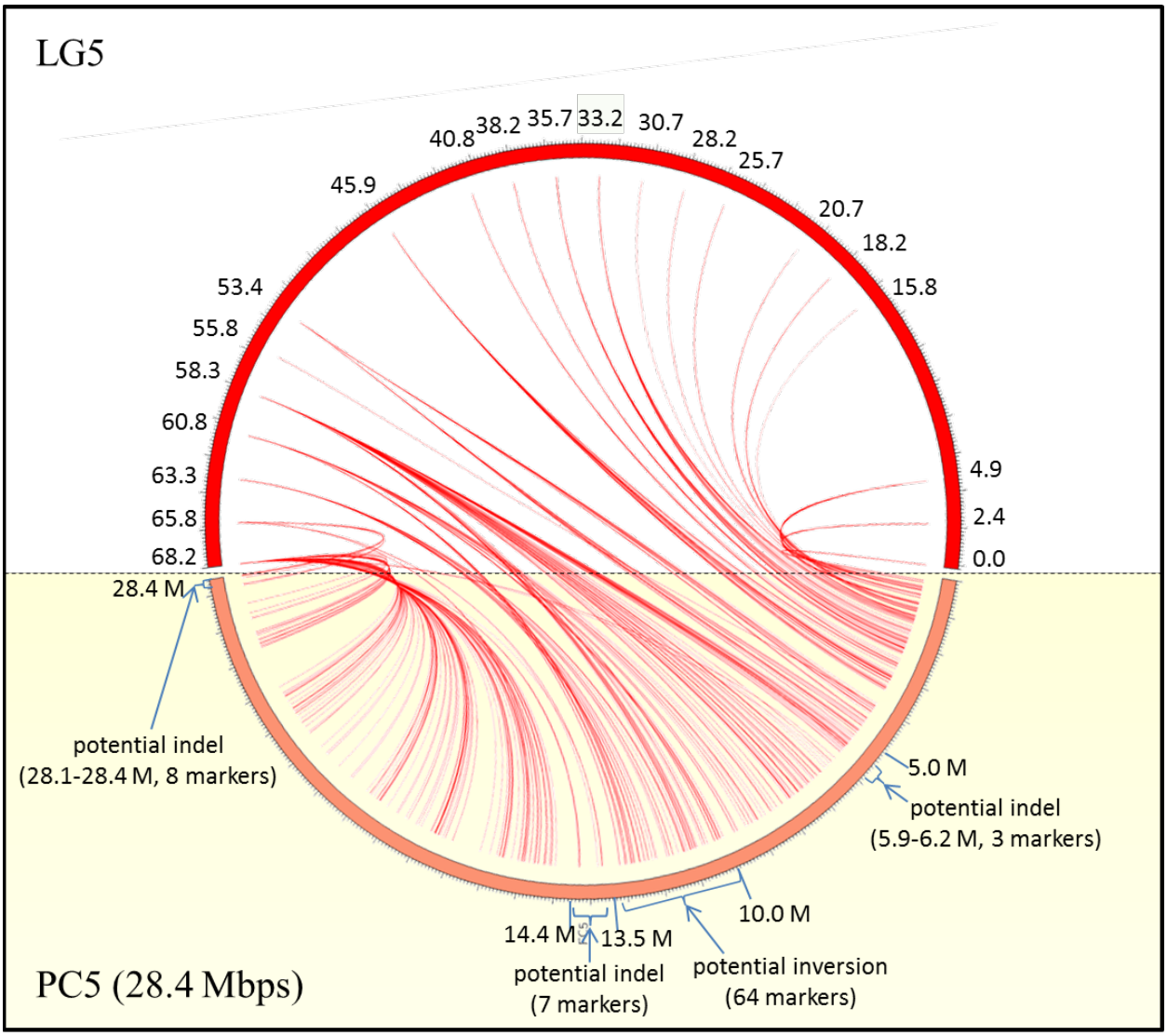


Figure 1.21: LG5 collinearity with PC5. On LG5, the 19 loci (273 markers) from 0.0 to 58.3 cM are collinear with the PC5 from 0.14 to 8.4 Mbps. However from 58.3 to 68.2 cM (5 loci, 54 markers), there is evidence of multiple inversion and rearrangements with respect to PC5.

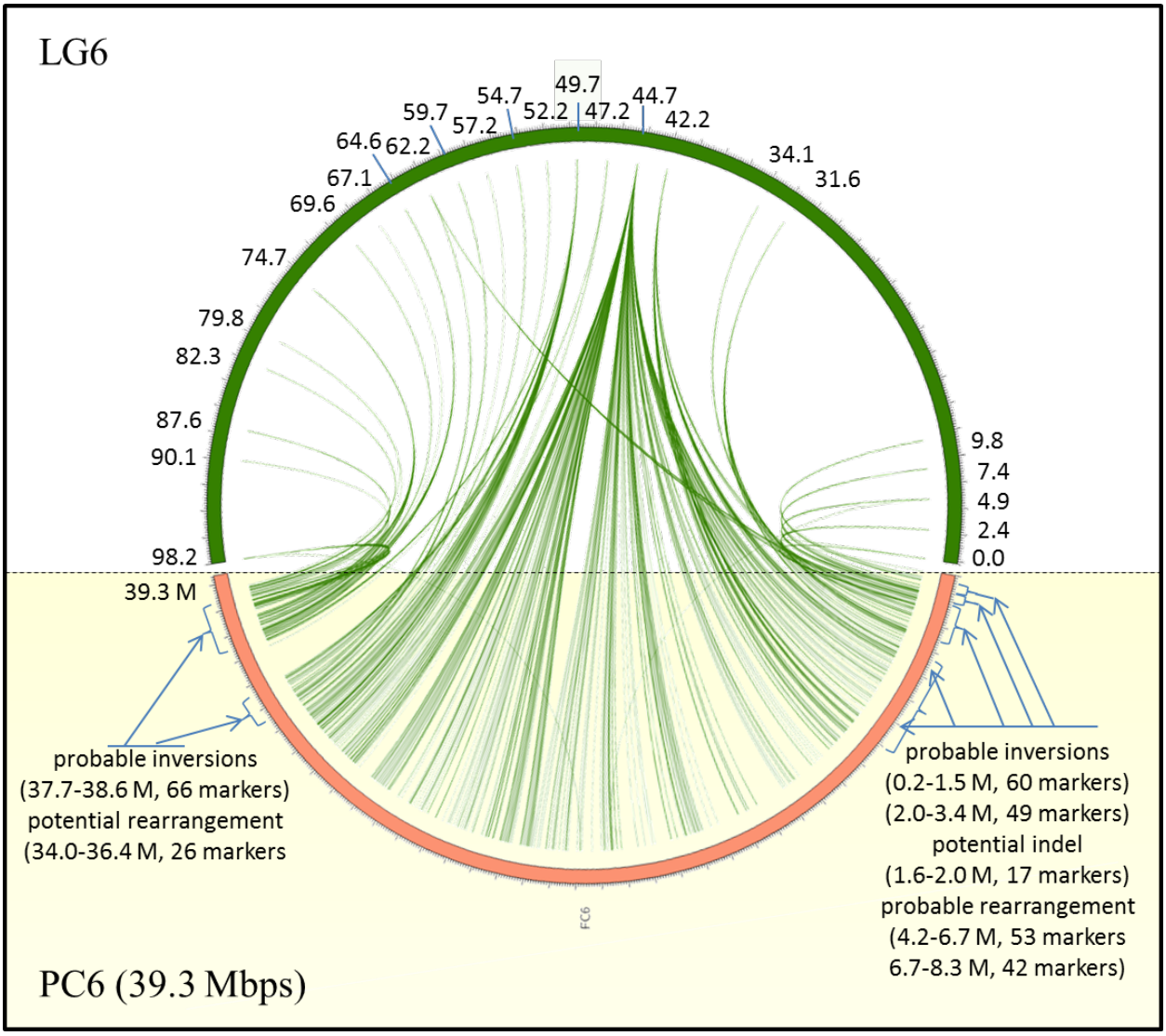


Figure 1.22: LG6 collinearity with PC6. On LG6, a number of loci appear inversely collinear with PC6: 56 markers at loci 0.0 to 9.83 cM to PC6 from 0.2 to 1.6 Mbps, 95 markers within loci 42.2 and 44.7 cM to PC6 from 4.2 to 8.3 Mbps, and 66 markers at loci 82.3 to 98.2 cM to PC6 from 37.6 to 38.7 Mbps. An indel is indicated at locus 62.2 cM with 17 markers with homology to PC6 from 1.5 to 2.0 Mbps inserted between the locus at 60.0 cM and part of the locus at 62.2 cM which have homology to PC6 from 33.6 to 33.8 Mbps and 33.9 and 34.0 Mbps, respectively.

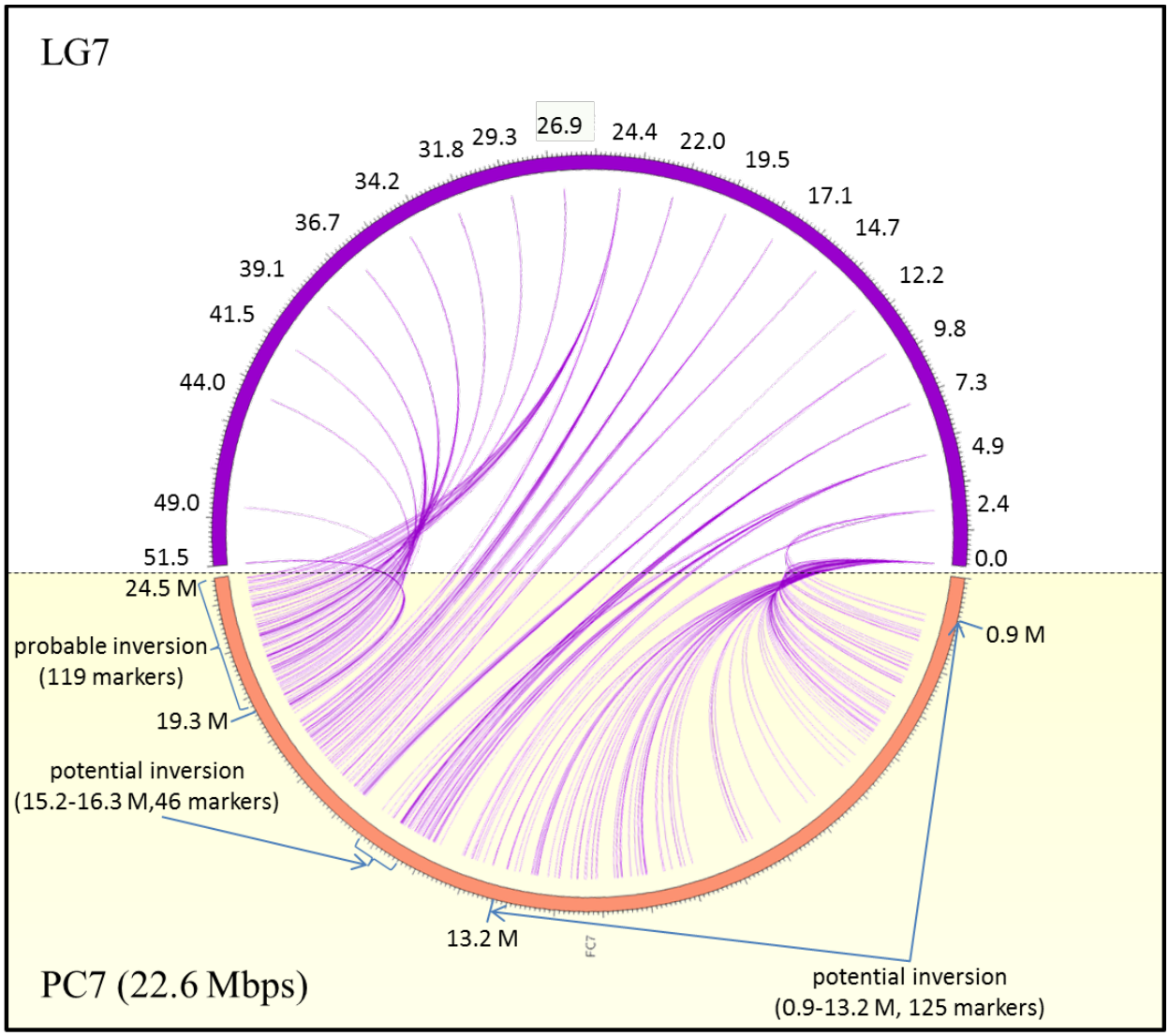


Figure 1.23: LG7 collinearity with PC7. On LG7, an inversion with PC7 is observed in three separate regions of sequential loci: 1) loci at 0.0 and 2.4 cM (125 markers) from 0.9 to 13.2 Mbps; 2) loci at 2.4 and 4.9 cM (36 markers) from 13.4 to 15.3 Mbps, and 3) the 11 loci from 24.4 to 51.5 cM (119 markers) from 19.3 to 22.5 Mbps.

Discussion

The construction of the first linkage maps in the ancestral diploid strawberry species, *Fragaria iinumae*, is reported here. The two constructed maps (Figure 1.6 and Table 1.9) converge on a mutually consistent description of linkage group structure and linkage map length in *F. iinumae*, but differ in two important ways: map resolution and numbers of markers. The 21F2D map (Table 1.9) incorporates the most markers (4,110), but these markers are separable into only 158 loci, resulting in an average map resolution of 2.70 cM/locus, as compared with the theoretical maximum of 2.38 cM/locus. The 21F2Dmap LOD averaged of 3, with a couple of troublesome linkages on LG3 and LG5 which had respective LOD scores of 2 and 1 respectively. The order of the problematic linkages in the map of 21F2D was affirmed in the map of 85F2D; the additional data permitted detection of additional recombination between markers. In contrast, the 85F2D map has a minimum LOD of 10 and has substantially fewer markers (895), but they were separable into 217 loci, resulting in an increased map resolution of 2.06 cM/locus as compared with a theoretical maximum of 0.58 cM/locus. Thus, the 85F2D map achieved better resolution, but the 21F2D map resolution of 2.70 cM/locus came closer to achieving its theoretical maximum resolution of 2.38 cM/locus. The comparative shortfall of the 85F2D map in achieving its maximum theoretical resolution is likely due to the low quality of the GBS data, as discussed later. It is anticipated that future incorporation of Array SNP data along with GBS data for all 85 plants used to construct the 85F2D map will result in a next generation map that achieves both high resolution and high marker number. That next generation map will serve to anchor the *F. iinumae* genome assembly that is now in progress.

The total map lengths of 486.7 and 447.3 cM, respectively, for the *F. iinumae* 21F2D and 85F2D maps are similar to the range of 406.3 to 445 cM reported for other diploid strawberry maps (Davis et al. 1997, Sargent et al. 2011, Tennessen et al. 2013). The linkage map used to anchor the FvH4 physical map is based on the FV×FB linkage map with 411 SSR loci for a total map length of 444.8 cM (Sargent et al. 2011). The FV×FB map is comparable in length to the *F. iinumae* map, although it has over twice the number of loci compared to the F1D maps.

Heterozygosity and segregation distortion

Analysis of both the linkage map for segregation distortion and for allelic representation shows close to a Mendelian segregation ratio of 1:2:1 as expected and close to the expected normal 50:50 ratio of A and B alleles (Table 11a and b, Figure 1.7 and 8, respectively). These normal segregation ratios contrast to the segregation distortion observed in the *F. vesca* × *F. vesca* and *F. vesca* × *F. bucharica* FV×FB maps (Davis et al. 1997, Sargent et al. 2006). The difference in segregation distortion between the maps may be due to a differences in nuclear-organelle genome compatibilities (Davis et al. 2009), which were more likely to be a factor in the wide intraspecific *F. vesca* × *F. vesca* (Davis and Yu, 1997) and interspecific *F. vesca* × *F. bucharica* (Sargent et al., 2006) crosses used to generate the respective mapping populations. In contrast, the *F. iinumae* J17 × J4 cross involved closely related, conspecific parents that would have been unlikely to have accumulated significant nuclear or organelle genomic divergences.

Marker performance

Construction of the two linkage maps provided numerous insights into the relative merits of various classes and categories of Array markers. In evaluating the performances of these marker classes and categories, it is important to recall that, of the 95,062 SNP markers (Table 1.1) interrogated by the IStraw90 array, only 3,751 were F1Dsnps, which were designed specifically to detect SNPs believed to be heterozygous in F1D and therefore expected to segregate in the F2D mapping population. In contrast, the 85,663 octoploid-based SNPs were known only to be polymorphic among the members of an octoploid germplasm panel, and the 5,648 speculative codon-based SNPs were not known to polymorphic in any particular population, so there was no *a priori* expectation that the octoploid- and codon-based Array SNPs would be informative in the F2D population. Thus, it was not at all surprising that 80.8% of the F1Dsnps were ultimately incorporated into linkage maps, while only 0.21% and 0.12% of the octoploid- and codon-based SNPs were so incorporated (Table 1.8). The high mapped conversion rate of 80.8% for F1Dsnps compared to the very low conversion rate of less than 1% for the octoploid SNP's (Table 1.8) indicates a strong correlation between the relatedness of the two types of discovery panels to that of the germplasm genotyped specifically; the lack of relatedness of *F. iinumae* to the *F. vesca* reference guided octoploid-based SNPs compared to the high relatedness of *F. iinumae* to the genotyped *F. iinumae* accessions.

Overall, 3.4% of the array markers were mapped (Table 1.7). Considering the performance of Array SNPs by cluster class, 94.1% of the *PHR* class was mapped, and very few with less than 1% of the other cluster classes were mapped (Table 1.7). The high conversion rate of the *PHR* class confirms the expected superiority of this class for utilization in mapping. Nevertheless, that fact that at least a few markers in other cluster classes achieved map

incorporation suggests that mapping should not be based exclusively on the members of the *PHR* class.

Array and GBS

The weakness and strengths of the Array and GBS process complemented each other in the assemblage of the *F. iinumae* map. Commonality of markers from the two approaches was very low, with only 21 markers in common (Table 1.8b), but common binning was very high, with GBS providing only 10 unique bins – i.e., bins that were not also defined by Array markers. A total of 30 bins did not have GBS markers. However, the GBS-specific bins were important because they added loci to the map, particularly in a region of LG4 that was not otherwise marked. The fact also points to a weakness of discovery-based technologies and a strength of the GBS technology. Genotyping of regions of the genome with a SNP array is limited to that contained in the reference genome. The weakness of the GBS approach is the large amount of missing data. LG4 was the most challenging linkage group to construct, and could only be assembled as one linkage group when the Array and GBS data were merged into one dataset.

21F2D map comparison to FvH4

A high degree of synteny (*or more properly conservation of synteny*) was observed between the marker distributions on the *F. iinumae* linkage groups (LGs) as compared with the *F. vesca* FvH4 pseudochromosomes (PCs). However, in more detailed comparisons between each LG and its corresponding PC, collinearity was not always evident, and evidence of paracentric inversional differences between *F. iinumae* and FvH4 was present near the ends of several LGs. The comparison of LGs and PCs indicates a putative translocation between

chromosome 1 and 6, such that *F. vesca* and *F. iinumae* have different arrangements of these two chromosomes. There also seems to be a translocation between PC6 and LG1 and PC1 and LG6 (Table 1.12) with 30 and 48 markers respectively and LG6 has the most number of markers (130) to non-homologous PCs, with the most homology with PC4 and PC1. Alternately, these putative rearrangements could actually be artifacts of mis-assembly of the FvH4 genome. In support of the latter hypothesis, there are a considerable number of markers in loci that have homology to non-homologous PCs as evidence by Table 1.12 and Figure 1.10 to 16. Interestingly, of the PCs, PC4 has the most markers on non-homologous LGs, and LG4 was the most challenging LG to assemble (Table 1.12). The difficulty with assemblage of LG4 and the homology of PC4 with non-homologous LGs suggests that FvH4 PC4 may be incorrectly assembled.

Overall, the observed differences between the *F. iinumae* LGs and the FvH4 PCs suggest two important questions. First, to what extent are the differences real, and to what extent if any do they indicate errors in the FvH4 genome assembly? Notably, LG4 of the HK map, an *F.* ×*ananassa* map, generated as part of the RosBREED project, also presented problems for linkage group construction using Array data (Bassil et al. manuscript submitted). Also, difficulty in assembling LG4 in another octoploid map has been encountered (Dan Sargent, personal communications). The re-occurring difficulty with LG4 suggests that at least PC4 is likely to be incorrectly assembled in the *F. vesca* FvH4 genome.

Of the 8,465 SNPs heterozygous in F1D and also heterozygous in the parents, only 20 segregated in the progeny and only these 20 were *PHR* class and mapped. The failure of 8,465 putatively heterozygous SNPs to map could be explained in relation to paralogy, such that the probe target sites are duplicated in the genome, and are polymorphic between sites. Similar but

non-identical paralogous sequences are likely to result in different annealing with the array probes, producing non-*PHR* cluster patterns. If these apparently heterozygous alleles are duplicated in the *F. iinumae* F1D genome, then they may also be duplicated in *F. vesca* FvH4, even though the duplication is not represented in the current reference genome. One possible way to address this hypothesis would be to recreate the population used to construct the linkage map that anchored the *F. vesca* FvH4 genome and genotype a population subset with the Array and GBS to construct a high density linkage map. Also the FvH4 genomic sequence could be reassembled using the *F. iinumae* linkage map as a comparator. The challenge with the FvH4 reference sequence is that the sequence scaffolds were anchored using an F2 population from an interspecific cross: FV×FB. So the question remains, is the FvH4 sequence correctly assembled?

CHAPTER II

PEDIGREE-BASED ANALYSIS OF FLOWER COLOR VARIATION USING SNP MARKERS FROM THE ISTRAW90 ARRAY

Abstract

This chapter explores the association of flower color traits with genetic markers detected using the IStraw90 strawberry SNP Array in a genome-wide approach. Populations were developed to advance selections for desired flower colors, fruit quality, and flowering cycles, with the ultimate goal of releasing new cultivars. A subset of these breeding lines was used to demonstrate the potential applicability of marker-assisted breeding (MAB) in strawberry with a focus on selection for non-white (NW) versus white (W) flower color.

A diverse population of ornamental hybrids segregating for NW versus W flower color, and for a wide spectrum of hues and color patterns in NW flowers, has been developed. The NW flowers varied in hue from pale pinks and corals to orange reds and scarlet red, and the anthers varied from yellow to darker red. Among the NW flowers, some petals contained darker shades of radial venations and others had petals margins with darker or lighter hues. The population is also segregating for other traits of interest, including flowering habit, fruit quality, and a number of pest and disease resistances. A population subset of 41 individuals called the ‘Select Set’ was genotyped on the IStraw90 Array. A pedigree-based analysis of the Select Set detected 5,674 segregating SNP markers, thirty-five of which are associated with NW flower color without recombination. Of these 35 markers, 28 are also located on pseudochromosome 5 of the *Fragaria vesca* 'Hawaii 4' reference genome.

Introduction

The project began with a question: why do the fruit of strawberry cultivars contain principally pelargonidin and very little cyanidin? Pursuit of the answer led to additional questions about the genetic controls of fruit and flower color, and to a primary focus on flower color because of its intrinsic horticultural interest as well as its comparative tractability as a subject of genetic research.

RosBREED and the IStraw90 Array

At the outset of my project, I became involved as a Project Associate in the USDA funded RosBREED project (http://www.rosbreed.org/), in which my advisor (Tom Davis) was a Co-P.I. The mission of the project was to bridge the gap between phenotyping and genotyping, and to advance marker-assisted breeding (MAB) in apple, peach, cherry, strawberry, and other members of the Rosaceae family.

As part of the RosBREED Project, we helped to develop standard phenotyping protocols for strawberry (Mathey et al. 2013), and phenotyped a broad range of germplasm and breeding lines. Most significantly, we contributed to the conceptual design and actualization of the IStraw90 strawberry SNP Array (Bassil et al. manuscript submitted). We are evaluating the performance of the IStraw90 SNP Array on diverse breeding and germplasm populations for the detection of segregating SNPs in strawberry, as described in (Bassil et al. manuscript submitted), as well as in Chapter I and in this chapter. Computational pipelines for SNP identification developed by the Davis lab were paramount to the design of the IStraw90 SNP

Array (Bassil et al. manuscript submitted). The strawberry SNP Array comprises 95,062 SNPs (Bassil et al. manuscript submitted), in contrast to SNP arrays for other Rosaceae crops; apple (Chagne et al. 2012), peach (Verde et al. 2012), and cherry (Peace et al. 2012), which have no more than 9,000 SNPs. Positive evaluations to-date justify the expectation that the exceptionally large size of the IStraw90 SNP Array will help compensate for the complexities of genotype calling in an octoploid.

The design of the IStraw90 Array, hereafter to be referred to as "the Array", was based predominantly on prior discovery of SNPs on the basis of sequence alignments and variant calling (Bassil et al. manuscript submitted). The design of the Array was based on three categories of markers (Table 2.1): 1) octoploid- based SNPs identified by discovery in an octoploid germplasm panel of 20, that included the three founders of the populations described in this chapter; 2) F1Dsnps - based on discovery in diploid *F. iinumae* (see Chapter I); and III) a speculative codon-based approach, which was not based on discovery, but on the third position nucleotide wobble of the amino acid proline within gene regions as annotated in the *F. vesca* FvH4 reference sequence (Shulaev et al. 2011). The octoploid-based category of markers was further subdivided into eight categories based on marker type, four of which were designed to identify segregation at the subgenomic level. The latter were called 'haploSNPs' (SnpSnp, IndelSnp, SnpinIns, SnpinDel), while the remaining four were designed to target di-allelic (Snp, Insertion, Deletion) or multi-allelic (mSnp) polymorphisms (Table 2.1).

The RosBREED IStraw90 SNP Array (Bassil et al. manuscript submitted) is a significant step towards reducing genotyping to manageable and hopefully attractive levels for MAB. With the IStraw90, the likelihood of finding robust marker-trait associations and quantitative trait loci in a genome wide scan was promising, offering an irresistible paradigm shift compared to one-

marker-at-a-time approaches with their concomitant multitudes of PCR reactions and gel-electrophoresis.

Table 2.1: Counts of IStraw90 Array SNPs by category. The primary categories are the octoploid-based, *F. iinumae* diploid-based F1Dsnps, and codon-based SNPs.

Marker name	Count	Description
Snp	63,263	SNP with two alternate alleles
mSnp	1,761	SNP with four alternate alleles
ins	4,615	An insertion
del	4,913	A deletion
SnpSnp	7,092	Subgenome-specific SNP adjacent to a marker SNP
indelSnp	1,176	Subgenome-specific indel adjacent to a SNP
SnpinIns	2,007	SNP inside a subgenome-specific insertion (insertion relative to *F. vesca* reference)
SnpinDel	836	SNP inside a subgenome-specific insertion (deletion relative to *F. vesca* reference)
Octoploid-based total	**85,663**	Discovered in octoploid germplasm panel
F1Dsnp	**3,751**	Discovered in F1D
Codon-based	**5,648**	Non-discovery based SNP candidates
Array Total	**95,062**	All SNPs on the Array

Marker-Assisted Breeding

Advancing marker-assisted breeding (MAB) of *Fragaria ×ananassa*, the principal strawberry of commerce, has been at the core of my applied research and breeding objectives. Marker-assisted breeding requires a genotyping platform for construction of a linkage map, as well as phenotypic data for identification of quantitative trait loci (QTL). An early feasibility study concluded that MAB would be cost prohibitive in strawberry, and more labor intensive than traditional breeding (Luby et al. 2001). But with the advent of next generation sequencing (NGS) platforms, the cost of sequencing has dramatically declined in the last ten years, from $8,000/Mbps to $0.10/Mbps in 2012 (Poland et al. 2012), opening opportunities for sequence-based genotyping strategies such as genotyping-by-sequencing (GBS) (Elshire et al. 2011, Poland et al. 2012), and for sequence-based, single nucleotide polymorphism (SNP) discovery. The expense and labor intensity of phenotyping has yet to be overcome, although inroads are

being made with imaging and computation software (Eberius 2009). Increasingly, streamlined pipelines for bioinformatics are being developed and improved to make effective application of MAB a foreseeable reality (Bink et al. 2012, Poland et al. 2012, Rosyara et al. 2013). Although MAB of strawberry is particularly challenging because of its octoploid genome, the use of state-of-the-art genotyping platforms such as the Array, GBS, and others promise to make MAB in strawberry practical in terms of cost and effort.

Linkage Maps - Setting the stage for MAB, a number of linkage maps for the octoploid strawberry have been published recently: (Rousseau-Gueutin et al. 2008, Spigler et al. 2008, Weebadde et al. 2008, Sargent et al. 2012, Zorrilla-Fontanesi et al. 2012, Isobe et al. 2013). Marker loci densities of 0.5 (Lerceteau-Kohler et al. 2012) and 0.8 per cM (Isobe et al. 2013) were achieved using PCR-based markers. Previous studies with other crops have recommended marker loci densities of 1 per cM or less to define a QTL with sufficient precision for use in MAB. Genome resolutions using current genome wide scan technologies are expected to easily exceed the target marker loci density of 1.0 per cM.

Quantitative trait locus (QTL) analyses - QTL analyses employ statistical methods to discover links between traits and marker loci in a mapping population segregating for the trait(s) of interest. Using two of the previously cited *F.* ×*ananassa* mapping populations: 'Capitola' x 'CF1116' (Rousseau-Gueutin et al. 2008), and '232' × '1392' (Zorrilla-Fontanesi et al. 2011), the Capitola' × 'CF1116' population (Rousseau-Gueutin et al. 2008) was phenotyped for 19 fruit quality traits, which resulted in the identification of 87 QTL. The '232' × '1392' population (Zorrilla-Fontanesi et al. 2011) was phenotyped for 17 agronomical and fruit quality traits, resulting in identification of 33 QTLs (Zorrilla-Fontanesi et al. 2011), and was also later

phenotyped for 48 volatiles in fruit, which resulted in an additional 70 QTLs (Zorrilla-Fontanesi et al. 2012).

Using pedigree based analysis and a combination of SSR and SNP markers, six QTLs for fruit size were located in cherry, another member of the Roseaceae family, confirming two QTLs previously identified in a single mapping population and discovering four new QTL (Rosyara et al. 2013). In the cherry study, pedigree relationships were visualized using Pedimap (Voorrips et al. 2012), and FlexQTL was used to discover QTLs (Bink et al. 2008). This work in cherry is highly relevant to my project because my approach is also pedigree-based, as distinct from the single population-based analyses previously conducted on strawberry as described above.

Plant pigments

The colors of flowers and fruit are the result of flavonoids (which include anthocyanins), carotenoids, and betalains (Mol et al. 1998). The betalains occur in only the Caryophyllales family and do occur simultaneously with anthocyanins (Mol et al. 1998). The colors and hues are further modified by co-pigmentation, pH, and cell shapes (Mol et al. 1998) and complexes with metal ions (Tanaka1 et al. 2008). The major pigments in Rosaceae flowers and fruit are usually the result of anthocyanins (Lin-Wang et al. 2010), and in strawberry fruit the anthocyanins are pelargonidin and cyanidin (Mahoney 2007, Wang et al. 2007, Mahoney et al. 2009).

Strawberry fruit

The strawberry is an accessory fruit composed of a swollen flower receptacle (the fleshy part) and seed-like achenes, which are the true botanical fruit (Perkins-Veazie 1975, Suutarinen et al. 1998, Fait et al. 2002). The achenes are derived from uni-carpellate pistils, and the

hardened pericarp encloses the seed (Perkins-Veazie 1975, Aharoni et al. 2002, Fait et al. 2002). In common usage and in this thesis, the swollen receptacle along with the achenes, are together referred to as the strawberry fruit.

Octoploid strawberry - The octoploid strawberry *F.* ×*ananassa* genome (2n=8x=56) has a 1C genome size of 780-800 million base pairs (Mbp) (Davis et al. 2007). *Fragaria* ×*ananassa* arose in France in the 1700's from an accidental hybridization between a white-fruited Chilean strawberry *F. chiloensis* ssp. *chiloensis* and a wild North American species, *F. virginiana* ssp. *virginiana* (Darrow 1966). Importantly, considerable diversity exists within both *F. chiloensis* and *F. virginiana*, each of which comprises four subspecies (Hancock et al. 2000). Thus, these wild species offer a rich germplasm pool for breeding (Hancock et al. 1993, Hancock et al. 1993, Hancock et al. 2010, Stegmeir et al. 2010). Both the white- and red-fruited forms of the South American *F. chiloensis* have been used in breeding and white-fruited cultivars of *F. chiloensis* are prevalent in Chile (Hancock et al. 2001, Carrasco et al. 2007). The white-fruited forms of *F. chiloensis* contain only trace levels of anthocyanins (Saud et al. 2009), although the achenes are red, while the red fruited form lacks the high cyanidin trait of interest to my research (Mahoney 2007, Mahoney et al. 2009). A source for the high cyanidin trait was found in North American *F. chiloensis* ssp. *lucida* (FRA1691) germplasm accession from Oregon (Mahoney 2007, Mahoney et al. 2009).

Diploid strawberry - There are currently twelve recognized diploid strawberry species (Hummer et al. 2011), one less than the previously considered thirteen (Folta et al. 2006, Staudt 2009) because *F. yezoensis* has been sub-classified under *F. nipponica* (Hummer et al. 2011). Many of the diploid species are red-fruited, but there are a number of exceptions including white-fruited *F. nilgerrensis* ssp. *nilgerrensis*, white-to-pink *F. daltoniana*, white-fruited *F.*

pentaphylla (Hummer et al. 2011)**,** and a few *F. vesca* ssp. *semperflorens* varieties that have yellow fruit (Darrow 1966). In addition, *F. tibetica* forma *alba,* a tetraploid, is also white- fruited (Hummer et al. 2011). The reference sequence for strawberry, based on yellow-fruited *F. vesca* ssp. *semperflorens* "Hawaii 4' (Shulaev et al. 2011). *F. vesca*, *F. iinumae,* and possibly a third as-yet-to-be-identified diploid are considered ancestral to the octoploid strawberry (Folta et al. 2006, DiMeglio et al. 2014).

Strawberry flowers

Strawberry flowers are normally white. The prior introgression of a "colored flower" trait from a wild source into a cultivated background (Ellis 1962) has opened an opportunity for breeders to add an ornamental quality to cultivated strawberry as the result of an interspecific cross of *F.* ×*ananassa* (previously known as *F. grandiflora*) with *Potentilla palustris*. *Fragaria grandiflora* (2n =8x=56) 'Sans Rivale' × *P. palustris* Scop (2n=6x=42) resulted in hybrids with pink flowers and a chromosome number of 2n = 49 (Ellis 1962). 'Sans Rivale' was an everbearing, very vigorous and large-fruited variety developed in 1937 (Darrow 1966). *Potentilla palustris* has large, spongy receptacles (Ellis 1962). *Fragaria* 'Frel', the first introduced pink-flowered ornamental was developed from this original cross, with five back crosses with *F. grandiflora* as a female, and thus considered to be 96% *Fragaria* (Ellis 1991). The introduction of pink-flowered cultivar 'Frel' (Ellis 1991), later known as 'Pink Panda', which has a continuous flowering habit albeit with small fruit, has inspired the development and continuing release of new ornamental strawberry cultivars with pink flowers, such as 'Serenata' (Ellis 1994), 'Rosalyne' (Khanizadeh et al. 2002), 'Roseberry' (Khanizadeh et al. 2002), 'Lipstick' (Northcrop name, verbal communications), 'Red Ruby', patented as 'Franor' (Bittner

2001), and ‘Tarpan’ (ABZSeeds 2014). I am taking advantage of this prior resource, which I have enhanced by identifying and utilizing new sources of hue variants to combine with a pink-flowered accession. Discovery of molecular marker associations for non-white (NW) versus white (W) flower color, for variant hues, and for variant fruit pigment composition will facilitate MAB of new cultivars with enhanced ornamental qualities and enhanced fruit quality. The presence of a strong ornamental industry, which is the single largest agricultural sector in NH, highlights an opportunity for developing locally adapted ornamental cultivars targeting homeowners, landscapers, and small scale producers.

Strawberry fruit and flower pigments

Cyanidin and pelargonidin are the two principle pigments in the fruit of strawberry. The absolute and relative contents of cyanidin and pelargonidin influence the hues of both flowers and fruit, with cyanidin imparting a pinkish component and pelargonidin an orange component. Cyanidin was reported to have twice the anti-oxidant potential of pelargonidin (Wang et al. 1997, Pietta 2000). Cyanidin and pelargonidin levels in strawberry fruit of various diploid and octoploid (wild and cultivated) species, and in the flowers and fruit of the F1 progeny of a pink-flowered ornamental × white flowered cultivar cross (‘Bountiful’ × ‘Pink Panda’) have been quantified (Mahoney 2007).

It had been reported that the fruit of strawberry cultivars contained low levels of cyanidin in comparison to pelargonidin (Nyman et al. 2001, Mahoney 2007, Wang et al. 2007). In contrast the fruit of an unidentified accession of diploid *F. vesca* contained equal amounts of cyanidin and pelargonidin (Sondheimer et al. 1956) and these finding are consistent with Mahoney (2007). However in a survey of wild accessions (Mahoney 2007, Mahoney et al. 2009)

identified an accession of octoploid *F. chiloensis ssp. lucida* with high fruit cyanidin content. Contrastingly, in the flowers of 'Bountiful' × 'Pink Panda' (B×PP) population segregating for NW (with hues from light to medium pink) versus W flower color¸ Mahoney (2007) found only cyanidin and no detectable levels of pelargonidin in the NW flowers. These findings led to four questions. 1) Why was there only cyanidin in the B×PP pink flowers? 2) Could a red flowered strawberry ornamental be developed and would the red flowers contain both cyanidin and pelargonidin? 3) Could the trait of high cyanidin content in the fruit be introgressed from the high cyanidin *F. chiloensis* ssp. *lucida* accession into the cultivated strawberry? 4) Could we develop markers to identify or predict the qualitative trait of color (presence/absence, where absence = white) and the quantitative trait of variable hue in relation to pigment composition?

Anthocyanin pathway

The anthocyanin pathway is controlled by structural and regulatory genes, which affect qualitative (presence/absence) and quantitative variation in color intensity and hue.

Anthocyanin biosynthesis structural genes - The basic anthocyanin biosynthetic pathway for the synthesis of cyanidin and pelargonidin in plants is well understood (Holton et al. 1995, Moss 2001), as illustrated in Figure 2.1. The pathway begins with the biosynthesis of tetrahydroxychalcone, mediated by chalcone synthase (CHS), from the condensation of a product of the phenyl-propanoid pathway, p-coumaroyl Co-A, and 3x of malonyl-CoA (Almeida et al. 2007). Tetrahydroxychalcone is then converted to naringenin by chalcone isomerase (CHI). The lack of specificity for substrates and the competition between the enzymes for common substrates results in the availability of multiple paths for the same intermediate (Holton et al. 1995). The pathway can branch three ways at naringenin to produce apigenin via flavone

synthase (FS), and/or eriodictyl via flavonoid 3'-hydroxylase (F3'H), and/or dihydrokaempferol via flavonone 3-hydroxylase (F3H). Dihydroquercetin may be produced via F3H from eriodictyl and/or from F3'H from dihydrokaempferol. Dihydroflavonol 4-reductase (DFR) reduces dihydrokaempferol to produce leucopelargonidin, and reduces dihydroquercetin to produce leucocyanidin. Flavonol synthase (FLS) oxidizes the dihydroflavonols to produce kaempferol and quercetin. The F3'H enzyme competes with DFR and FLS (Holton et al. 1995) for substrates, and kaempferol (a flavonol), naringenin (a flavanone), and epigenin (a flavone) all serve as substrates for F3'H (Moss 2001), competing with dihydroquercetin. Leucocyanidin and leucopelargonidin are both synthesized from dihydrokaempferol, but leucocyanidin can also be synthesized from dihydroquercetin. Leucocyanidin and leucopelargonidin are converted subsequently to cyanidin and pelargonidin by leucoanthocyanidin oxgenase (ANS) and/or to the proanthocyanidin pathway to produce catechin and afzelechin, respectively, by leucoanthocyanidin reductase (LAR). Cyanidin and pelargonidin may also be diverted to the proanthocyanidin pathway via anthocyanidin reductase (ANR) (Almeida et al. 2007) or to the final step of the anthocyanidin pathway where they are converted to cyanidin-3-glucoside and pelargonidin-3-glucoside during glucosylation mediated by 3-*O*-glucosyltransferase (3GT) (Pourcel et al. 2010) and transferred in the vacuoles via glutathione S-transferase (GST) (Pourcel et al. 2010).

Tetrahydroxychalcone is yellow, whereas naringenin is colorless (Holton et al. 1995). Kaempferol and quercetin act as co-pigments to intensify flower color and generally shift it towards blue (Brugliera et al. 1999). The intermediate products are colorless until the glycosylation of the anthocyanidin by 3GT to anthocyanidin 3-glucosides (Holton et al. 1995), accompanying the transfer of the anthocyanidin to the vacuole by GST (Pourcel et al. 2010).

Anthocyanin biosynthesis regulatory genes - The *r* and *c1* families of regulatory genes in maize, analogous to *an1*, *an2*, *an4* and *an11* in petunia, control the transcription of all the structural genes of the anthocyanin pathway (Quattricchio et al. 1998). The petunia *JAF13* is orthologous to the maize *r* genes, which encode bHLH (basic helix-loop-helix) proteins, and the *c* family, which encodes MYB transcription factors (Quattricchio et al. 1998). In a comparison of R2R3 MYB transcription factors in Rosaceae, Lin-Wang et al. (2010) concluded that *MYB1* and *MYB10* are alleles of each other in an apple red × white flesh segregating progeny.

Flower color - Flower color has been modified in numerous plants using traditional breeding as well as molecular approaches. The suppression of *CHS* gene expression in petunia, chrysanthemum, carnation and rose (Gutterson 1995) has resulted in white flower color. A modification of *CHS* gene expression impacted the flower color intensity in *Petunia ×hybrida* (Hanumappa1 et al. 2007), but did not produce white flowers. In petunia, high levels of cyanidin derivatives accumulate only in accessions that possess F3'H activity but that lack flavonoid 3'5'-hydroxylase (F3'5'H) (not shown in Figure 2.1) and FLS activity (Holton et al. 1995). The *F3'H* transgene was introduced into a homozygous recessive petunia with pale lilac flowers which resulted in a F3'H transgenic line of petunia with highly pigmented pink flowers and anthers (Brugliera et al. 1999). Of regulatory gene products, transcription factors such as bHLH alone or in combination with MYB transcription factors have been found to control pigmentation in flowers (Quattricchio et al. 1998).

Strawberry anthocyanin genes

Although the anthocyanin biosynthetic pathway has been described in generalized form (Figure 2.1), in strawberry its specific details continue to be refined (Halbwirth et al. 2006, Almeida et al. 2007).

Gene characterization in *Fragaria ×ananassa* – Gene names in *Fragaria ×ananassa* are prefixed with '*Fa*'. All of the pathway structural genes including *FaCHS1*, *FaCHS2*, *FaCHS3*, *FaCHS5*, *FaCHI*, *FaANS*, *FaANR*, *FaDFR*, *FaLAR*, *FaFGT* (aka *3GT*), *FaFHT* (*F3H*), and *FaFLS* have been sequenced and the relative transcriptional activities of each have been characterized and compared in roots, leaves, flower petals and ripening fruit of 'Queen Elisa' and 'Korona' (Almeida et al. 2007). *CHI*, *CHS*, and *ANS* gene sequences have also been isolated from 'Elsanta' as cDNA (Aharoni et al. 2002), *DFR* from 'Chandler' (Moyano et al. 1998), and *FaGT1*, *UFGT* (*FaGT1* through *FaGt7*) from 'Elsanta' (Griesser et al. 2008). In addition, phenyl-propanoid pathway genes (*FaPAL*, *FaC4H*, and *Fa4CL*) have been sequenced and their transcriptional activities have been similarly characterized (Almeida et al. 2007). The regulatory transcription factor *FaMYB1* has been sequenced from *F.* × *ananassa* 'Elsanta' and characterized in strawberry, as well as in tobacco and yeast using transformants (Aharoni et al. 2001).

Gene characterization in *Fragaria chiloensis* –Transcriptional activity levels of white-fruited *F. chiloensis* ssp. *chiloensis* structural genes of the phenyl propanoid pathway (*PAL*, *C4H*, *4CL*) and the anthocyanidin pathway (*CHS1*,*CHS2*,*CHS3*, *CHS5*, *CHI*, *F3H*, *DFR*, *ANS*, *FGT* (aka *3GT*), and one regulatory gene (*MYB1*) were compared to their counterparts in *F.* ×*ananassa* 'Chandler'(Saud et al. 2009). Transcript levels in the ripening strawberry fruit were generally lower in the white-fruited *F. chiloensis* compared to *F.* × *ananassa* (Saud et al.

2009). Transcript levels of *CHS2, CHS3, CHI, F3H,* and *FGT* were minimally expressed in *F. chiloensis* (Saud et al. 2009). A similar comparison of transcript levels of structural genes (*PAL, C4H, 4CL, CHS, CHI, F3H, DFR, ANS, UFGT, FLS, LAR, ANR*) was made on ripening fruit of *F. chiloensis* ssp. *patagonica* (red fruited) to white-fruited *F. chiloensis* ssp. *chiloensis* (Moyano et al. 1998). Transcript levels of anthocyanidin pathway structural genes were generally higher in the ripening fruit of *F. chiloensis* ssp. *patagonica* particularly at the ripe stage (Moyano et al. 1998). Transcript levels of the phenyl-propanoid pathway (*PAL, C4H, 4CL*) gene generally tracked together downward with degree of ripening (Moyano et al. 1998).

FcMYB1, an F. chiloensis ortholog of *FaMYB1,* was isolated from white fruited *F. chiloensis* ssp. *chiloensis* and its impact on the activity of structural genes *F3H, DFR, ANS, UFGT* (aka *3GT*), *LAR,* and *ANR* were determined. The transient suppression of *FcMYB1* using RNAi caused a slight reddening of the fruit and a most significant down regulation of *LAR* and *ANR* gene expression.

Gene characterization in diploid strawberry - Intron-containing segments of anthocyanin pathway genes *CHS, CHI, F3H, DFR,* and *ANS* and *RAN* (a *Del*-like regulatory gene) were cloned from *F. vesca* and sequenced (Deng et al. 2001) and the complete sequence of *F3'H* was cloned from *F. vesca* ssp. *americana* (Mahoney unpublished). Subsequently, the complete sequences of these genes have been revealed in the *F. vesca* 'Hawaii 4' reference genome (Shulaev et al. 2011).

In *F. vesca*, there are yellow and red fruited accessions and varieties. In two F2 mapping populations *F. vesca* × *F. vesca* (DN1C × YW) and *F. vesca* × *F. nubicola* (YW x FRA520) (Deng et al. 2001), which were segregating for red versus yellow fruit, anthocyanin candidate genes were mapped in an effort to identify a gene-trait association between an anthocyanin

pathway structural or regulatory gene and the color locus (*c*). Co-segregation without recombination between the *c* locus and the *F3H* gene was reported (Deng and Davis, 2001), suggesting that a mutation in the *F3H* gene was responsible for the yellow fruit trait. More recently, recombination between the *c* locus and the *F3H* gene on LG1 was detected (Shields and Davis unpublished), undermining the hypothesis of identity between *c* locus and *F3H.*

Segregating populations for flower color and fruit quality have been developed with the objectives of 1) understanding the genetic control of cyanidin and pelargonidin pigment levels in flowers and fruits, and 2) developing cultivars adapted to the Northeast region for the ornamental market. A pedigreed 'Select Set' of 41 members was chosen to include the three parental founders and a sampling of floral NW and W members and the spectrum of fruit pigment composition from each of the four generations. The NW members were chosen to represent the diversity of flower color and hue (variant colors and color patterns). The 'Select Set' of 41 individuals was genotyped on the Phase 1 test of the IStraw90 Axiom Array (Bassil et al. manuscript submitted). Long-term goals are to advance MAB and to introduce NW flower color and desirable flower hues and fruit pigment composition traits into cultivated strawberry backgrounds in order to develop a marketable collection of day-neutral cultivars with a palette of flower hues and desirable fruit size and quality. Herein, is described the first study of marker-trait association for flower color in strawberry.

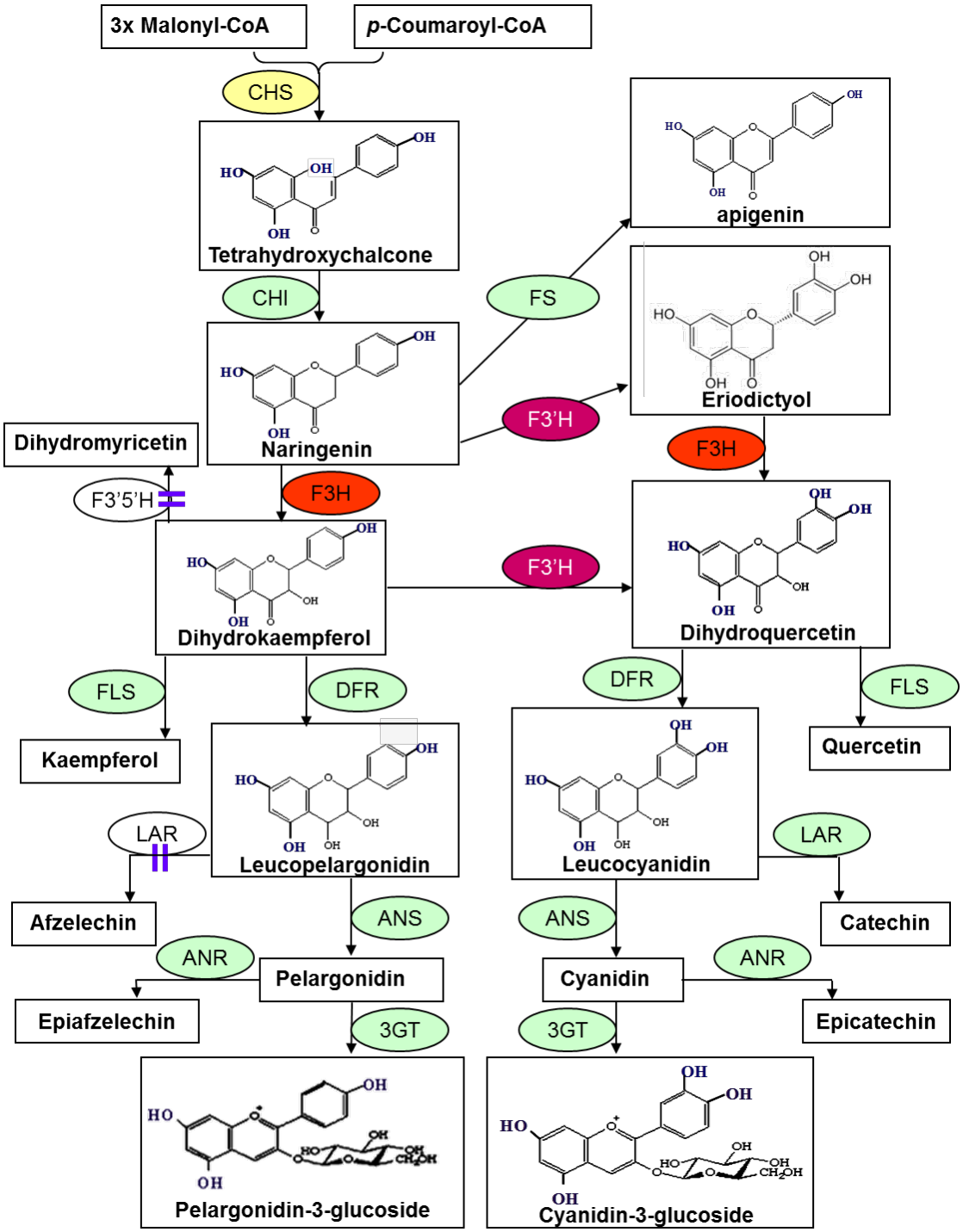


Figure 2.1: Anthocyanin biosynthetic pathway. Enzyme abbreviations: CHS (chalcone synthase); CHI (chalcone isomerase); FS (flavone synthase); F3H (flavonone 3-hydroxylase); FLS (flavonol synthase); F3'H (flavonoid 3'-hydroxylase); DFR (dihydroflavonol 4-reductase); LAR (leuco-anthocyanidin 4-reductase); ANR (anthocyanidin reductase); ANS (leucoanthocyanidin oxygenase); 3GT (anthocyanidin 3-*O*-glucosyltransferase).

Materials and Methods

Plant Materials

Three population founders, FC1, FC2, and FC3 were selected as crossing parents based upon their desirable traits. Founder FC1, an accession of *F. chiloensis* ssp. *lucida*, has W flowers and is the source of genes influencing the hue and cyanidin composition of fruit (Mahoney 2007, Mahoney et al. 2009). FC2, an *F.* ×*ananassa* derivative, presumably of 'Pink Panda', with pink-flowers, is the source of the genetic determinant(s) for NW flower color. FC3, an accession of *F. virginiana* ssp. *glauca*, has W flowers and is the source conferring day-neutrality. FC1 was obtained from the NCGR germplasm collection, while FC2 and FC3 were collected by Tom Davis in 2001, from cultivated and wild locations, respectively, near Prince George, British Columbia. The three founders were used to generate the Closed Pedigree Set consisting of four generations. Select individual members of the Closed Pedigree Set based on flower color were crossed with cultivars in phase 2 to generate hybrids with desirable color and fruit quality. Breeding lines were intercrossed towards the goal of increasing cyanidin content in the fruit.

Generating hybrids

Making a cross – A flower on a plant to serve as the female (i.e., pollen recipient) was selected just before anthesis, at the bud stage but just before opening. A flower on a plant to serve as the male (i.e., the pollen donor or pollen parent) was selected at anthesis when the anthers were bursting with pollen, optimally in late morning on a sunny day. The recipient flower was emasculated, and the pollen-bearing anthers from the pollen parent flower were

brushed onto the recipient flower. The pollinated recipient flower was tagged and isolated with a small polyester mesh bag tightened with a draw-ribbon around the pedicel to prevent chance extraneous pollination by visiting insects.

Harvesting and storing achenes - The fruit were harvested approximately 30-50 days post pollination, depending on the season. For harvesting of achenes, a fruit was cut open, the flesh was carved-out, and the fruit exterior was pressed epidermis side up onto recycled non-craft paper and allowed to dry for a few days. The achenes were harvested by rubbing them off the paper and cleaning off debris by manually vibrating the seeds on a clean sheet of paper. The harvested seeds were stored in small envelopes within a zip-lock bag or plastic box and refrigerated at 4 C.

Seed propagation with potting media – Achenes/seeds selected for planting were refrigerated for a minimum of 2 weeks, providing a measure of vernalization in the event that some of the seeds might not germinate at all or not very well without such treatment.

The procedure that follows was intended to disinfect achenes from pests or microbes. The seed starting mix was moistened and placed in an autoclave tray and covered with foil and autoclaved using liquid autoclave settings. The cleaned seeds were placed in labeled 1.5 ml micro-centrifuge tubes, then soaked for 10 minutes with 200 ml of aqueous using Tween 80 at 0.05%. The 0.05% Tween 80 solution was removed. The seeds were then sanitized by adding 200 µl of 30% bleach solution (Chlorox liquid bleach, 5.25% sodium hypochlorite) to each tube and agitated for 10 minutes at 30-50C. The bleach solution was removed and the seeds were rinsed three times with dH2O, again 200 µl each time. The last rinse was used to remove the seeds from the tubes, by mixing to suspend seeds and dumping the contents onto a paper towel.

The seeds were planted in the seed-starting mix in seedling trays or 4" pots and covered with fine-powdered sterile peat-moss to prevent damping off.

The seeds were then germinated using one of two options under grow-lights or in the greenhouse: Under the grow lights option, the seedling trays or pots were covered with a clear slotted (for ventilation) plastic cover. At 7-10 days post-planting, the cover was taken off and grow lights were turned on for a daily photoperiod of 16 hours. The mix was sprinkled with a little more peat moss periodically. With the greenhouse option, the seedling trays or pots were placed under mist on the greenhouse mist bench and regularly checked for germination. Once seedlings were established, the pots were removed from the mist bed but maintained elsewhere in the misted greenhouse until ready to transplant.

DNA isolation

One sample containing three furled leaves of approximately 50-100 mg fresh weight from each individual were freeze-dried and shipped to N. Bassil group at the National Germplasm Repository, where the DNA was isolated using the E-Z® 96 Plant DNA kit (Omega bio-tek, Inc) following (Gilmore et al. 2011); the same protocol as was followed for *F. iinumae* as described in detail in Chapter I.

Phenotyping for presence/absence of flower color

The presence or absence of flower color (pigmentation), a qualitative trait, was determined visually and was classified as NW or W. To be categorized as W, the flower petals had to be entirely white. For example, a flower with otherwise white petals but with colored rays or venations was considered NW.

Phenotyping for flower and fruit pigmentation

The phenotyping of flower and fruit pigment composition was performed by High Performance Liquid Chromatography (HPLC) for contents of pelargonidin and cyanidin. The preparation of the fruit for analysis, and the HPLC analysis itself were performed following a previously developed protocol (Mahoney 2007, Mahoney et al. 2009). The protocol reported below is reproduced verbatim from (Mahoney 2007) with only minor edits for clarification and with the following exceptions: 1) the fruit was frozen at -20C and was not lyophilized; instead a wedge of fruit sample was cut and weighed. Upon addition of the 7 ml of 2N HCl, the samples was vortexed until homogenized; and 2) 'Earliglow' instead of 'Jewel' was used as an external standard. The assay of flowers was performed using 0.2 g fresh petals and using 5 ml instead of 7 ml of 2N HCl for hydrolysis. The moisture content of the petals was assumed to be comparable to that of rose, at 65% (Schmitzer et al. 2010). The protocol for the sample preparation and HPLC analysis reproduced verbatim from Mahoney (2007) is as follows:

> Fruit sample preparation for anthocyanidin assay - hydrolysis of anthocyanins (Mahoney 2007). The fruit was pulverized (Wang et al. 2003) to achieve a uniform composite sample. The acid hydrolysis process was performed using aqueous 2N HCl (Durst et al. 2001), as opposed to the use of 2N HCl in methanol (Nyman et al. 2001), to avoid use of highly hazardous methanol at elevated temperatures and in proximity to non-explosion proof electrical devices. Each 0.5 g sample of lyophilized strawberry fruit was mixed with 7 ml of 2N HCl in a 15 ml polypropylene centrifuge tube (VWR SuperClear™ Catalog #21008), hydrolyzed at 90^{o}C for 50 minutes (Nyman et al. 2001) in a Nitrogen Evaporator™ 111 (Organomation Associates, Inc) used as a hot water bath, and then cooled in a separate cold tap-water bath for 5 minutes. The hydrolyzed samples were spun for 20 minutes in an Eppendorf 5804R centrifuge at 15,500 xg and 4^{o}C. The centrifuged samples were filtered, using syringe-adapted filter housings with F6801 Sigma-Aldrich 100 µm mesh nylon fabric, to recover the liquid extract containing the anthocyanidins.
>
> Extraction of anthocyanidins (Mahoney 2007) - The procedure used to extract the anthocyanidins was patterned after those previously described (Rodriguez-Saona et al. 2001, Wang et al. 2003, Wang et al. 2003), with modifications as indicated below. Sep-Pak® C18 cartridges (Waters Corp, Ireland) were activated with 2 ml of 0.01% HCl in methanol, but the additional rinses of deionized water (Rodriguez-

Saona et al. 2001, Wang et al. 2003) or formic acid (aqueous) (Wang et al. 2003) were not employed. Each supernatant sample was poured into a Sep-Pak® C18 cartridge to bind the anthocyanidins, then the sugars and starches were eluted with 10 ml of 3% formic acid (aqueous). The anthocyanidins and other phenolic compounds were recovered from the C18 Sep-Pak® cartridges with 2.5 ml acidified methanol containing 0.01% HCl (Rodriguez-Saona et al. 2001).

The recovered anthocyanidins were then filtered with a 0.2 µm syringe filter, in lieu of the 0.45 µm filter (Wang et al. 2003), to prolong the life of the HPLC separation column. Sample aliquot volumes of 750 µl were transferred to 1.5 ml HPLC vials for analysis. In order to minimize decomposition of the anthocyanidins, the processed samples were immediately analyzed by HPLC, or held in a -20°C freezer before warming to room temperature for 15 to 20 minutes before analysis by HPLC. The purified samples were stored at -80°C according to Rodriguez-Saona and Wrolstad (2001), who recommended storage of purified samples at less than -15°C, preferably less at -70°C.

Preparation of anthocyanidin standard solutions (Mahoney 2007) – "Standard solutions needed for calibration of the HPLC for assays were prepared from concentrated master stock solutions. The master solutions were prepared by dissolving certified HPLC grade powder standards (Indofine Chemicals, Hillsborough NJ) of pelargonidin chloride and cyanidin chloride in acidified methanol (0.01% HCl) to make master solutions. The master solutions were made at a concentration of 1000 µg/g in acidified methanol as follows: the powder standards were weighed (scale accuracy of four decimal places) and then the required amount of acidified methanol was used to police the powder standard into a dark colored vial. The required amount of acidified methanol was determined as follows:

$$\text{Y mls of methanol} = \frac{\text{X gms of powder standard} \times \text{purity of standard}}{(\text{density of methanol} \times 1000\ \mu g/g)}$$

The purity of the powder standards was obtained from the certificates of analysis (COA): Pelargonidin COA = 0.998; Cyanidin COA = 0.972. The density of methanol (0.7875 g/ml) was obtained from the manufacturer's technical data sheet.

Standard solutions with concentrations of 10, 50, 90, 100, and 150 µg/g of cyanidin and pelargonidin chloride were each made directly from the master solutions For instance, to make a standard solution concentration of 10 µg/g of acidified methanol, 10 µl of the master batch was added to 990 µl of acidified methanol. Aliquots of the standard solutions were stored at -20°C.

Using freshly made standards, the HPLC was calibrated to develop a calibration curve for 5 µl sample injections. Aliquots of anthocyanidin extract of cultivar 'Jewel' fruit, prepared as described earlier and stored at -80°C, were used as an external standard for all assays in Phase 3, to assure run-to-run repeatability. Cyanidin and pelargonidin were identified by comparing the retention times of the standards with those of the strawberry fruit extract.

High Performance Liquid Chromatography method (Mahoney 2007) – The separation and quantification of cyanidin and pelargonidin were conducted following a modified protocol (Miyazawa et al. 1999) with a Hewlett Packard Series 1100

HPLC equipped with a Diode Array Detector. A reverse-phase Nova-Pak®C18 column 150 x 3.9 mm with 4µm particle size equipped with a Nova-Pak®C18 20 x 3.9 mm guard column (Waters Corp, Ireland) (Wang et al. 2003) was used for the separation of cyanidin and pelargonidin. Due to its smaller size (lower cost) and corresponding lower chemical and sample volume requirements, this configuration was preferred to a commonly used reverse-phase C18 250 x 4.6 mm ODS (Miyazawa et al. 1999, Durst et al. 2001).

The photodiode array was set to scan the range of 240 to 570 nm with detection at 320, 350 and 528 nm, similar to Wang et al. (2003), whose scan was set at 240 to 550 nm with detection at 320, 350 and 510 nm, as compared with single point detection at 520 nm (Durst et al. 2001), or 532 nm (Miyazawa et al. 1999)

The temperature of the columns was maintained at 30^{o}C to operate above fluctuations in the room temperature which might impact results, in contrast to the use of ambient temperature (Durst et al. 2001), 20^{o}C (Wang et al. 2003), or 40^{o}C (Miyazawa et al. 1999). Cooling the column was not an option with the utilized HPLC system.

The solvents chosen for mobile phases A and B were formic acid (aqueous) and 100% methanol, respectively, (Miyazawa et al. 1999), in contrast to Wang et al.(2003) mobile phases A 2.5% formic acid (aq) and B (acetonitrile) or mobile phases A (acetonitrile) and B (10% acetic acid, 5% acetonitrile, and 1% phosphoric acid) (Durst et al. 2001) to coincide with the chemicals used in the sample preparation and thus minimize the variety of chemicals required.

The mobile phase A concentration of formic acid was reduced to 0.3% v/v from 6.9% v/v (1.5 molar)(Miyazawa et al. 1999) or from 2.5% v/v (Wang et al. 2003) in order to minimize corrosion of the HPLC plumbing system and to extend the life of the column, as well as to minimize use of chemicals, while maintaining an acidic pH for pigment stability and maximum absorption (Cabrita et al. 2000). The mobile phase B methanol was diluted to 95% v/v to reduce gas bubbles in the column at the point of mixing of the two mobile phases.

Isocratic elution as opposed to gradient elution was chosen to maintain steady state and thus minimize the run cycle time to 15 minutes. The mobile phases were optimized to 52% as mobile phase A (0.3% formic acid) and 48% as mobile phase B (95% methanol) in contrast to (Miyazawa et al. 1999) compositions of 14% A containing 1.5 mol/l (6.9%) formic acid and 86% B (100% methanol) and in contrast to gradient elution and alternative mobile phase solvents as described above (Wang et al. 2003). The mobile phase total flow was reduced to 0.7 from 1.5 ml/min (Miyazawa et al. 1999) based on the smaller column size and from 1.0 ml/min (Wang et al. 2003) based on sample peak shape. The initial volume of the sample injection was 20 µl (Phase 1) in accordance with Wang et al.(2003) much less than the 50 µl used by Durst and Wrolstad (2001) or 100 µl by Miyazawa et al.(1999). The volume of the sample injections was later optimized to 5 µl (Phases 2 and 3) to reduce the load on the columns, with the intent of reducing the potential for overload and improve peak shape.

A volume of 5 µl of the prepared anthocyanidin samples, were auto-injected into an isocratic 0.7 ml/min elution stream containing 52% mobile phase A (0.3% formic acid) and 48% mobile phase B (95% methanol).

Genotyping

The SNPs were genotyped (Bassil et al. manuscript submitted) using Affymetrix GTC and SNPolisher bioinformatics software. The quality of the genotyping results relied on categorization of cluster plots according to the Affymetrix rating system. The genotype calls for each marker was represented as a cluster plot and the quality of the plots was categorized into six classes (Chapter I, Figure 1.5) as follows. 1) In the highest quality class, the *Poly High Resolution* (*PHR*) *class,* cluster plots are required to contain no more than three highly distinct clusters, including both of the expected homozygous genotyping clusters. 2) The *Call Rate Below Threshold* (*CRBT*) class contains both of the expected homozygous genotyping clusters, but is considered lower quality because of dispersed sample points within clusters. 3) In the *Mono High Resolution* (*MHR*) class, there are less than two occurrences of the minor allele. 4) The *No Minor Homozygous* (*NMH*) class displays only two clusters and lacks one of the expected homozygous clusters. 5) The *Other* (*Oth*) class has distinct clusters but they are shifted off center and/or the individual samples dots within the three cluster plots are dispersed. 6) In the *Off-Target Variant* (*OTV*) class, the cluster plot displays a fourth, vertically displaced cluster that precludes confident genotype calling. In addition, a seventh group of genotyping results for mSNPs (designed to reduce complexity in the octoploid germplasm) were provided but these were not classified, and these are grouped as *Not Classified* (*NOCLS*).

Pedigree based marker-trait analysis

In order to be used for pedigree analysis, the SNPs had to be qualified as concordant in the pedigree for each family and generation using the same methodology as used in Chapter I for the mapping population and founding parents. The pedigree with flower color information was

displayed using Pedimap (Voorrips et al. 2012). The genotypic calls of the NW and W progeny were compared to each other and to the three founders, FC1, FC2 and FC3 to identify an association between the NW phenotype and genotype. A marker-trait association was identified as a consistent pattern of alternate genotypes of W colored flowers from the genotypes of NW flowers across the four generations. Specifically to be considered a marker-trait association, the genotyping pattern would be as follows: 1) both W founders (FC1 and FC3) and all of the W progeny would have the same genotype; 2) the NW founder (FC2) and all of the NW progeny would have the same genotype; and 3) the NW and W would not have the same genotype.

Comparison to FvH4

The sequences of genes identified as related to the anthocyanin pathway were obtained from various sources as cited in the introduction. Using the deposited sequence accession identification number, the sequence fasta file was obtained from either NCBI blastx (Altschul et al. 1997) at http://www.ncbi.nlm.nih.gov or EMBL_EBI at http://www.ebi.ac.uk. The sequences were then subjected to Blastn searches on GDR NCBI blast (Jung et al. 2013) at http://www.rosaceae.org to obtain the location on FvH4 v1.1. The GeneMark ID was obtained on GBrowse (Jung et al. 2013) by zooming on the FvH4 v1.1 PC and base-pair location.

Results

Population development

Population development through crossing and selections was partitioned into two distinct phases. Phase 1 has generated over 1000 progeny plants from crosses involving wild germplasm and one cultivated variety, FC2, which was the source of the NW trait. Within Phase 1, the 455-member Closed Pedigree Set, was derived exclusively from FC1, FC2, and FC3 (Figure 2.2). The Closed Pedigree Set included the 41 members of the 'Select Set' chosen for genotyping on the Array. Phase 2 involved crosses between selected individuals from Phase 1 and some commercial cultivars.

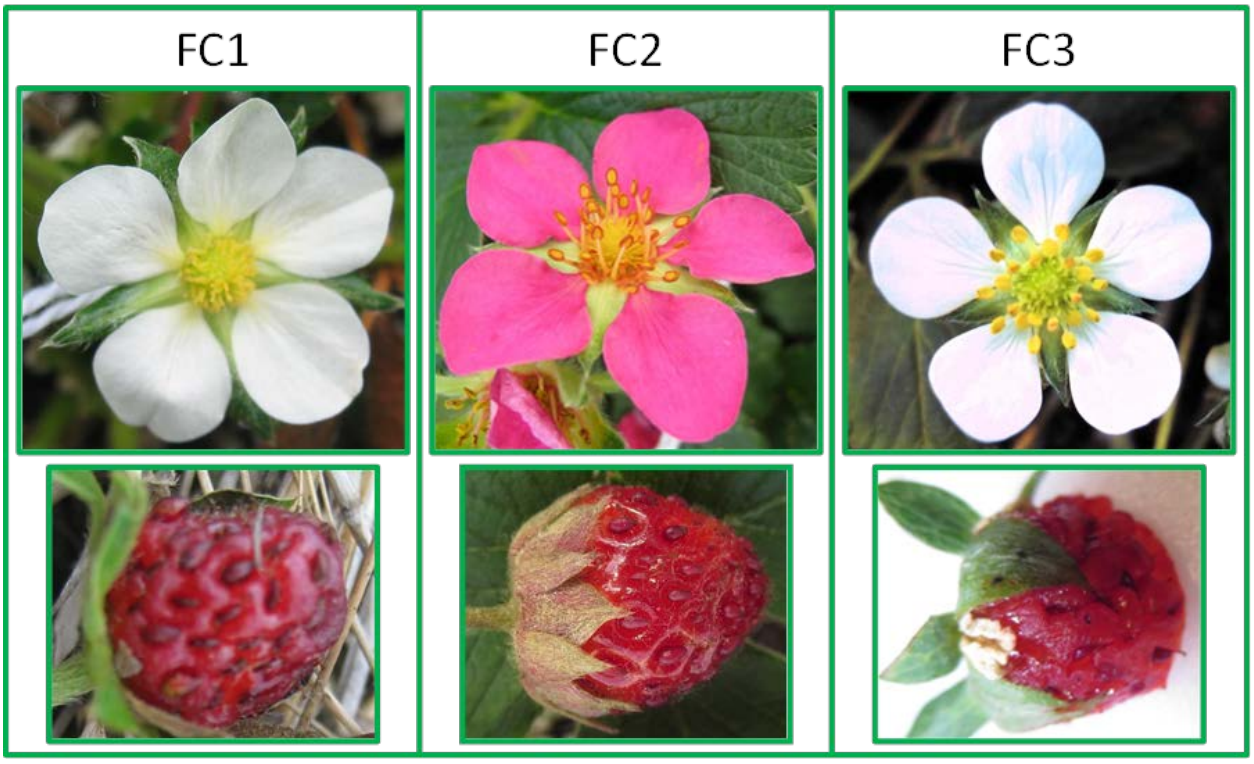


Figure 2.2: Founders of the Closed Pedigree Set. The photos display typical flowers and fruit from each of the three founders: FC1, FC2, and FC3.

Phase 1 – The Closed Pedigree Set (Figure 2.3) encompassed four generations and 18 progeny families. The Closed Pedigree Set is segregating for numerous traits in addition to NW versus W flower color, and include floral hue, sex (female versus hermaphrodite), flowering habit (day-neutral versus short day), and aspects of fruit quality. The families of the Closed Pedigree Set averaged N = 25 in size, with a range of N = 6 to 100 (Table 2.2 and Figure 2.3). Overall, the percentage of NW members increased with each generation, ranging from 13 to 17% in the second generation and from 56 to 100% in the fourth generation. In NW × W crosses, the percentage of NW progeny ranged from 13 to 17% in the second generation, and from 42 to 100% in the fourth generation. In NW × NW crosses, the percentage of NW progeny ranged from 71 to 72% in the third generation, and from 56% to 100% in the fourth generation. Crosses between two W members resulted in only W progeny. In some progeny families, and particularly in the self of LMJ6, some members have never been observed to flower, and therefore their floral characteristics are unknown. The families also segregated for a rainbow of hues starting in the second generation, with the first incidence of red flower color occurring in the third generation.

Phase 2 – In Phase 2, selected members of Phase 1 families were crossed with various cultivars, and among the progeny were hybrids with desirable flower hues and fruit quality. So far, particular attention has been given to one promising Phase 2 family. The LM49 family (N=93) derived from Cavendish × LMJ6 (third generation selection from Closed Pedigree Set) had 47% NW progeny. This family is typified by a broad range of flower hues and attractive and flavorful fruit. Members of the LM49 family have been selected by Pleasant View Gardens for evaluation. Phase 2 is ongoing, and its full description goes beyond the scope of this thesis.

Table 2.2: Phase 1 segregation for flower color and hue. The columns (left to right) report generation (Gen) number, the family name (Name), the counts of members with the flower hues according to the color code below, NW versus W versus unknown (Unk) flower color, and the family size (FamSize) are provided. The hues are as follows:

White Scrlt SlPk DSlPk Red Pk LPk Dpk Fush Lav LCor Cor Unk

Family		Parents				Progeny Count														Family	
		Parents		Flower Color		Flower Hues											Flower Color				
Gen	Name	Female	Male	Female	Male	Scrlt	SlPk	DSlPk	Red	Pk	LPk	Dpk	Fush	Lav	LCor	Cor	NW	W	Unk	Size	%NW
2	LMA	FC3	FC2	W	NW	0	3	0	0	0	0	0	0	0	0	0	3	15	3	21	17%
2	LMB	FC1	FC2	W	NW	0	0	0	0	2	0	0	0	2	0	0	4	26	4	34	13%
3	LMG	LMB1	LMB2	NW	W	0	2	0	3	2	0	0	0	0	0	1	8	17	0	25	32%
3	LMS	LMA1	LMB22	NW	W	0	0	0	1	4	0	1	0	0	0	0	6	12	0	18	33%
4	LM51	LMJ6	LMJ9	NW	W	1	1	0	2	13	0	3	1	0	0	0	21	29	1	51	42%
4	LM36	LMJ6	LMI9	NW	W	2	1	1	0	3	0	0	0	0	0	0	7	1	0	8	88%
4	LM30	LMJ6	LMI10	NW	W	0	5	4	3	3	1	1	0	0	0	0	17	0	1	18	100%
3	LMJ	LMB1	LMA1	NW	NW	0	6	4	3	1	0	1	0	3	0	0	18	7	2	27	72%
3	LMH	LMB1	FC2	NW	NW	0	1	0	0	5	1	0	2	1	0	0	10	4	1	15	71%
3	LMT	LMB3	LMA1	NW	NW	1	2	0	0	0	5	0	0	0	0	0	8	1	0	9	89%
4	LM128	LMJ6	LMJ6	NW	NW	0	0	0	3	1	0	0	1	0	0	0	5	4	9	18	56%
4	LM18	LMJ7	LMA1	NW	NW	0	0	0	0	4	1	2	0	0	0	0	7	5	0	12	58%
4	LM9	LMG16	LMJ6	NW	NW	0	3	1	0	0	0	0	0	1	1	0	6	2	0	8	75%
4	LM12	LMJ6	LMG16	NW	NW	3	2	9	11	3	0	7	0	2	2	0	39	2	0	41	95%
4	LM69	LMJ12	LMJ6	NW	NW	4	0	0	2	0	0	2	0	2	1	0	11	0	0	11	100%
2	LM107	FC1	FC3	W	W	0	0	0	0	0	0	0	0	0	0	0	0	100	0	100	0%
3	LMI	LMB22	LMB22	W	W	0	0	0	0	0	0	0	0	0	0	0	0	30	0	30	0%
3	LMK	FC1	LMB2	W	W	0	0	0	0	0	0	0	0	0	0	0	0	6	0	6	0%
	Total					11	26	19	28	41	8	17	4	11	4	1	170	261	21	452	

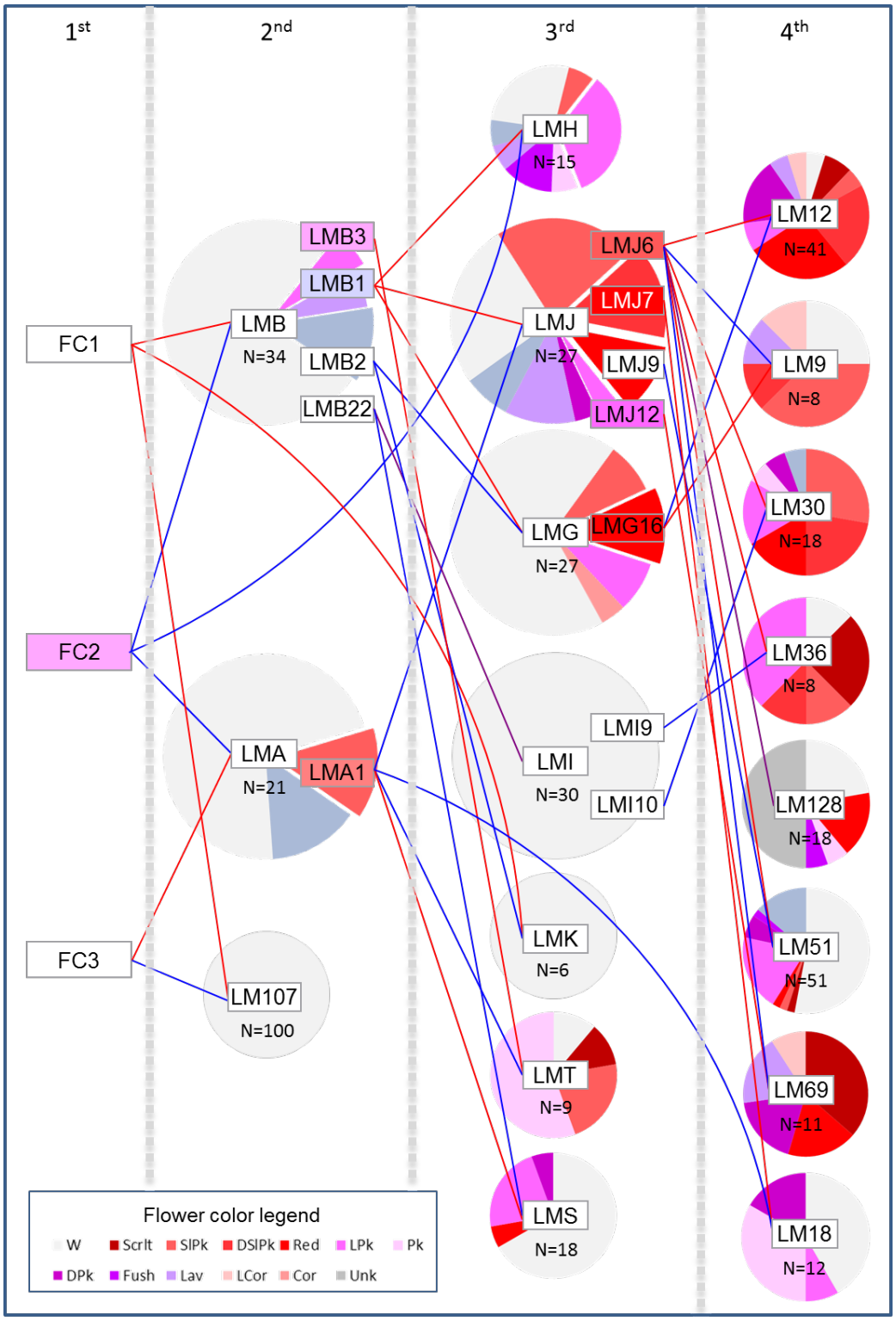


Figure 2.3: Flower colors in the four generation Closed Pedigree Set. The pie-charts represent the distribution of W and NW members by hue within families, by generation (left to right). N = number of individuals per family. The female parent is connected to its progeny with a red line, while the male parent is connected with a blue line.

The Closed Pedigree Set provides a diverse germplasm resource for advancement of marker-assisted strawberry breeding, and is being used in Phase 2 of my program to develop hybrids with desirable flower colors, flowering habits, and favorable fruit shape, size and quality.

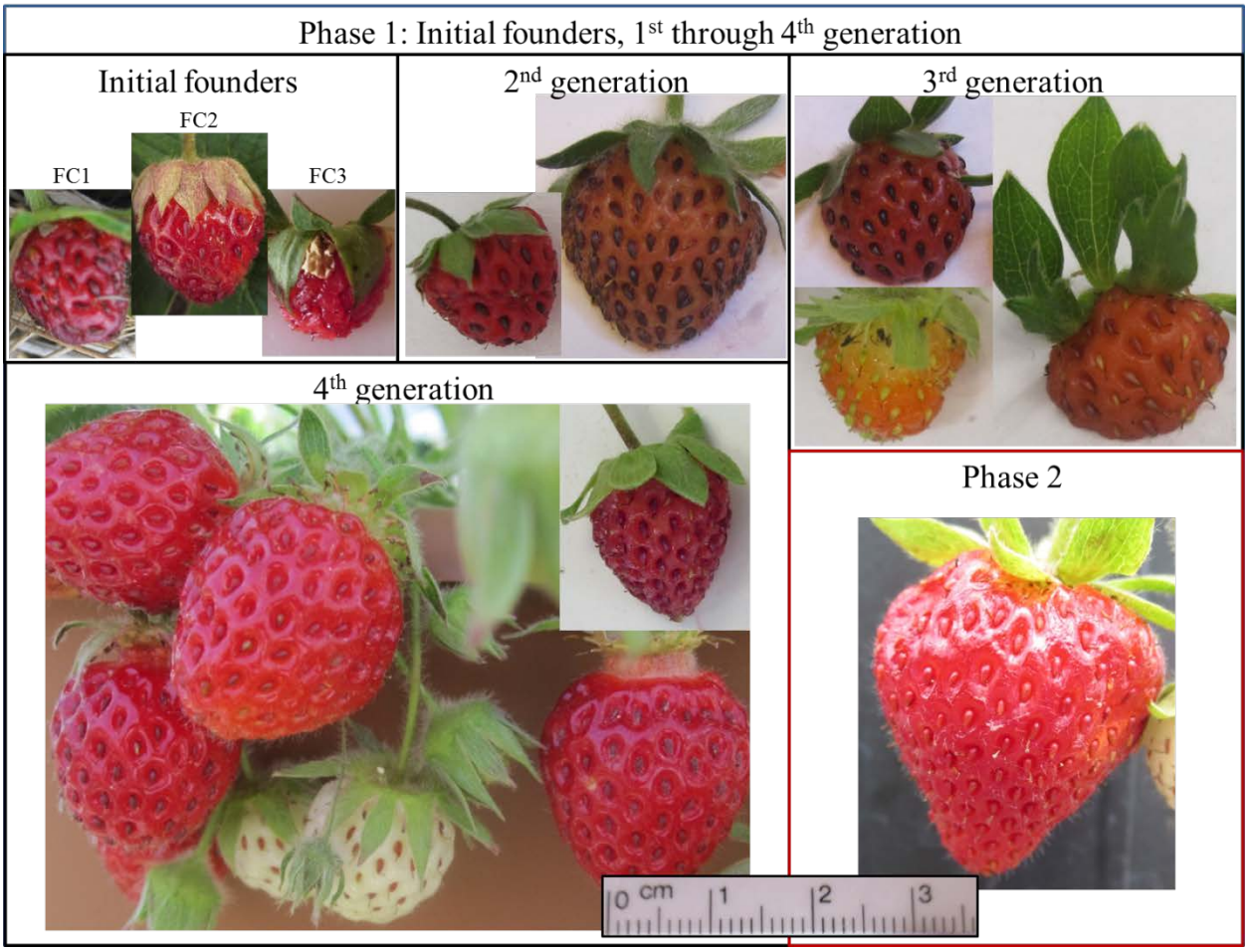


Figure 2.4: Fruit quality improvements under selection. These photos display visually proportional variation in fruit shape and size. The sizes are according to the displayed scale in cm. The fruit size in the first three generations of Phase 1 was very small, while in the fourth generation there were instances of attractive and reasonably good-sized fruit. At the lower right, a fruit from a selected, red-flowered LM49 (Phase 2) family member is shown, depicting the gain in fruit size in combination with desirable flower hue.

Phenotyping – Flower color and pigment composition

Presence/absence of flower color – In general, flowering plants displayed either NW or W flower color (as in Figure 2.2) and could be unambiguously categorized as such. However, there were also numerous examples of irregular flower color patterns on plants with otherwise uniformly pigmented flower petals, including bicolored petals and flowers (Figure 2.5). The occurrence of 'twin spots', which consist of paired white and highly pigmented streaks and spots (panel c of Figure 2.5) is particularly noteworthy as will be discussed later. In one instance half of a flower was white with yellow anthers, and other half was red with red anthers (panel h of Figure 2.5).

The hues of NW flowers – NW flower hue displayed a pattern of continuous (i.e., quantitative) variation in the Closed Pedigree Set. The NW flowers (Figure 2.6) had variant shades of color, and variable color patterns such as darker rays, venations (panel h of Figure 2.6) or margins (panel b of Figure 2.6). The colors and color patterns of anthers were also variable among plants (Figure 2.6). Flowers of some plants have vestigial anthers or lack anthers entirely, thereby influencing the overall appearance and color pattern of the flower (Figure 2.6).

Cyanidin and pelargonidin contents of flowers – Floral cyanidin and pelargonidin contents were determined in 31 NW plants of the Closed Pedigree Set, including 27 from the Select Set. Four of the NW Select Set members were not flowering during the course of pigment analysis and could not be assayed. For comparison, one W-flowered member of the Select Set was also assayed. Flower petals that were entirely white had no detectable cyanidin or pelargonidin.

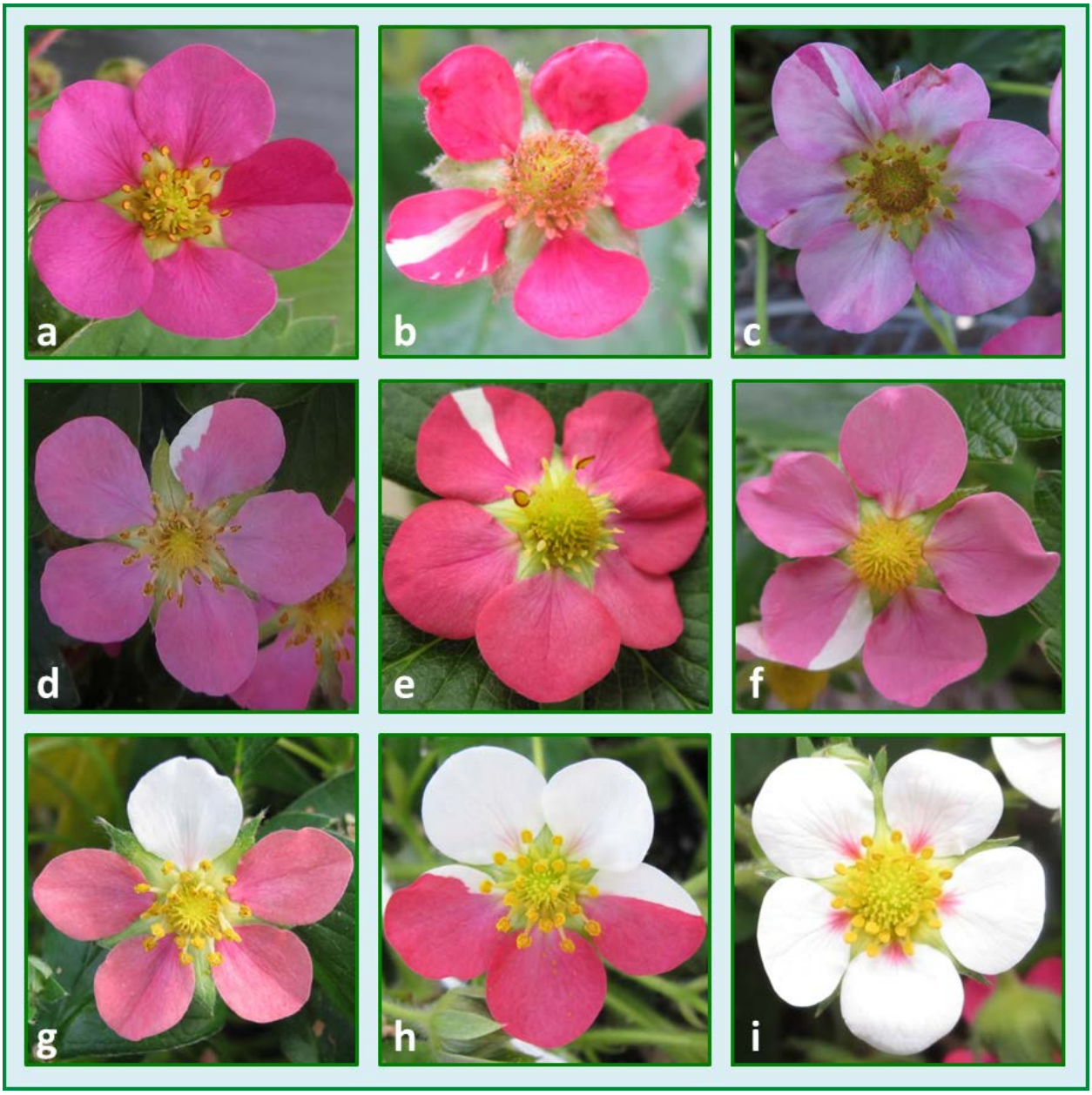


Figure 2.5: Sampling of flowers with unusual color patterns. These flowers were on plants with otherwise uniformly pigmented NW flowers. The flower shown in panel i was part of an inflorescence upon which all flowers had pink axial rays, while the rest of the plant had red flowers. In panel c, the flower has an apparent "twin spot" phenotype. Other flowers display various mosaic forms.

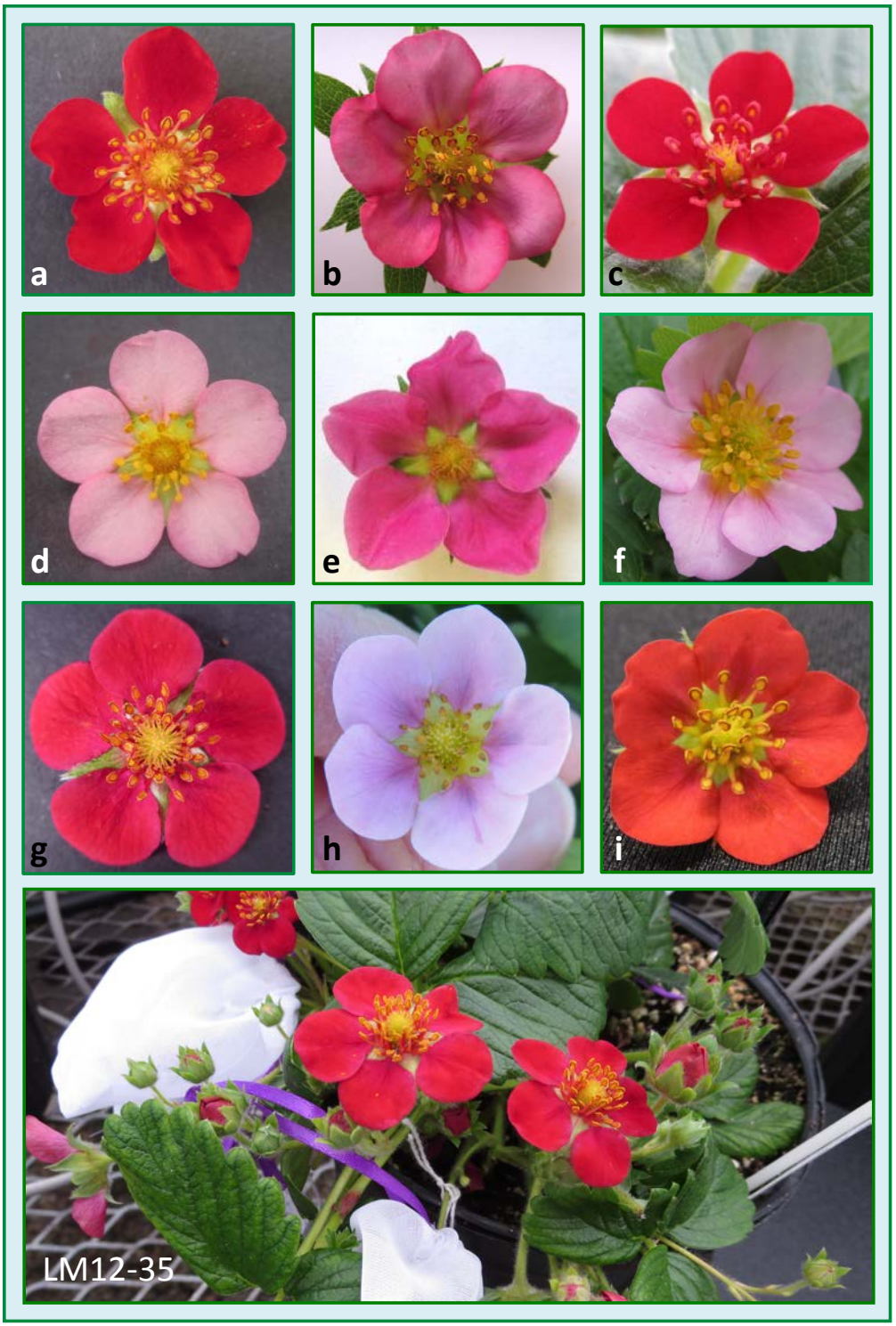


Figure 2.6: A sampling of the hues of NW flowers. The flower pictures display a sampling of the diversity of flower hues in Phase 1 and Phase 2 members. The pictures also show a diversity of anther presence/absence, and anther colors and color patterns. LM12-35, the member with the highest floral content of cyanidin and pelargonidin is shown in the bottom photo. The white mesh bags are enclosing a flower bud which has been emasculated and pollinated.

The variation in cyanidin and pelargonidin contents for the NW flowers Closed Pedigree Set is shown in Table 2.3 and Figure 2.7. The NW flowers varied over a wide range of anthocyanidin contents161 to 4256 µg/g: including 88 to2419 µg/g cyanidin and 15 to 1837 µg/g pelargonidin contents (Table 2.3 and Figure 2.7). FC2 had intermediate contents of cyanidin and pelargonidin, 1,200 and 170µg/g, respectively, for a total of 1370 µg/g anthocyanin. Most notably, fourth generation selection, LM12-35, with deep red flower petals (Figure 2.6 bottom photo and panel g), had exceptionally high cyanidin and pelargonidin contents of 2,419 and 1837 µg/g, respectively. Conversely, LM69-3 pink flower petals (Figure 2.6 panel f) had the lowest cyanidin and pelargonidin contents of 146 and 15 µg/g, respectively.

Among assayed NW flowers in Phase II individuals of the LM49 family, cyanidin and pelargonidin contents ranged from 165 to 669µg/g and 41 to 640µg/g, respectively. For comparison, one W-flowered member of the LM48 family was also assayed. Flower petals that were entirely white had no detectable cyanidin or pelargonidin. Plant number LM49-64 stood out as having a a particularly high floral cyanidin content of 669 µg/g (Figure 2.8).

Phenotyping – Fruit color and pigment composition

Fruit pigmentation could not be assayed in the Select Set or other Closed Pedigree Set members due to poor and irregular fruit set. There was however visible evidence of variation in fruit hue and some fruit were very light, but not W. In the Phase 2 LM49 family, fruit cyanidin and pelargonidin contents were 56 to 163 and 159 to 1178 µg/g, respectively (Table 2.4). Plant number LM49-64 stood out as having particularly high fruit pelargonidin content (Figure 2.8). The previously tested cultivars had fruit cyanidin contents ranging from 27 to 120µg/g, while their pelargonidin contents ranged from 402 to 761µg/g (Table 2.5).

Phenotyping – Additional traits

Fruit size - Fruit size was variable within families, and increased under selection from the second through the fourth generation of Phase 1 (Figure 2.4). Thus far, the largest fruit have been found in members of the LM18 family, while one member of the LM9 family (LM9-6) produced the most fruit and the most attractive fruit over the longest duration (fourth generation larger panel in Figure 2.4). In Phase 2 of my program, hybrids with desirable fruit shape, size and quality are being developed, with initial focus on the LM49 family (Phase 2 panel in Figure 2.4).

Other traits - Sex expression (female versus hermaphrodite) segregated in some progeny families, while in others only hermaphrodites were seen. The seasonal flowering pattern varies: starting early (mid-April to mid-May) to late (late-June), with or without repeated flowering. In addition, there is variability among the progeny for presence/absence of flowering on the runners, an important trait for ornamental potted plants.

Table 2.3: Flower petal cyanidin and pelargonidin contents for Closed Pedigree Set listed by generation. Key to column headings: Cyn = cyanidin; Plr = pelargonidin; Anth = total anthocyanins.

Generation	Sample	Cyn (µg/g dry wt)	Plr (µg/g dry wt)	Anth (µg/g dry wt)
1	FC2	1,200	170	1,370
2	LMA1	257	384	641
2	LMB1	88	227	315
3	LMG16	337	348	686
3	LMJ6	301	613	914
3	LMJ12	425	143	568
4	LM12-15	-	-	-
4	LM12-3	257	782	1,039
4	LM12-23	565	670	1,235
4	LM12-12	1,325	1,296	2,621
4	LM12-34	2,227	251	2,477
4	LM12-35	2,419	1,837	4,256
4	LM30-1	110	466	576
4	LM30-10	340	383	723
4	LM30-12	251	38	288
4	LM30-13	407	531	937
4	LM30-17	165	737	902
4	LM30-18	441	537	979
4	LM30-5	156	260	417
4	LM30-9	132	553	685
4	LM69-3	146	15	161
4	LM69-1	224	38	262
4	LM69-5	682	579	1,260
4	LM69-2	787	705	1,492
4	LM69-7	893	553	1,446
4	LM69-4	1,103	166	1,269
4	LM69-12	1,366	173	1,539
4	LM69-11	1,441	980	2,421
4	LM69-10	1,800	691	2,491
4	LM9-5	190	347	537
4	LM9-6	175	121	296
4	LM9-8	160	289	449

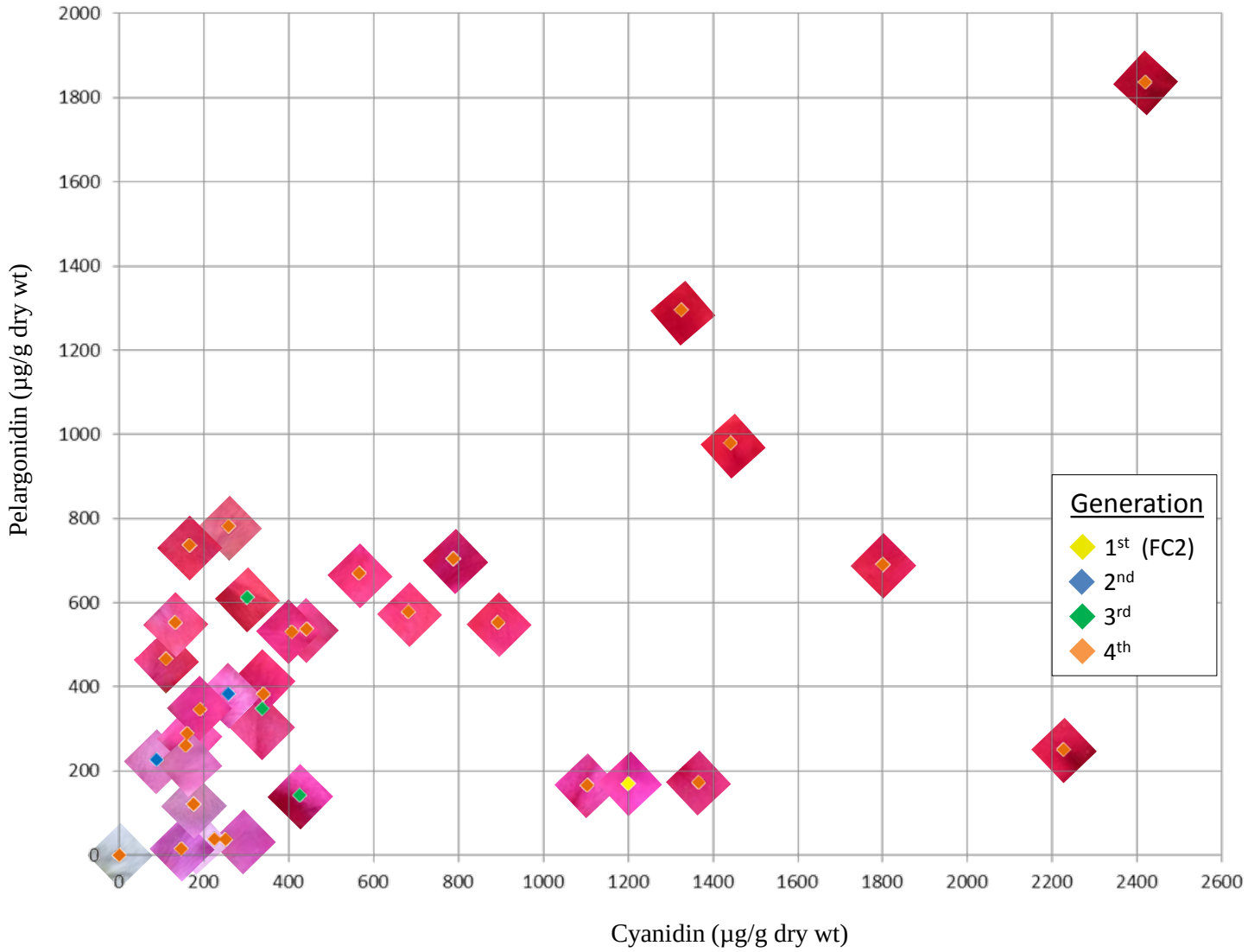


Figure 2.7: Cyanidin and pelargonidin contents in flower petals of members of the Closed Pedigree Set. Samples show variations in pelargonidin (y axis) and cyanidin (x axis) concentrations in NW flowers.

Table 2.4: Flower and fruit cyanidin and pelargonidin contents in representative members of Phase 2 family LM49. Key to column headings: Cyn = cyanidin; Plr = pelargonidin; Anth = total anthocyanins). The members selected for assay represent a diversity of hues as observed visually in the LM49 family.

Sample	Flower			Fruit		
	Cyn (µg/g dry wt)	Plr (µg/g dry wt)	Anth (µg/g dry wt)	Cyn (µg/g dry wt)	Plr (µg/g dry wt)	Anth (µg/g dry wt)
49-16	-	-	-	58	513	571
49-03	165	332	498	68	161	229
49-02	171	141	312	67	437	504
49-55	185	251	436	77	393	470
49-08	214	162	377	78	159	237
49-91	276	158	433	163	448	611
49-04	284	390	674	99	347	446
49-10	288	148	436	95	272	366
49-05	288	176	464	92	253	345
49-94	316	636	952	122	385	507
49-68	384	176	560	143	644	787
49-80	420	640	1,060	98	466	564
49-64	669	481	1,150	56	1,178	1,234

Table 2.5: Fruit cyanidin and pelargonidin contents in an assortment of commercial cultivars. The data for the cultivars is from (Mahoney 2007) is provided for purposes of comparison.

Sample	Cyn (µg/g dry wt)	Plr (µg/g dry wt)	Anth (µg/g dry wt)
Seascape	120	524	644
Tristar	81	761	842
Sparkle	74	512	586
Earliglow	62	588	650
Seneca	53	484	537
Honeoye	50	697	747
Winona	50	598	648
Jewel	48	671	719
Northeaster	47	499	546
Tribute	45	402	447
Delmarvel	43	727	770
Raritan	27	532	559

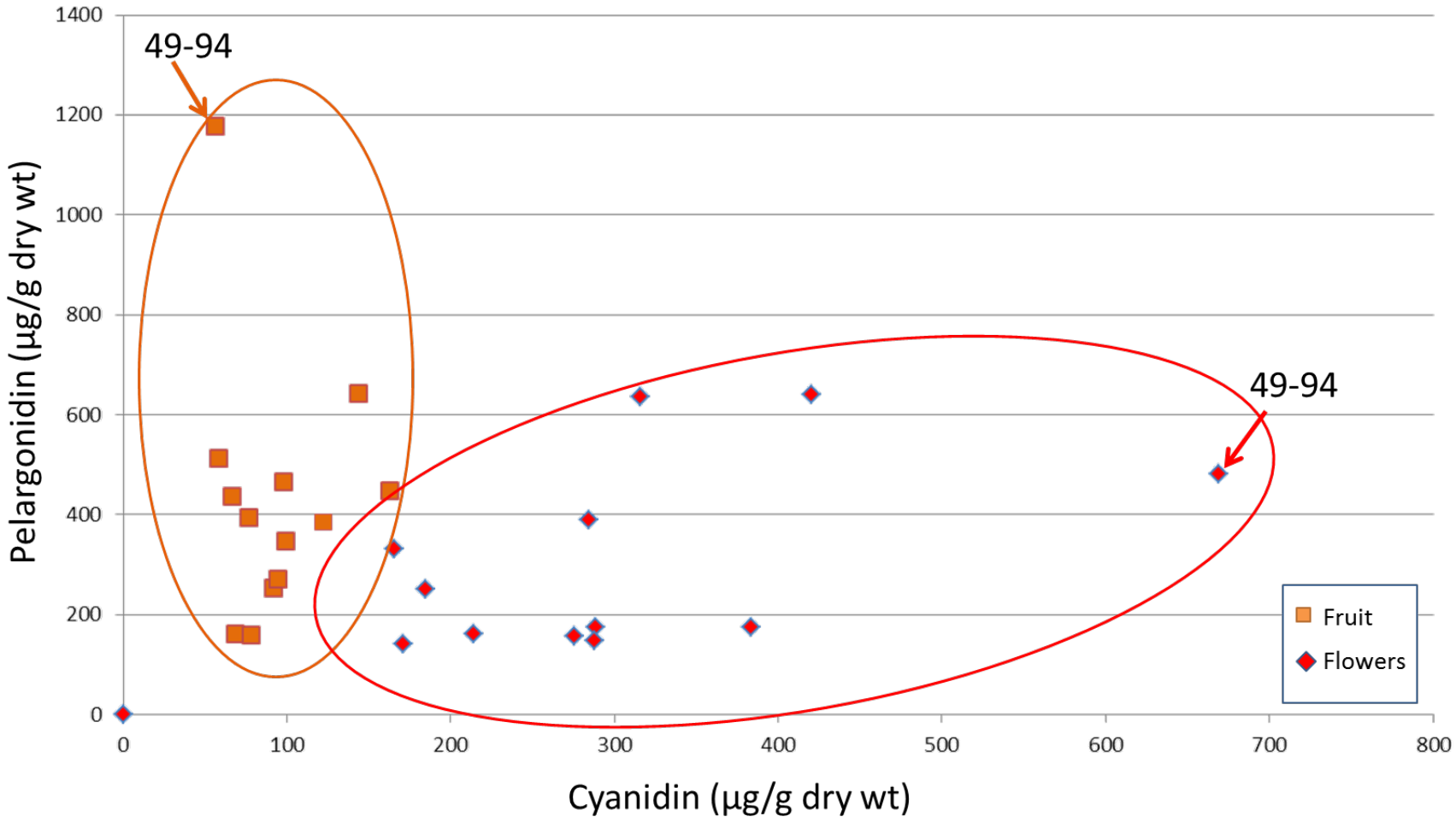


Figure 2.8: Flower and fruit anthocyanidin (cyanidin and pelargonidin) contents in representative members of Phase 2 LM49 family. The two shaded ovals outline anthocyanidin ranges for flowers (red diamonds) and fruit (orange squares). Arrows indicate the extreme positions of plant LM49-64 with respect to flower cyanidin and fruit pelargonidin contents.

Genotyping

SNP Array genotyping results obtained for 51 individuals included the following: a Select Set of 41 plants comprised of the one NW- and two W- flowered parents and 31 NW- and 8 W-flowered progeny individuals (Table 2.6 and Figure 2.9); and a diverse sampling of 10 other W-flowered "non-ananassa" germplasm accessions representing *F. virginiana* and *F. chiloensis* and a few hybrids thereof.

Segregating markers in the Select Set - A total of 5,674 parentally concordant, segregating markers were identified in the Select Set. These 5,674 concordant markers constitute 6.2% of the 95,062 marker sites on the Array, and include all of the recognized marker categories (Table 2.7). The octoploid-based SNPs had a higher success rate (6.5%) compared to the diploid-based (1.3%) and codon-based (1.1%) SNP groups (Table 2.7). The markers were fairly well distributed in relation to the seven pseudochromosomes (PCs) of the *F. vesca* FvH4 reference genome as indicated by the distribution of markers on the array, and the success rate ranged from a low of 4.7% for PC7 to high of 7.4% for PC1 (Table 2.8).

Table 2.6: Pedigree of Select Set. The members are identified by generation, name, female and male parentage, flower color category (NW versus W), and flower hue, where Petal1 indicates the overall hue of the petals, and Petal2 indicates a second tone in the flower petal, usually at the central axis. The abbreviations for the hue categories are provided to the right of the table.

Generation	Name	Female	Male	Color	Petal1	Petal2
1	FC1	-	-	W	W	W
1	FC3	-	-	W	W	W
1	FC2	-	-	NW	Pk	Pk
2	LMA1	FC3	FC2	NW	SlPk	DSlPk
2	LMB1	FC1	FC2	NW	Lav	Lav
2	LMB2	FC1	FC2	NW	W	W
2	LMB22	FC1	FC2	NW	W	W
2	LM107-4	FC1	FC3	W	W	W
2	LM107-6	FC1	FC3	W	W	W
3	LMI10	LMB22	LMB22	W	W	W
3	LMG16	LMB1	LMB2	NW	Red	Scrlt
3	LMJ6	LMB1	LMA1	NW	DSlPk	DSlPk
3	LMJ12	LMB01	LMA1	NW	DPk	Scrlt
4	LM12-15	LMJ6	LMG16	NW	W	W
4	LM12-23	LMJ6	LMG16	NW	DPk	DPk
4	LM9-1	LMG16	LMJ6	NW	SlPk	SlPk
4	LM9-3	LMG16	LMJ6	NW	W	W
4	LM9-4	LMG16	LMJ6	NW	W	W
4	LM9-5	LMG16	LMJ6	NW	LCor	SlPk
4	LM9-6	LMG16	LMJ6	NW	Lav	Lav
4	LM9-7	LMG16	LMJ6	NW	SlPk	SlPk
4	LM9-8	LMG16	LMJ6	NW	DSlPk	SlPk
4	LM30-1	LMJ6	LMI10	NW	Red	Red
4	LM30-5	LMJ6	LMI10	NW	Pk	Pk
4	LM30-9	LMJ6	LMI10	NW	SlPk	SlPk
4	LM30-10	LMJ6	LMI10	NW	DSlPk	Red
4	LM30-12	LMJ6	LMI10	NW	LPk	LPk
4	LM30-13	LMJ6	LMI10	NW	DSlPk	Red
4	LM30-17	LMJ6	LMI10	NW	Red	Red
4	LM30-18	LMJ6	LMI10	NW	Pk	Pk
4	LM69-1	LMJ12	LMJ6	NW	Lav	DPk
4	LM69-2	LMJ12	LMJ6	NW	Scrlt	Scrlt
4	LM69-3	LMJ12	LMJ6	NW	Lav	Pk
4	LM69-4	LMJ12	LMJ6	NW	DPk	Scrlt
4	LM69-5	LMJ12	LMJ6	NW	Scrlt	Scrlt
4	LM69-6	LMJ12	LMJ6	NW	Scrlt	Scrlt
4	LM69-7	LMJ12	LMJ6	NW	Scrlt	Scrlt
4	LM69-8	LMJ12	LMJ6	NW	LCor	Pk
4	LM69-10	LMJ12	LMJ6	NW	Red	Red
4	LM69-11	LMJ12	LMJ6	NW	Red	Scrlt
4	LM69-12	LMJ12	LMJ6	NW	DPk	Scrlt

Whte
Scrlt
SlPk
DSlPk
Red
Pk
LPk
Dpk
Fush
Lav
LCor
Cor
Unk

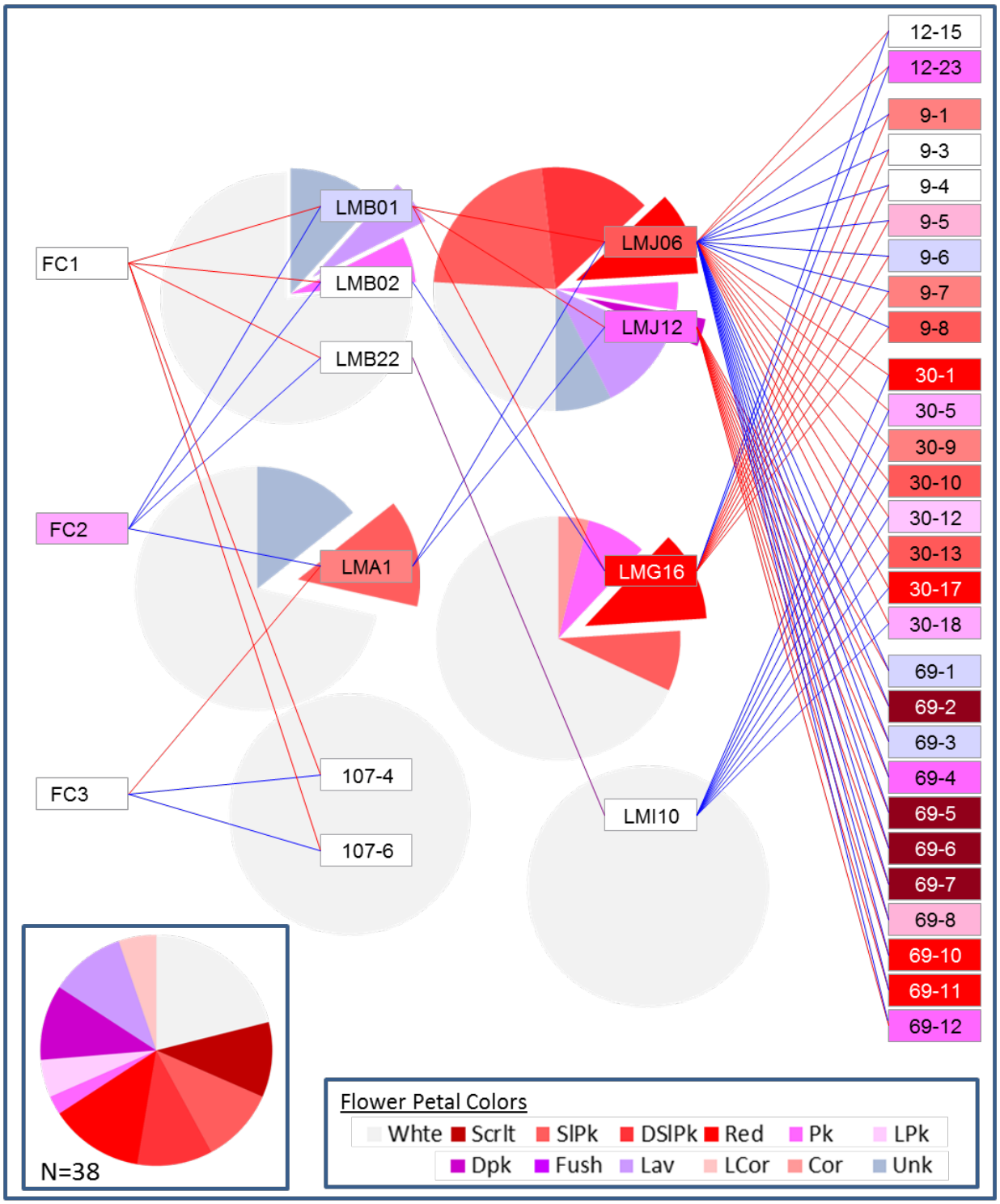


Figure 2.9: Pedigree relationships of the Select Set. Box colors represent flower petal hues. The pie charts represent distributions of flower color (NW versus W) and hues among the members of the respective family. The red (female) and blue (male) lines indicate parentage.

Table 2.7: Marker distribution in the Select Set. The distribution of 5,674 pedigree-informative markers is shown in terms of absolute counts, as percentages in relation to the total number on the array, and by design group.

Marker Type		Total # of segregating markers	Total # of Array markers	% Array
Octoploid-based				
	snp	4,360	63,263	6.9%
	mSNP	176	1,761	10.0%
	Ins	237	4,615	5.1%
	Del	216	4,913	4.4%
	SnpSnp	462	7,092	6.5%
	indelSnp	41	1,176	3.5%
	SnpinIns	60	2,007	3.0%
	SnpInDel	9	836	1.1%
	Total	5,561	85,663	6.5%
Diploid-based	F1D	49	3,751	1.3%
Codon Based		64	5,648	1.1%
Pedigree total		5,674	95,062	6.0%

Table 2.8: Distribution of pedigree markers in the Select Set relative to *F. vesca* FvH4. The counts of markers, the number of segregating markers in the Select Set, and the success rate as a percentage % of total Array markers is provided for each of the FvH4 PCs.

FvH4 PC	# Markers on Array	# of Pedigree Markers	Pedigree/Array Markers
1	10,384	768	7.4%
2	12,439	797	6.4%
3	15,190	788	5.2%
4	12,011	676	5.6%
5	14,429	838	5.8%
6	19,131	1,266	6.6%
7	11,478	541	4.7%
Total	95,062	5,674	6.0%

Pedigree based marker-trait analysis

In a marker-trait analysis of NW versus W flower color in the Select Set pedigree using 5,674 concordant Array markers, initially only 5 markers displayed an absolute association with NW flower color. However, among the 41 members of the Select Set, the phenotype and genotype of one individual, LM69-4, was in question, and required closer consideration. A review of photos of LM69-4 showed that the plant generally produced dark pink flowers, but on at least one occasion produced an inflorescence with lighter salmon pink flowers and on another occasion produced a dark pink flower with one white petal with red rays or venation (Figure 2.10). In addition, in the SNP genotyping data set, LM69-4 had a borderline QC quality of 96% compared to the general cutoff of 97%, as recommended by Affymetrix. Examination of the cluster plots of the initially identified five markers showed that the LM69-4 cluster diagram sample "dots" were generally falling outside the range of what is considered good quality genotyping calls (Figure 2.11). LM69-4 was thus excluded from further consideration in the marker trait analysis, based on the observed seemingly unstable phenotype for the color trait and the low quality genotyping calls.

The exclusion of LM69-4 resulted in identifying an additional 30 markers that were co-segregating without recombination with the NW trait, for a total of 35 trait-associated markers (Table 2.9). Overall, at these 35 marker sites, the NW founder, FC2, and the 30 NW progeny possessed the NW-associated allele and genotyped as heterozygous (Table 2.9), while the W founders FC1 and FC3 and all W progeny lacked the NW-associated allele, and genotyped as homozygous for an allele that did not come from FC2. These 35 markers included 30 octoploid-based (28 Snps, two mSnps), two diploid-based and three codon-based SNPs. An additional 14

markers numbered 36 through 49 in Table 2.9 were identified as loosely associated but with some recombination to the NW trait.

Figure 2.10: LM69-4 variable phenotypes. The larger picture shows two inflorescences, each with a different hue on the same plant; an inflorescence with the typical dark pink flower color of LM69-4 (left) and an inflorescence that is a lighter coral color (right).The inset picture on the lower left shows two single flowers taken from LM69-4: one flower with a single white petal with dark pink rays or venation, and the other flower with the typical LM69-4 dark pink.

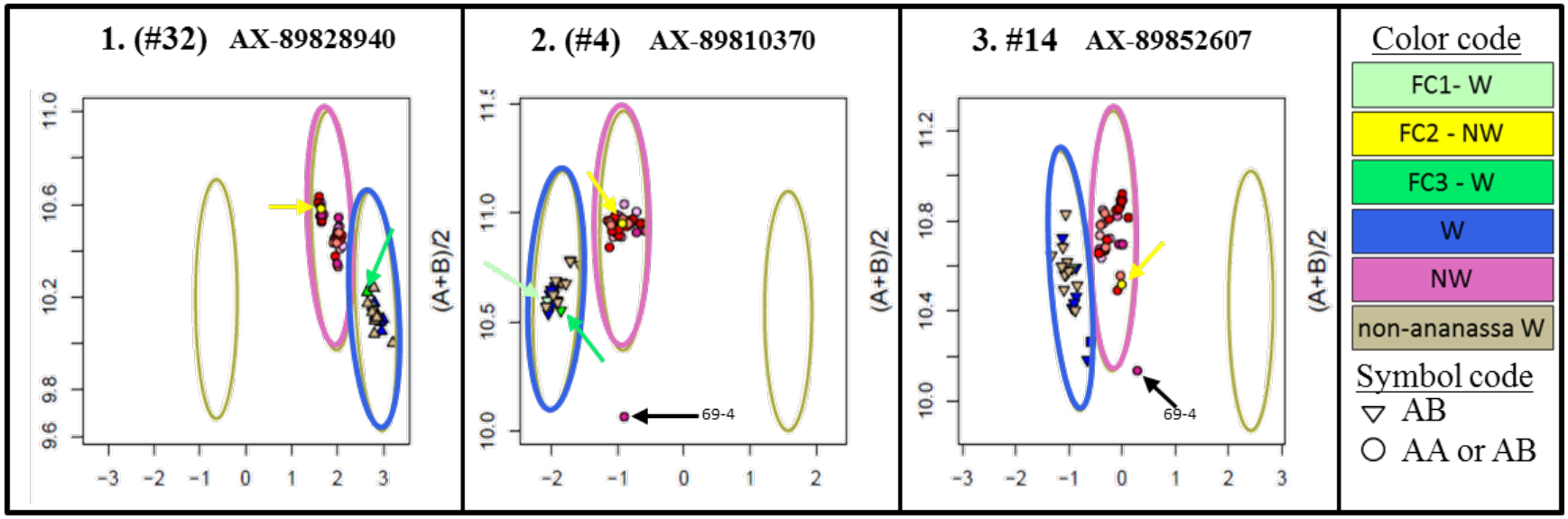
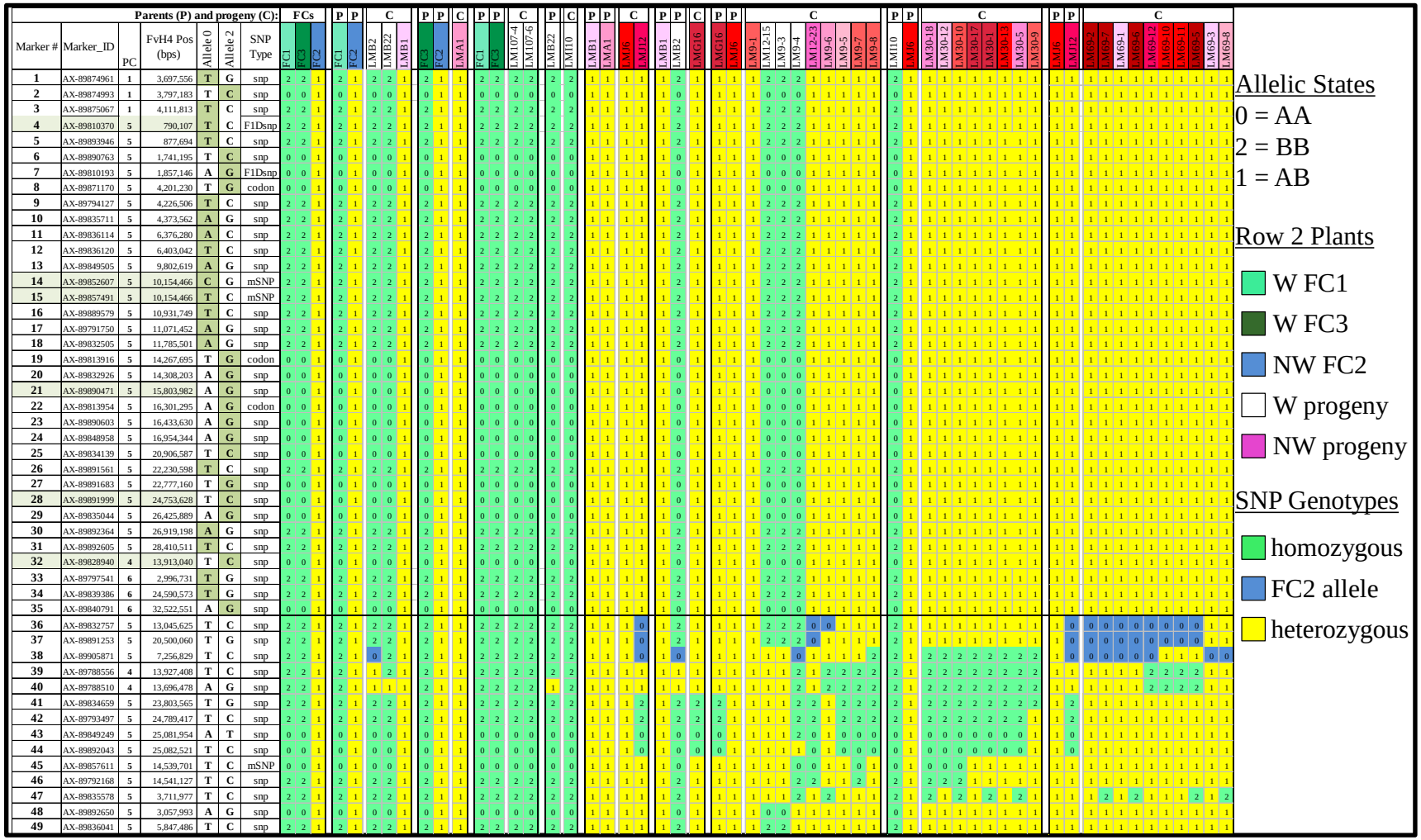


Figure 2.11: Typical Array cluster plots for markers associated with the NW flower color trait. For each of three markers from Table 2.6, the plots include the genotyping of the Select Set of 41 and 10 W "non-ananassa" genotypes. The arrows point to corresponding genotype/phenotype colored according to the Color Code legend. The lower intensity (quality) of LM69-4 can be seen by the lower displacement of the respective dots in the plots for markers 2 and 3. The least frequent allele considered the minor allele. The shift of the plots away from 0 on the x-axis is indicative of the background allele copy number, such that the genotype for an octoploid is shifted away from the 0 on the x-axis. The plots are shifted relative to the x-axis as influenced by the underlying octoploid genotype; marker 1 is shifted to the positive indicating an 'A' background allele, marker 2 to the negative indicating a 'B' background allele, and marker 3 is shifted just slightly negative, indicating a reduced ploidy site with a 'B' background allele. For example, marker 1 is shifted to the positive and therefore has the genotype BA AA AA AA which corresponds to CT TT TT TT (Table 2.9), with 'C' minor allele and the marker allele being one and the same. Marker 2 is shifted to the negative, and therefore has the genotype AB BB BB BB, which corresponds to TC CC CC CC, with 'T' minor allele again being one and the same as the marker allele (Table 2.9).

Table 2.9: Marker-trait associations. Thirty-five markers (numbered #1-35 in column 1) are linked without recombination to the NW color trait. Only markers #4, 14, 15, 21, 28, and 32 were associated with NW color before exclusion of LM69-4. Markers #36-49 are associated but with some recombination with the NW trait. The marker allele associated with NW is highlighted dark green (Allele 0 and Allele 2 columns).



Comparison to *F. vesca* FvH4

The marker-trait associations for NW flower color include 35 markers that are associated without recombination. Of these 35 markers, 28 are syntenous with PC5 of the *F. vesca* FvH4 reference genome (Table 2.9), and their positions span the entire chromosome (Figure 2.12). A single associated marker, #32 AX-89828940, is syntenous with PC4, but appears to be mislocated in the FvH4 genome because it is clearly positioned within a block of 39 contiguous markers on LG5 of the *F. iinumae* map (Table 2.9, Figure 2.12, and Chapter I). Of the remaining 6 markers, three (#1, 2, and 3 in Table 2.9) are syntenous with PC1 and three with PC6 in FvH4. These three markers with synteny to PC1 are positioned among six other markers that are proximally located in FvH4 PC1 and are also mapped to LG1 of the *F. iinumae* map (Chapter I). The three markers (#33, 34 and 35 Table 2.9) with synteny to PC6 are scattered in PC6, and their locations could not be assigned on the *F. iinumae* map.

On the basis of a homology search, 19 genes related to the anthocyanin pathway were located on various PCs of the FvH4 reference genome (Table 2.10). Six of these genes are located within the color-trait association, and all six of these genes are located on PC5 of FvH4, and are therefore of the greatest interest as candidate genes with respect to the NW trait. The six genes include four structural genes, *ANR*, *ANS*, *F3'H*, and a *Ph* gene; and two regulatory genes *JAF13* and *FaMYB1* (Table 2.10).

Table 2.10: Location of identified anthocyanin related structural and regulatory genes on FvH4 PCs. The GeneMark ID for the genes that were annotated is provided. No GeneMark IDs are available for PC0, which consists of unplaced scaffolds and therefore has not been annotated. The start and end position of the annotated genes are indicated in base-pairs (bps).

Gene Type	Gene	GeneMark	FvH4 PC	FvH4 start (bps)	FvH4 end (bps)
Structural	*4CL*	No GeneMark ID, blasts to PC0	0	10,632,371	10,636,740
Structural	*F3H*	mrna14611.1-v1.0-hybrid	1	7,929,548	7,931,288
Regulatory	*MYB113-like*	mrna31407.1-v1.0-hybrid	1	14,027,705	14,029,775
Regulatory	*MYB10*	mrna31413.1-v1.0-hybrid	1	14,060,846	14,061,556
Structural	*FLS*	no GeneMark ID	2	16,383,681	16,378,349
Structural	*DFR*	no GeneMark ID	2	22,427,918	22,428,173
Structural	*C4H*	mrna28093.1-v1.0-hybrid	3	20,085,403	20,088,772
Regulatory	*PRX27*	mrna19544.1-v1.0-hybrid	3	140,381	143,386
Structural	*LAR*	mrna03877.1-v1.0-hybrid	4	25,703,897	25,706,081
Structural	*ANR*	mrna24665.1-v1.0-hybrid	5	66,916	68,842
Structural	*ANS*	mrna32347.1-v1.0-hybrid	5	831,406	832,669
Structural	*F3'H*	mrna25801.1-v1.0-hybrid	5	7,611,689	7,614,828
Structural	*pH gene*	mrna02301.1-v1.0-hybrid	5	26,584,340	26,595,426
Regulatory	*JAF13*	mrna32494.1-v1.0-hybrid	5	1,624,881	1,628,070
Regulatory	*FaMYB1*	mrna09407.1-v1.0-hybrid	5	10,191,971	10,193,640
Structural	*PAL*	mrna09753.1-v1.0-hybrid	6	8,934,129	8,937,388
Structural	*CHS*	mrna26826.1-v1.0-hybrid	7	6,154,395	6,155,736
Structural	*CHI*	mrna23367.1-v1.0-hybrid	7	15,113,802	15,115,265
Structural	*3GT*	mrna12591.1-v1.0-hybrid	7	19,513,486	19,515,049

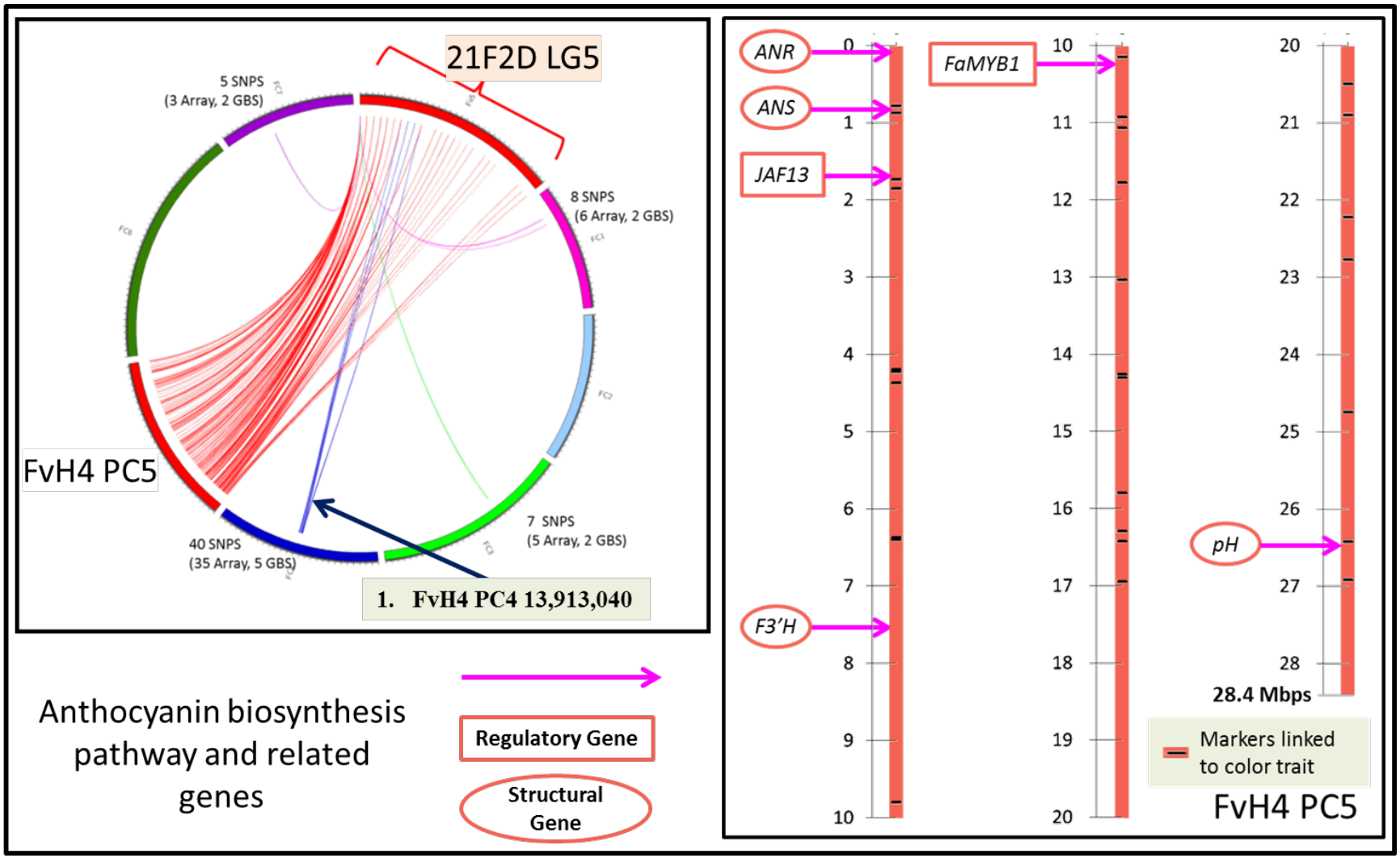


Figure 2.12: Markers associated with color and anthocyanin related genes on *F. iinumae* 21F2D LG5 and *F. vesca* FvH4 PC5. One marker located FvH4 PC4 (left diagram) linked to flower color is located on LG5 of the 21F2D map. Thirty of the 35 markers are syntenous with FvH4 PC5. The locations of five anthocyanin related genes are indicated on PC5 (right).

Discussion

The population development effort began with the initial cross made in 2007, and has resulted in the establishment of over one thousand progeny, thereby leading to the advancement of breeding objectives for flower color and fruit quality. The primary focus of phenotyping has been flower color and hues, as determined visually and complemented by HPLC analysis of pigment composition to the extent possible. Fruit quality was also of central interest. The numbers of plants subjected to both SNP Array genotyping and HPLC analysis of flower and fruit pigment contents is as yet comparatively small. The populations and results described here provide a foundation for a marker-assisted strawberry breeding program emphasizing the integration of ornamental value and fruit quality for specialty markets. The Select Set of 41 individuals has provided the basis for identifying marker-trait associations and identifying candidate genes for potential identity with the locus governing NW versus W flower color.

Genetic basis of the NW trait

In the Closed Pedigree Set, the outcomes of NW × NW, NW × W and its reciprocal (W × NW), and W × W crosses provide the basis for inferring that the presence of non-white (NW) flower color is genetically dominant to its absence, white (W) flower color. This conclusion is supported by the fact that W × W crosses gave only white progeny, while 7 out 8 NW × NW crosses generated segregating progenies. In the exceptional case, all members of the small (N = 11) LM69 family were NW, perhaps by chance alone. The fact that segregation occurred in the

second generation LMA and LMB families indicates that FC2, the original source of the NW flower color trait, was itself heterozygous. Moreover, the presence of segregation in all but one progeny family involving at least one NW parent suggests that homozygosity for the NW trait was rare or absent in the NW members of the Closed Pedigree Set. If so, an explanation for such genotypic bias will be sought through future investigations.

Presence/absence of flower color - The occasional presence of mosaic flowers of plants with NW flowers (Figure 2.5 panels a through h) suggests that the presence of color is conferred by a single gene copy, the loss or inactivation of which results in a white sector. This hypothesis is consistent with the widespread heterozygosity for the NW trait as noted above. On this basis, doubling of the gene copy number, perhaps by a somatic recombination event, could produce a very dark sector, as seen in Figure 2.5, panels a and c. The increasing frequency of NW individuals in the advancing generations of the Closed Pedigree Set is likely the result of the imposed selection for NW flower color, in combination with repeated opportunities for genetic recombination in the advancement of one generation to the next.

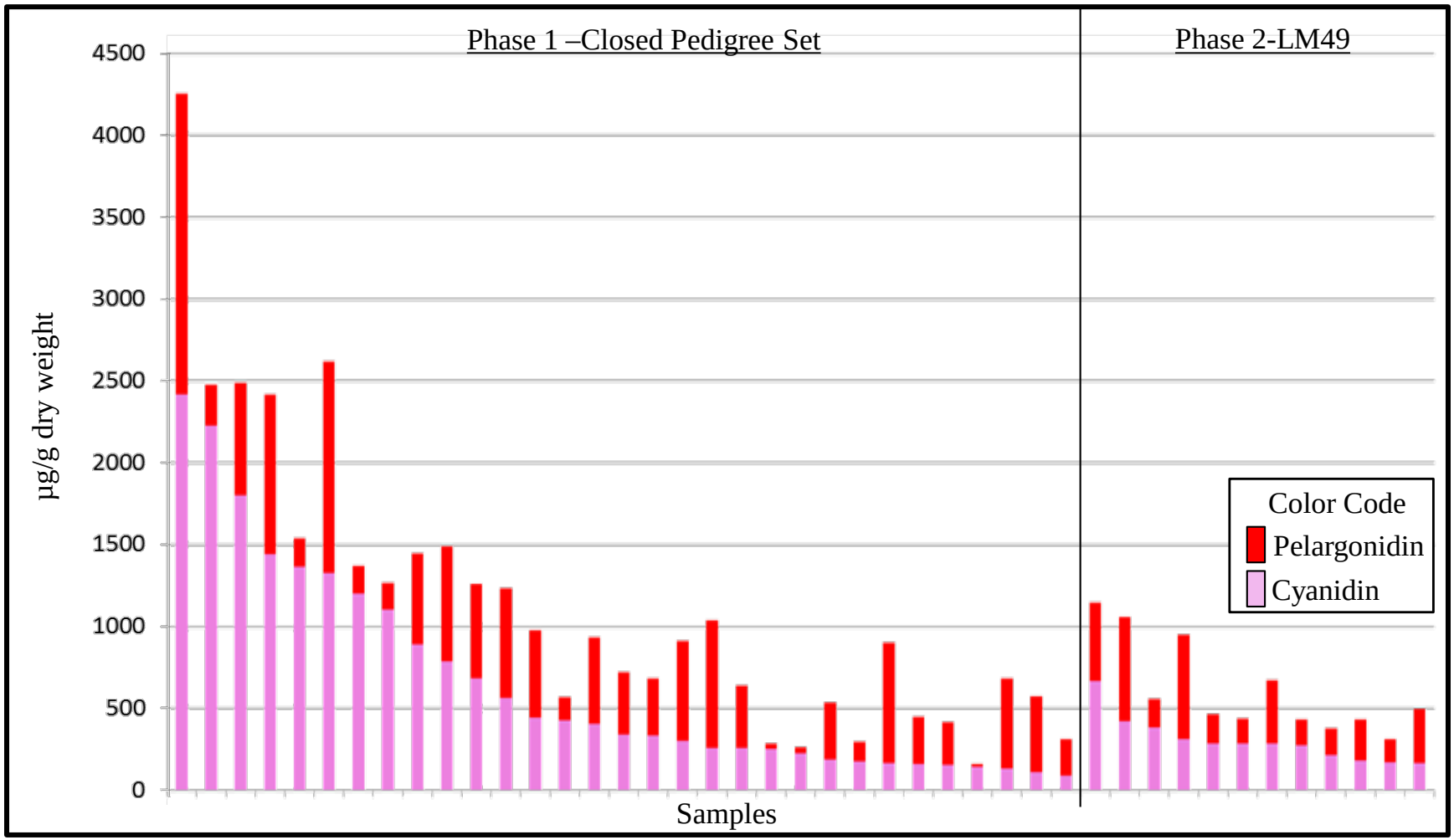
Variation in floral hue

In addition to the presence/absence of color, a broad spectrum of floral variations in hue, color intensity, and color pattern was evident (Figure 2.6), offering immense scope for selection of ornamental types. Figure 2.6 (panels a, c, g, and i) displays examples of red flowered selections, but with subtle differences in petal color intensity and hue accompanied in some cases by distinct differences in stamen color (compare panels a and c to panels g and i). There appears to be an association between petal hue and anther hue, as in Figure 2.6 (panels a, b, c, g, and i) where the darker colored flowers have reddish to red anthers, while the more pastel-shaded

flowers have yellow anthers (panels d, f, and h). Figure 2.6 panel c displays a strikingly attractive flower with deep red petals and stamens to match. Floral patterns with darker edges on the flower petals (Figure 2.6, panel b) look as though the petals had been outlined or painted with a darker shade of the same color, while in contrast, panel h shows a flower with dark axial rays that transition gradually to a lighter shade of the same hue toward the petal edges. The variation of hues and floral patterns among progeny family members is indicative of segregation at multiple loci, presenting a challenge to genetic analysis.

Cyanidin and pelargonidin contents of flowers - The fact that the NW founder parent FC2 had intermediate levels of cyanidin and low levels of pelargonidin contents suggests that the white-flowered parental founders, FC1 and FC3, may be contributing hereditary factors influencing floral hue in the subsequent progeny generations, including the appearance of red flower color in the third and fourth generation of the Closed Pedigree Set. The ranges of cyanidin and pelargonidin in the flowers of the Phase 2 LM49 family were much lower than those of the Phase 1 Closed Pedigree Set (Figure 2.13), as might be expected because the LM49 family samples the alleles of only one Select Set member, LMJ6, which has an intermediate level of floral pigments. In the LM49 family, which was derived from a W cultivar Cavendish x NW LMJ6, some progeny members had floral cyanidin contents as much as twice that of their NW parent LMJ6, yet progeny pelargonidin levels were much less than or equal to that of the NW parent, suggestive of contributory hereditary factors from ‘Cavendish’ for cyanidin but not for pelargonidin in this family.

Figure 2.13: Flower cyanidin and pelargonidin contents in NW flowers of representative Phase 1 and Phase 2 population members. A broader range of both cyanidin and pelargonidin contents is seen in Phase 1 (Closed Pedigree Set) as compared with Phase 2.



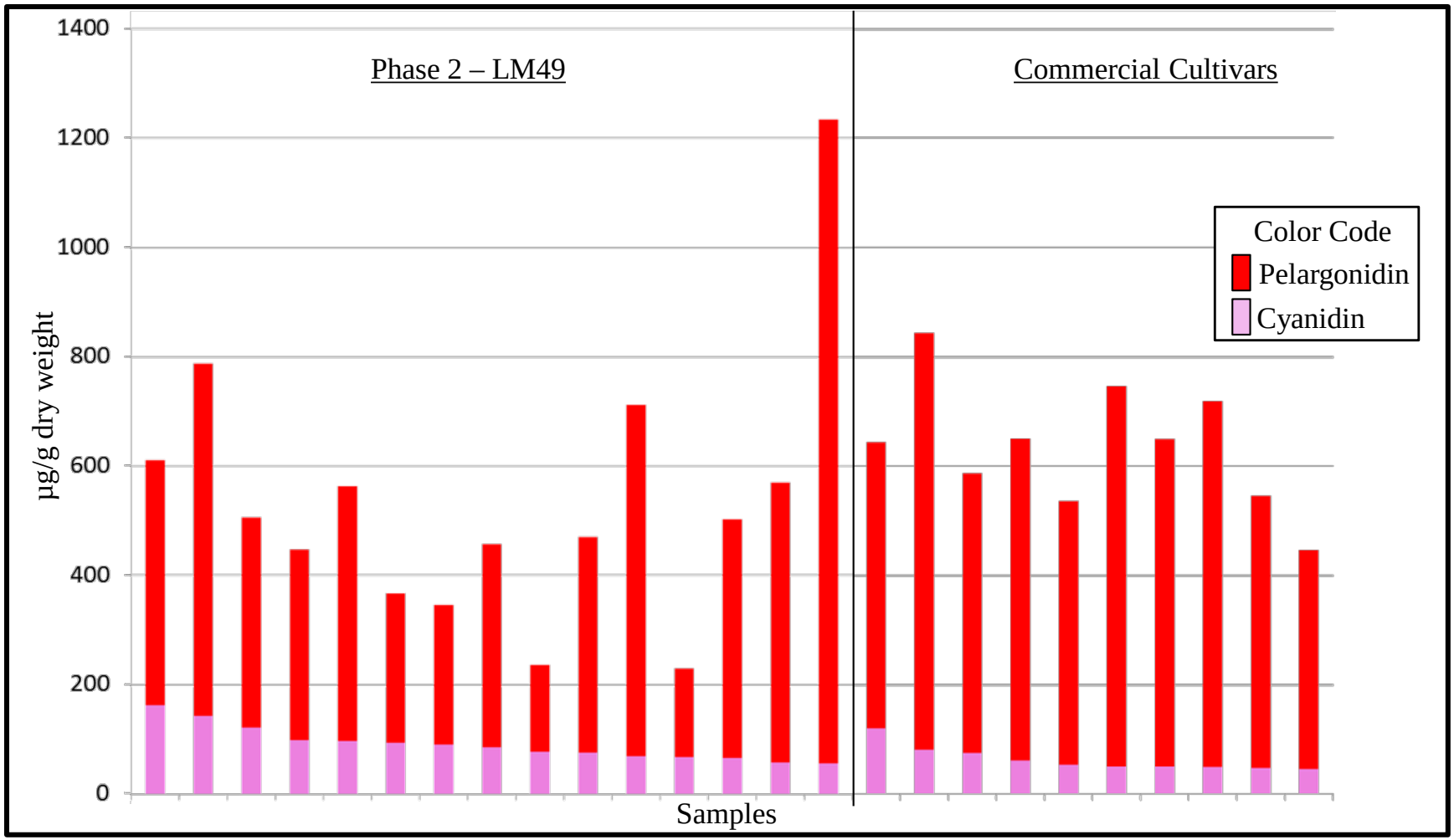


Figure 2.14: Cyanidin and pelargonidin contents in fruit. The anthocyanin content of fruit of members of Phase 2 (LM49 family) and an assortment of cultivars tested previously (Mahoney 2007).

Comparison of flower and fruit pigment contents

Fruit set was generally not abundant or consistent in Phase 1, precluding the generation of useful data on fruit pigment composition. In contrast, improved fruit production and quality in the Phase 2 LM49 family enabled acquisition of fruit (Figure 2.14) as well as flower pigment composition data, permitting useful comparisons between flower and fruit pigment composition in that family. The ranges in cyanidin and pelargonidin contents in a sampling NW flowers and fruit from members of the LM49 population contrasted with each other in interesting ways (Figure 2.8, Table 2.4). Plant LM49-64 was an outlier, having exceptionally high floral cyanidin and fruit pelargonidin (Table 2.5). Excluding this exceptional plant, the range of cyanidin contents was higher and broader in NW flowers than in fruit (Figure 2.8, Table 2.4). Contrastingly, the range of pelargonidin contents was similar in both NW flowers and fruit, again with the exception of plant LM49-64 (Figure 2.8). The comparison of flower and fruit pigment compositions suggests an elevation of cyanidin biosynthesis in flowers as compared to fruit, while no such elevation is seen with pelargonidin. Interestingly, the ranges of cyanidin and pelargonidin contents in the fruit of the LM49 family (Table 2.4) are comparable to those of commercial cultivars previously assayed (Mahoney 2007) (Table 2.5, Figure 2.14).

The LM49 NW progeny display a palette of floral hues, suggesting that one or both parents must be heterozygous for loci influencing floral hue, providing opportunity for recombination in future generations. The very good fruit quality in some of the members is indicative of inheritance from Cavendish, but also of complementation with LMJ6, as the fruit did not resemble that of either parent. Moreover, the interest of Pleasant View Gardens in evaluating ten members of this family as ornamental selections and in continuing our

relationship towards further varietal improvement justifies continued intensive breeding efforts involving the LM49 family.

Phenotyping - Additional traits

The Select Set is also segregating for other traits, including flowering habit (day-neutrality versus short-day), and fruit size and shape. It is reasonable to expect that these populations are also segregating for other fruit quality traits of interest, such as fruit pH, titratable acid, and soluble solids. In the Phase 2 LM49 family, the fruit size (8-12 g/berry) was comparable to that of cultivars, ranging from 7.2 to 15.5 g/berry (Gent 1990), and similar to that obtained at UNH of 4.2 to 11.2 g/berry for an assortment of cultivars during the RosBREED phenotyping project (Mathey et al. 2013).

Genotyping

The number of concordant markers (5,674) in the Select Set is comparable to the 6,594 concordant markers mapped in the *F.* ×*ananassa* Holiday × Korona cultivar cross, of which 80 progeny members and the parents were also genotyped on the evaluation phase of the Array (Bassil et al. manuscript submitted). The sequence files of 'Holiday' and 'Korona' and six of their progeny were a major part of the discovery panel used in the design of the Array. Although the founders of the Closed Pedigree Set were part of the discovery panel, the low depth of coverage on the sequence data precluded them as major contributors to the design. The final result however indicates that there contribution to the design may have been a factor in the identification of a significant number of markers in the Select Set.

Marker trait association for flower color

The 28 markers associated with NW flower color are distributed over the entire length of reference chromosome PC5. This finding suggests that a chromosome derived from FC2 and containing the flower color locus is being transmitted in the Select Set without recombination. Presumably the NW flower color locus is located somewhere on this chromosome, in close proximity to a particular marker or markers. However, the absence of detected recombination in the limited number of 38 Select Set progeny individuals (Table 2.9) precludes the determination of more narrowly defined marker-trait associations, and also precludes the establishment of linear marker order except as defined by the marker locations on PC5 of the diploid reference genome.

In prior studies conducted by two research groups, quantitative trait loci (QTLs) for fruit quality have been identified on one of the LG5 homoeologues of *F.* ×*ananassa* ((Zorrilla-Fontanesi et al. 2011, Lerceteau-Kohler et al. 2012). Zorrilla-Fontanesi et al. (2011) found QTLs on a homoeologue of LG5 for each of the following traits; total anthocyanin, pH, titratable acidity, and color values (a*, b*, and C*) and markers for candidate genes co-localized with some of these QTLs. In another QTL study (Lerceteau-Kohler et al. 2012) of 19 strawberry fruit quality traits, 115 QTLs were detected; 4 QTLs for acidity traits and one for the color value a* were located on one of the homoeologues of LG5. However, QTLs for anthocyanin contents and fruit color (L a* b*) variation and additional QTLs for fruit acidity traits, were also found on linkage groups other than LG5 (Lerceteau-Kohler et al. 2012).

Candidate genes for flower color

The marker-trait association for NW versus W flower color involving 28 markers on PC5 suggests that the gene(s) conferring functional capacity for anthocyanin production in the flower is located on a homoeologue of chromosome 5, and that this chromosome was derived from the original source of NW flower color, founding parent FC2. Therefore, genes with potential influence on pigmentation characteristics and also located on chromosome 5 of the FvH4 reference genome are candidates for potential identity to the "NW locus". As identified by literature and homology searches, the identified candidate genes centered on PC5 include four structural genes, *ANR*, *ANS*, *F3'H*, and a *Ph* gene, and two regulatory genes, *JAF13* and *FaMYB1* (Table 2.10 and Figure 2.14). Candidate gene products influencing NW versus W might compete for the same substrate, and/or an enzyme might have tissue specific functionality or an enzyme might be non-functional. The likelihood of such enzymes influencing color is briefly discussed below within the context of the literature.

ANR - ANR activity was found to be three times higher on cyanidin as a substrate than on pelargonidin in strawberry, producing many times more epicatechin (from cyanidin) compared to epiafzelechin (from pelargonidin) (Almeida et al. 2007) (Figure 2.1). These findings suggest that *ANR* variants could influence hue but not NW versus W color in flowers and/or fruit.

ANS - ANS is at the point of conversion from colorless to colored compounds in the anthocyanin biosynthetic pathway (Figure 2.1) (Holton et al. 1995). It is conceivable that the *ANS* gene is duplicated and sub-functionalized into fruit-specific and flower-specific forms in strawberry. Loss of flower but not fruit pigmentation could result from a mutation in the floral-specific gene copy. A functional gene copy of *ANS* may exist in FC2. On this basis, *ANS* is a viable candidate gene.

F3'H – F3'H can catalyze the conversion of eriodictyol and dihydroquercetin precursors to cyanidin (Figure 2.1). A mutant line of petunia transformed with an overexpressed F3'H had pink flowers with pink anthers and pollen containing peonidin (an anthocyanin derived from a cyanidin), compared to pale lilac control which contained very little anthocyanin (Brugliera et al. 1999). Only the hue of the transgenic petunia flower was affected, but not whether the flower was NW or W. Thus, these finding do not support *F3'H* as a candidate gene for the NW flower trait.

Ph gene - Griesbach (1996) found in *Petunia ×hybrida* that vacuolar pH affected flower hue and not the presence or absence of color and thus the *Ph* gene is not a likely candidate gene for the NW flower trait.

JAF13 and *FaMYB1* - The *c* and *r* family of genes control the transcription of all the structural genes of the anthocyanin pathway (Quattricchio et al. 1998). The *c* family encodes MYB transcription factors. *JAF13,* by NCBI blast homology to *Arabidopsis thaliana* (gb|AAB72192.1|), is part of the *r* gene family, the members of which encode basic helix-loop-helix (bHLH) regulatory proteins. The bHLH transcription factors alone or in combination with MYB factors have been found to control presence versus absence of anthocyanin pigmentation in flowers (Quattricchio et al. 1998).

Expression of *FaMYB1* in *F. ×ananassa* 'Elsanta' strawberry was found to be the highest in ripe red fruit and to be low in the flowers (Aharoni et al. 2001). Tobacco was used as a model system for ascertaining the function of FaMYB1 (Aharoni et al. 2001). Heterologous expression of *FaMYB1* in tobacco reduced anthocyanin and quercetin (a flavonol) levels. The overexpression of FaMYB1 in tobacco was found to be inversely correlated with the synthesis of anthocyanin pigments in the tobacco flowers (Aharoni et al. 2001). Overexpression of FaMYB1

in tobacco resulted in flowers ranging from white, white with red venations, to slightly colored, in comparison to the dark pink flowers of the wild type (Aharoni et al. 2001), suggesting that FaMYB1 acts as a repressor of the anthocyanin expression in flower. The flower in panel i of Figure 2.5 is nearly identical to that shown by (Aharoni et al. 2001) for transgenic overexpression of FaMYB1 in tobacco by introduction of 3-4 copies of the transgene in the plant resulted in a white flower.

In a comparison of co-constructs using a yeast two hybrid system, Aharoni et al. (2001) determined that *FaMYB1* and *AN2* do not contain an active *bHLH* binding domain, in contrast to *AN1* and *JAF13* which do contain an active *bHLH* binding domain. The lack of an active *bHLH* binding domain on *FaMYB1* may imply that the regulation of the anthocyanin pathway genes is in conjunction with JAF13. In *FaMYB1* transgenic tobacco, the active *bHLH* may have been present, allowing repression of the anthocyanin pathway and resulting in white flowers. Therefore, are strawberry flowers white because FaMYB1 works together with JAF13 to repress the anthocyanin pathway in strawberry flowers, so that a non-functional MYB1 or a non-functional JAF13 would enable NW flower color? With the introgression of NW flower color trait from FC2, the capacity for NW was introduced into the strawberry flowers. Unlike tobacco with normally pink flowers, the overexpressed FaMYB1in transgenic tobacco displayed white flowers, implying that tobacco already contained an active *bHLH* domain. Has a non-functional type of *MYB1* or a non-functional *bHLH* transcription factor similar to *AN2* been introgressed in the NW strawberry from FC2, thereby preventing the full expression of FaMYB1 and the concomitant repression of the anthocyanidin pathway genes such as *ANS* and *F3'H*, resulting in NW flowers? Exploration of these hypotheses will require gene expression analysis, and could be an attractive objective for future research.

In conclusion, the most likely candidate genes influencing NW versus W trait are the two regulatory genes *FaMYB1* and *JAF13*, and the structural gene *ANS*, while the remaining structural genes, *ANR*, *F3'H*, and a *Ph* gene are better suited as candidate genes for influencing quantitative variation in floral hue.

The identification of a marker-trait association for NW flower color in this analysis with only 38 progeny members offers promise for discovery of additional trait associations with the anticipated analysis of genotypic data for additional members of the Closed Pedigree Set. The anticipated analyses may elucidate the identity of the locus conferring NW flower color, as well as loci conferring variation for flower hues.

At this writing, I am anticipating Array genotyping data for an additional 104 members of the Closed Pedigree Set, which will provide a sufficient population to construct a linkage map of LMJ6, a third generation red-flowered member that has all three founders in its heritage, and to complete quantitative trait loci analyses for NW flower trait and fruit quality traits.

CHAPTER III

GERMPLASM RESOURCES FOR VERTICILLIUM WILT RESISTANCE BREEDING AND GENETICS IN STRAWBERRY (*FRAGARIA*)[1]

Abstract

We screened 26 octoploid, 1 decaploid, and 23 diploid Fragaria (strawberry) genotypes for response to root-dip inoculation with Verticillium dahliae isolate V1. Inoculated plants were individually rated at eight weeks post-inoculation in comparison to uninoculated controls using a categorical scale: 1 = healthy; 1.5 = slightly symptomatic; 2 = moderately symptomatic; 2.5 = very symptomatic; 3 = dead. Qualitative classifications were assigned to genotypes on the basis of their respective mean disease resistance ratings. The rating ranges and corresponding classifications (in parentheses) were: 1.0 to 1.3 (very resistant = VR), 1.4 to 1.7 (moderately resistant = MR), 1.8 to 2.2 (intermediate = I), 2.3 to 2.6 (moderately susceptible = MS), and 2.7 to 3.0 (very susceptible = VS). Considerable variability in inoculation response existed within and between species at both the diploid and octoploid levels. VR or MR genotypes were found within each of the following species: diploids F. vesca, F. iinumae, and *F. nipponica*); and octoploids *F. chiloensis, F. virginiana,* and *F. ×ananassa*. MS and VS genotypes were

[1] This chapter is revised from a manuscript is submission process to Genetic Resources and Crop Improvements Vining, K.J., T.M. Davis, A.R. Jamieson, L.L. Mahoney. **Verticillium** wilt resistance varies within ploidy levels in strawberry (*Fragaria* spp.)

documented within *F. vesca*, within each octoploid species, and in a genotype of decaploid *F. cascadensis.*

We then compared our screening results to those of previous studies, aided by a constructed pedigree of evaluated and related octoploid cultigens (cultivars and breeding clones). We also made resistant × susceptible crosses at both the diploid and octoploid levels as a step toward genetic analysis of wilt resistance/susceptibility and resistance gene identification in strawberry.

Introduction

The fungal disease verticillium wilt has been a major obstacle to U.S. strawberry production since first identified and described by Thomas (1931). In most major U.S. strawberry production areas, methyl bromide and chloropicrin have been the foundation for control of soil-borne disease organisms (Samtani et al. 2012), including *Verticillium dahliae* Kleb., the causal agent of verticillium wilt. However, the classification of methyl bromide as an ozone depleting chemical under the Montreal Protocol in 1987, and by the U.S. Environmental Protection Agency in 1993, has prompted the development of alternative chemical treatment practices (Environmental_Protection_Agency 2013). Non-chemical alternatives such as steam and solarization treatments have shown promise, but have not been demonstrated to be cost effective (Samtani et al. 2012). Verticillium wilt was a serious disease before the advent of soil fumigation (Shaw et al. 1997, Sjulin 2003), and it continues to be a significant problem for strawberries.

At least partial relief from the problems posed by verticillium wilt could be provided by incorporation of genetic resistance into new commercial strawberry varieties. While enhanced wilt resistance has been obtained in strawberry via the introduction of a chitinase gene (Chalavi et al. 2003), the genetic engineering approach would also negate the opportunity to exploit the burgeoning organic production niche. The skyrocketing demand for organic strawberries from $2 million in 1997 to $55 million in 2009 has stimulated intensive interest among breeders in the prospect of developing wilt resistant strawberry varieties (Koike et al. 2012). The foregoing realities emphasize the need to

identify and exploit naturally occurring sources of genetic resistance and the need to breed for resistance.

Quantitative genetic variation for field resistance to verticillium wilt was documented in cultivated strawberry breeding populations in the mid-twentieth century (Varney et al. 1959, Bringhurst et al. 1961, Bowen et al. 1968) and more recently by (Shaw et al. 1996), Shaw et al. (1997), (Shaw et al. 2003), indicating the potential for enhancing resistance through breeding. Shaw et al. (2005) asserted that genetic resistance to wilt is best regarded as one component of an integrated management system that also includes efforts to reduce pest populations at all growth stages. Nevertheless, it is evident that considerable potential exists for improving wilt resistance through germplasm evaluation and breeding, and that the full potential for genetic resistance to verticillium wilt in the cultivated strawberry has yet to be defined or realized.

The strawberry genus *Fragaria* is remarkably diverse, encompassing more than 23 species and spanning ploidy levels from diploid ($2n = 2x = 14$) to decaploid ($2n = 10x = 70$) (Staudt 2009, Nathewet et al. 2010). The octoploid ($2n = 8x = 56$) cultivated strawberry, *Fragaria ×ananassa*, is known to have arisen via hybridization between its octoploid ancestors, *F. chiloensis* and *F. virginiana*, in the mid-1700s (Darrow 1966). Phylogenetic and genomic studies have implicated ancestral forms of diploids *F. vesca* and *F. iinumae* as likely genome donors to the octoploids (Folta et al. 2006); however, the evolutionary pathway from the diploid to the octoploid level is yet to be delineated (Davis et al. 2009). Each of the ancestral octoploids has multiple subspecies: *F. chiloensis* has subspecies *chiloensis*, *patagonica*, *lucida*, and *pacifica*; while *F. virginiana* has subspecies *virginiana*, *grayana*, *glauca*, and *platypetala* (Staudt 1999).

An effort to reconstruct *Fragaria* ×*ananassa* by crossing representatives of *F. chiloensis* and *F. virginiana* was initiated (Hancock et al. 1993) and is ongoing (Hancock et al. 2010).

A broad sampling of the diversity present in *F. chiloens*is and *F. virginiana* is represented by the 38 accessions comprising the USDA "supercore" collection (Hancock et al. 2000). We have obtained this collection from the National Clonal Germplasm Repository (NCGR) in Corvallis Oregon, and maintain it as part of a broader collection of over 600 genetically unique strawberry plants, including species, hybrids, and segregating populations, at the University of New Hampshire. In the present study, we evaluated representatives of five diploid species, three octoploid species, and – serendipitously – one representative of decaploid *F. cascadensis*. At the time that this study was initiated, NCGR accession CFRA 110 was identified as octoploid *F. virginiana* ssp. *platypetala*. However, it has since been determined to be decaploid (Nathewet et al. 2010), and to belong to the newly defined decaploid species, *F. cascadensis* (Hummer 2012).

Our ongoing investigations are concerned with defining new sources of resistance in cultivated and wild strawberry germplasm, and with advancing genetic studies on the basis of resistance/susceptibility. This communication is conceptually divided into two components. First, we present the results of our own inoculation screens aimed at identifying new sources of resistance: at the octoploid level as resources for breeding, and at the diploid level to facilitate efforts to isolate and characterize resistance genes. Second, we submit a compendium of previous verticillium wilt studies in strawberry, both wild and cultivated e.g. (Varney et al. 1959, Varney et al. 1960, Bringhurst et al.

1961, vanAdrichem et al. 1962, Maas 1984, Maas et al. 1989, Hancock et al. 1991, Shaw et al. 1996, Olbricht et al. 2009). As a means of effectively positioning our study within this historical context, we have constructed an extensive pedigree depicting the ancestries of the tested cultivars, and wherever possible, including their previously reported verticillium wilt resistance ratings. Although differing rating terminologies have been employed by previous authors, we have integrated the findings of previous investigators with our own.

Materials and Methods

Plant and fungal materials

Information about the studied plant accessions, their geographic origins (wild-collected materials) or breeding program sources, and their identification numbers (local and/or Plant Introduction) is provided for diploids and polyploids, respectively, in Tables 1 and 2. Subspecies designations are not provided for California accessions of *F. vesca* due to uncertainty in differentiating the subspecies *Fragaria vesca* ssp. *bracteata* from *F. vesca* ssp. *californica* and their possible hybrids. Among diploid accessions (Table 3.1); CFRA364.002, CFRA333.001, and CFRA520.001 were obtained from the NCGR, accessions from Hokkaido, Japan were collected by Thomas M. Davis and Kim Hummer (Hummer et al. 2006), and GS1J was collected by Gunter Staudt. All other UNH-numbered accessions were collected by Davis. The polyploid accessions of octoploids *Fragaria virginiana* and *F. chiloensis*, and decaploid *F. cascadensis* belonging to the *Fragaria* supercore collection were obtained from the NCGR. The studied *F.* ×*ananassa* accessions were of interest to our breeding programs. Plants of 'Sparkle' and 'Tristar' were purchased from Nourse Farms, Whately MA, while the other cultivars and breeding lines were provided by Andrew R. Jamieson. As distinct from wild germplasm, we refer collectively to advanced breeding selections and named cultivars as cultigens. *F.* ×*ananassa* cultivars 'Annapolis', 'Cavendish', 'Evangeline', 'Mira', 'Wendy' (aka 'AC Wendy'), and 'Laurel' (tested as K93-20), and numbered breeding clones K05-9 and

M903 were developed at the Agri-Food Canada Kentville Research Station, Nova Scotia, Canada. Cultivar 'Sparkle' is a 1942 release from the New Jersey State University breeding program (Darrow 1966), and was included as an old time Northeastern favorite. 'Tristar' is a 1981 release from the USDA Beltsville program and was included as a day-neutral variety.

Screening methods

A series of trials was conducted in which from five to 20 genotypes were screened. In each trial, each genotype was represented by three-to-four inoculated and two uninoculated (control) plants. Pots containing inoculated or uninoculated plants were maintained within separate containment trays, and plants were randomly distributed within the trays. Some genotypes were included in multiple trials.

Verticillium dahliae isolate V1 was obtained from Mansun Kong at Driscoll Strawberry Associates, Watsonville, CA, USA, and was originally isolated from an infected strawberry plant (M. Kong, personal communication). Plants were maintained in the UNH MacFarlane Greenhouse facility in Pro-Mix Mycorrhizae™ (Premier Tech Horticulture LTD, Canada), and were propagated by rooting stolons that were still attached to mother plants to produce runner plantlets. Runner nodes were pinned onto the surface of Metro-mix 360 (Hummert™ International, Missouri) medium in 4" standard round polypropylene pots (Dillen Products Company, Ltd., Middlefield, Ohio) using staples made from plastic-coated wire. Plantlets were allowed to root for two weeks prior to separation from the mother plant and inoculation. Ten plantlets were rooted from each mother plant, and eight were ultimately used in each trial (four inoculated plantlets and four uninoculated controls). Concurrent with plant propagation, fungal

inoculum was cultured in an appropriate volume (~10 ml for each plant to be inoculated) of autoclaved Difco™ Czapek-Dox broth (BD Biosciences). The broth, contained in 1L flasks, was inoculated in a laminar flow hood with two to four ~1 cm^2 pieces of fungus-covered Czapek-Dox agar from fungal culture plates. The inoculated broth was then incubated for two weeks at room temperature on an orbital shaker at 200 RPM.

On the day of inoculation, the fungal culture was strained through two layers of cheesecloth and one layer of Miracloth (EMD Millipore, Billerica, Massachusetts), and then centrifuged at 10,000 x g for 5 min. The culture medium was decanted and the conidial pellet was resuspended in a volume of sterile distilled water equivalent to that of the decanted culture medium. Conidia were quantified using a hemacytometer (Bright Light Counting Chamber Improved Neubauer, Hausser Scientific, Horsham Pa), and the suspension was diluted, if necessary, with sterile distilled water to ~2 x 10^7 conidia/ml. Immediately prior to root dipping, rooted plantlets were separated from mother plants and trimmed to remove runners. Soil was shaken from roots prior to dipping. Root dipping was performed in 50-ml polyvinyl chloride pipet basins (Fisher Scientific, Pittsburgh, PA). Root systems were immersed, two at a time per basin, for 5 min in either 20 ml fungal spore suspension or 20 ml sterile distilled water (uninoculated control). After dipping, the plants were replanted in new 4" pots containing sterile (autoclaved) Metromix medium, and then moved to a greenhouse under ambient light and temperature conditions or to a 22 ^{o}C temperature-controlled growth room under broad-spectrum (140 µmoles/m^2/sec) fluorescent lights. Plants were then maintained in containment trays with minimal watering for a period of at least eight weeks.

Plant verticillium wilt disease rating

At the end of the observational period, each individual plant was rated relative to controls according to the following rating scale, as exemplified by plants shown in Figure 3.1. A rating of 1.0 (healthy) was given to plants closely resembling uninoculated controls. A rating of 1.5 (slightly symptomatic) indicated mild stunting and/or mild outer leaf necrosis and/or browning. A rating of 2.0 (mildly symptomatic) indicated distinct stunting and/or distorted growth, more leaf necrosis and browning, and perhaps one or two dead leaves. A rating of 2.5 (very symptomatic) was given to plants with severe stunting, leaf necrosis and browning, yet still having one to a few green leaves. A 3.0 (dead) rating indicated that all of the leaves were necrotic and the plant was considered to be nearly or completely dead. Each accession was initially represented in each trial by four inoculated plants, plus controls; however, in a few

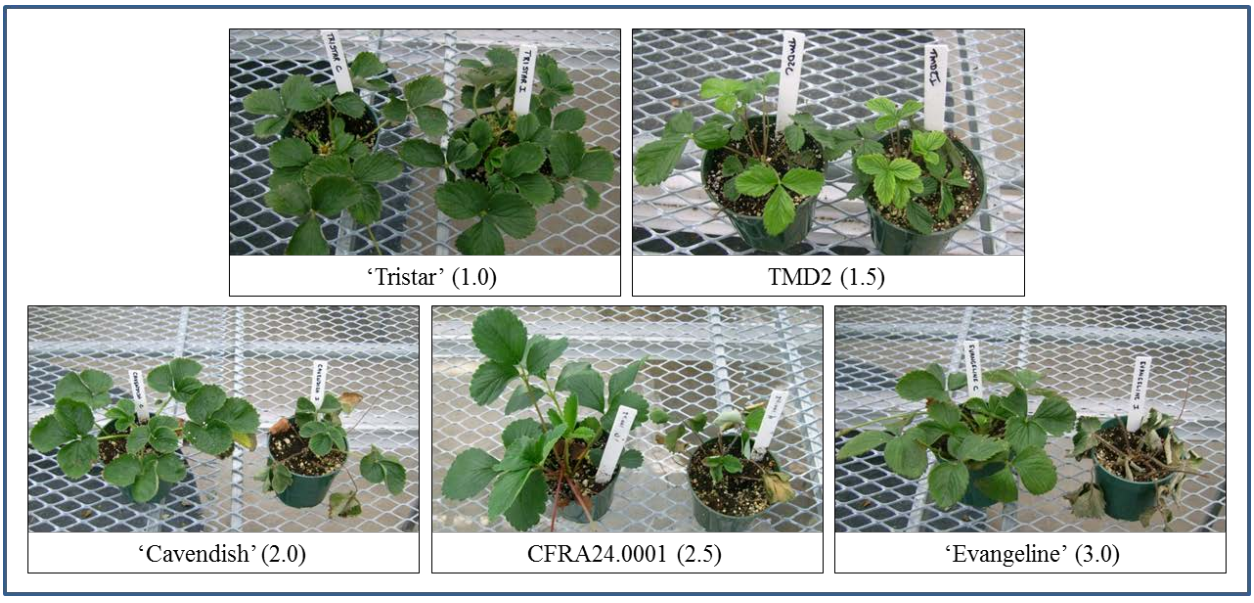


Figure 3.1: Disease ratings and examples of their respective verticillium wilt phenotypes. Within each panel, a control plant is shown on the left, and an inoculated plant of the same variety is shown on the right along with its disease rating (number in black box).

cases, a plantlet was lost due to causes not related to verticillium wilt, and only three inoculated plants were rated. For each accession, the mean rating and associated standard deviation were calculated over the total number of replicates.

As guided by previous literature (Bringhurst et al. 1961, Bringhurst et al. 1966, Olbricht et al. 2009), we then assigned a classification to each genotype based upon its mean disease rating. The rating ranges and corresponding classifications (in parentheses) were: 1.0 to 1.3 (very resistant = VR), 1.4 to 1.7 (moderately resistant = MR), 1.8 to 2.2 (intermediate = I), 2.3 to 2.6 (moderately susceptible = MS), and 2.7 to 3.0 (very susceptible = VS).

Summary of published sources of verticillium wilt resistance ratings in octoploid strawberry

Relevant information sources were identified using searches of scientific literature and the USDA Germplasm Resources Information Network (GRIN) database (http://www.ars-grin.gov/), and keyword web searches. The pedigree relationships of the rated cultigens were then determined by extracting relevant information from the RosBREED "Breeding Information Management System" (BIMS) crop reference set for *Fragaria* (http://www.rosaceae.org/breeders_toolbox), and integrating it with information from published cultivar release announcements to create a project-specific database. Verticillium resistance ratings from the present study (Table 3.2) and resistance categories from various literature sources (Table 3.3) were then added to the database. We traced the pedigrees of the studied cultivars and breeding clones to find common ancestors. Finally, the pedigree relationships and verticillium resistance ratings, where available, were depicted in the form of an annotated pedigree map, which was constructed using Pedimap™ software (Wageningen UR – Plant

Breeding). The development of the BIMS crop reference data set and current Pedimap resource are products of the USDA-NIFA-SCRI RosBREED and EU-FruitBreedomics (www.fruitbreedomics.com) projects.

Results

The results of our verticillium inoculation response screenings are summarized for the diploid and polyploid genotypes, respectively, in Tables 1 and 2. In the tables, the accessions are ordered by species, subspecies, and mean disease rating, where the latter value is the mean of the individual plant scores for the accession in question. On the basis of their mean disease ratings, the assayed genotypes were then classified as VR, MR, I, MS, or VS, and our classifications of octoploid germplasm were integrated where appropriate into Table 3.3 for comparison with those of previous investigators.

Some accessions that displayed relatively high levels of resistance or susceptibility were screened more than once, with the aim of confirming their suitability for use as parents in resistant × susceptible crosses. In early trials, diploid *Fragaria vesca* accession TMD2 was identified as moderately resistant and BC30 was identified as very susceptible, while among octoploid accessions *Fragaria virginiana* CFRA1699 was identified as very resistant and CFRA1455 and CFRA1408 were identified as very susceptible. These five accessions were used as resistant and susceptible controls, respectively, in subsequent trials, and therefore are represented by larger numbers of inoculated plants as indicated in the "N" column in Table 3.2. Importantly, these comparator accessions displayed consistent resistant or susceptible responses under both greenhouse and growth room conditions.

At the diploid level, the mean ratings of the 15 *F. vesca* accessions ranged from 1.5 to 3.0 (Table 3.1). The most resistant *F. vesca* accessions, all with mean ratings of 1.5, were one accession from British Columbia (BC5) and two from Mendocino County, California (U2A and TMD2); while the most susceptible, all with mean ratings of 2.9 to 3.0, were three accessions from British

Columbia (BC3, BC30, and GS1J), two from California (DN2A and HP3A) and one from New Hampshire ('Pawtuckaway'). The three representatives of *F. vesca* subsp. *americana* (WC6, WC8, and 'Pawtuckaway') all had mean ratings in the moderately-to-very susceptible range (2.6 to 3.0), while both resistance and susceptibility was seen among the *F. vesca* accessions from California and among those from British Columbia. The other diploid accessions included three species (*F. bucharica*, *F. iinumae*, and *F. viridis*) and one interspecific hybrid (CFRA364) that were each represented by a single accession and had mean ratings in the very-to-moderately resistant range of 1.0 to 1.7 (Table 3.1). Among the four accessions of *F. nipponica*, mean ratings ranged from 1.3 (very resistant) to 2.0 (intermediate).

Among the wild polyploid accessions, the mean ratings of octoploids *F. chiloensis* and *F. virginiana* ranged from 1.6 to 3.0 and 1.2 to 3.0, respectively (Table 3.2). The only wild octoploid accession categorized as "very resistant" was *F. virginiana* subsp. *virginiana* CFRA1699, while three and four accessions of *F. chiloensis* and *F. virginiana*, respectively, were categorized as "very susceptible". The single representative of decaploid *F. cascadensis* (CFRA110) was also categorized as very susceptible (mean rating 3.0). Among the ten cultigens of octoploid *F.* ×*ananassa*, mean ratings ranged from 1.0 to 3.0 (Table 3.2). 'Tristar' (1.0) and breeding clone M903 (1.3) were categorized as very resistant, while 'Mira', 'Evangeline', 'Laurel', and breeding clone K05-9 were categorized as very susceptible. Of the remaining four cultigens, three were intermediate and one was moderately susceptible. We examined the ancestries of rated cultigens with the aid of the constructed pedigree (Figure 3.2), with the exception of very susceptible rated breeding clone K05-9 which, as an open-pollinated selection from an unknown Driscoll variety has unknown parentage and so could not be integrated into the

pedigree. Previous verticillium resistance ratings were unavailable for both parents of 'Tristar', 'Evangeline' and 'M903', while ratings for only one parent each were available for 'Wendy', and 'Annapolis'. Among the four cultigens for which both parents had available ratings, the very susceptible 'Mira' had very susceptible parents 'Scott' and 'Honeoye'; the very susceptible 'Laurel' had intermediate parents 'Allstar' and 'Cavendish'; the very susceptible 'Sparkle' had as parents intermediate 'Fairfax' and very resistant 'Aberdeen'; and the intermediate 'Cavendish' had as parents very susceptible 'Glooscap' and intermediate 'Annapolis'. Similarly, in some instances where all ratings came from literature sources, very resistant 'Etna' had very susceptible parents 'Belrubi' and 'Marlate'; moderately resistant 'Temple' had as parents very resistant 'Aberdeen' and intermediate 'Fairfax'; and very susceptible 'Bounty' had as parents very susceptible 'Jerseybelle' and very resistant 'Senga Sengana' (Figure 3.2).

Based upon the foregoing results, we identified promising intra-specific crossing combinations between moderately (MR) or very resistant (VR) and very susceptible (VS) parents, at the diploid (F. vesca) and octoploid (F. virginiana) levels, respectively: diploid TMD2 (MR) × BC30 (VS); octoploid CFRA1408 (VS) × CFRA1699 (VR), and octoploid CFRA1455 (MS) × CFRA1699 (VR). We have performed the indicated crosses and generated F1 hybrid progeny. The results from an initial screening (to be reported elsewhere) are indicative of segregation for resistance/susceptibility in the F1 progeny of each cross, suggesting that one or both parents in each cross are heterozygous for genetic determinants of resistance.

In our literature survey, ratings were found for 67 cultigens in studies performed during the period of 1955-2013 (Table 3.2). There were 33 instances wherein a given cultivar was rated by two or more studies. The present study added ratings for five cultivars that had not been previously evaluated for verticillium resistance and complemented ratings for four cultivars that

had been previously studied. The prior investigations employed varying terminologies for qualitative classification of resistance/susceptibility. The terminologies we have used in summarizing ratings reports from these prior studies in Table 3.3 are those of the respective investigators and/or conversions or extrapolations of prior ratings to those categories used in the present study.

Table 3.1: The inoculation responses of diploid *Fragaria* genotypes.

Taxon	Origin	PI numbers[z]	CFRA[z]	Local name[y]	N[x]	Mean[x]	STD[x]
F. vesca	BC, Canada	660763	1988.00	BC5	4	1.5	0.0
F. vesca ssp.[w]	Mendocino, Co. CA	660765	1990.00	TMD2	32	1.5	0.5
F. vesca ssp.[w]	Mendocino Co.,CA	NA	NA	U2A	4	1.5	0.6
F. vesca ssp.[w]	BC, Canada	NA	NA	BC7	4	2.0	0.0
F. vesca	Santa Cruz Co., CA	TBD	2185	HP6A	4	2.3	0.5
F. vesca ssp.	Santa Cruz Co., CA	NA	NA	HP7B	4	2.5	0.6
F. vesca ssp.	Coos Co.,NH	TBD	2186	WC6	4	2.5	0.6
F. vesca ssp.	Coos Co.,NH	TBD	2187	WC8	4	2.8	0.3
F. vesca ssp. [w]	Humboldt Co., CA	NA	NA	H1B	4	2.8	0.5
F. vesca ssp. [w]	Del Norte Co.,CA	TBD	2188	DN2A	7	2.9	0.2
F. vesca ssp.	Santa Cruz Co., CA	TBD	2189	HP3A	4	2.9	0.3
F. vesca ssp.	BC, Canada	660764	1989.00	BC30	11	2.9	0.2
F. vesca ssp.	BC, Canada	TBD	2190	BC3	8	3.0	0.0
F. vesca ssp.	BC, Canada	TBD	2191	GS1J	4	3.0	0.0
F. vesca ssp.	Rockingham Co., NH	657856	1948.00	Pawtuckaway	4	3.0	0.0
F. bucharica	Pakistan	551851	520.001	880083 Pakistan	4	2.0	0.0
F. iinumae	Hokkaido, Japan	637964	1850	J7	4	1.3	0.5
F. nipponica	Hokkaido, Japan	637979	1866	J32	4	1.3	0.3
F. nipponica	Hokkaido, Japan	637980	1868	J34	12	1.3	0.4
F. nipponica	Hokkaido, Japan	637977	1864	J30A	3	1.7	0.6
F. nipponica	Hokkaido, Japan	637975	1862	J25	4	2.0	0.0
F. vesca× *F. viridis*	uncertain*	551744	364.002	CA 1450	4	1.6	0.3
F. viridis	Germany	551741	333.001	CA 72.501-2	4	1.8	0.5

[z] NCGR *Fragaria* accessions have National Plant Germplasm System (NPGS) PI numbers and local numbers with the prefix CFRA. TBD = Awaiting assignment of PI number. NA = not applicable, not part of NPGS.

[y] Local names/numbers used by original collectors (all UNH numbers in Table 3.1 and various collectors' local numbers in Table 3.2).

[x] N = number of replicate plants; Mean = the mean disease score for the indicated N; SD = standard deviation of the mean.

[w] California accessions of *F. vesca* subspecies are difficult to differentiate and may be either ssp. *bracteata*, ssp. *californica*, or hybrids thereof.

Table 3.2. Inoculation responses of 8*x* and 10*x* (*F. cascadensis*) *Fragaria* genotypes. The superscript definitions are as in the footnotes of Table 3.1.

Taxon	Origin	PI no.[z]	CFRA[z]	Local name[y]	N[x]	Mean[x]	SD[x]
F. chiloensis f. chiloensis	Peru	551736	372.002	CA1541	4	1.6	0.3
F. chiloensis ssp. *lucida*	CA, USA	551728	357.002	CA1367	16	1.7	0.6
F. chiloensis ssp. *patagonica*	Chile	236579	24.001	Darrow 72	8	2.4	0.5
F. chiloensis ssp. *patagonica*	Chile	602570	1108.002	2 CAR 3B	4	2.5	0.6
F. chiloensis ssp. *patagonica*	Chile	612316	1088.002	2 BRA 1A	4	2.5	0.6
F. chiloensis ssp. *lucida*	OR,USA	612489	1691.001	HM1	12	2.9	0.4
F. chiloensis ssp. *patagonica*	Chile	552091	796.001	Termas de Chillan-TDC	4	3.0	0.0
F. chiloensis ssp. *lucida*	CA, USA	551445	34.002	RCP 37	6	3.0	0.0
F. virginiana ssp. *virginiana*	ON, Canada	612497	1699.001	Montreal River 10	9	1.2	0.3
F. virginiana ssp. *grayana*	MS, USA	612569	1414.001	NC 95-19-1	6	2.2	1.0
F. virginiana ssp. *grayana*	FL, USA	612570	1435.002	JP 95-1	4	2.5	1.0
F. virginiana ssp. *grayana*	GA, USA	612320	1455.001	JP 95-9-6	26	2.6	0.7
F. virginiana ssp. *virginiana*	NC,USA	612325	1620.001	NC96-5-3	4	2.8	0.5
F. virginiana ssp. *grayana*	MS, USA	612486	1408.001	NC 95-19-1	7	2.9	0.4
F. virginiana ssp. *grayana*	FL,USA	612570	1435.001	JP95-1	3	3.0	0.0
F. virginiana ssp. *glauca*	MT, USA	612495	1697.001	LH 50-4	4	3.0	0.0
F. cascadensis (10*x*)	Oregon	551527	110.001	-	4	3.0	0.0
F. ×*ananassa* 'Tristar'	USDA-MD	551954	663.001	EB60	4	1.0	0.0
F. ×*ananassa* 'M903	NS, Canada	NA	NA	M903	3	1.3	0.6
F. ×*ananassa* 'Cavendish'	NS, Canada	616560	1169.000	K83-4	4	2.0	0.0
F. ×*ananassa* 'Annapolis'	NS, Canada	552257	964.001	K78-4	4	2.0	0.0
F. ×*ananassa* 'Wendy'	NS, Canada	NA	NA	K98-6	4	2.0	0.0
F. ×*ananassa* 'Sparkle'	NJ, USA	551559	183.001	'Paymaster'	3	2.5	0.6
F. ×*ananassa* 'Mira'	NS, Canada	NA	NA	K84-5	4	2.8	0.5
F. ×*ananassa* 'Evangeline'	NS, Canada	NA	NA	K93-1	4	3.0	0.0
F. ×*ananassa* K05-9	NS, Canada	NA	NA	K05-9	4	3.0	0.0
F. ×*ananassa* 'Laurel'	NS, Canada	NA	NA	K93-20	4	3.0	0.5

Table 3.3: Information sources for members of pedigree shown in Figure 3.2. In the Information Sources column, results from the present University of New Hampshire (UNH) study are **underlined in bold**.

Cultigen	Qualitative Score[z]	Information Sources
Aberdeen	VR[1], VR/MS[2]	[1]Bringhurst et al.1961, Maas et al 1989; [2]Eastern/California isolates, Maas and Galletta 1989
Allstar	I[1], I-T[2], MR[3]	[1]Maas et al 1989; [2] (Galletta et al. 1981) , Maas 1984; [3]Galletta et al. 1982
Annapolis	MR[1], I[2]	[1]Jamieson and Nickerson 1989, [2]Maas et al 1989, **UNH result**
Belrubi	VS	Gaggioli et al., 1989
Blakemore	MR	GRIN, (Amenduni et al. 2004), Wilhelm 1955a, Maas 1984, Maas et al. 1989
Bounty	VS[1], I[2]	[1]Jamieson and Nickerson 1989, Maas 1984; [2]Maas et al. 1989
Cal_39.117-4	I	Bringhurst et al.1961
Cal_42.8-16	VR[1], MR[2]	[1]Bringhurst et al.1961; [2]Bringhurst et al. 1966
Cal_43.1-36	MR	Bringhurst et al. 1961
Cal_53.10-2	I	Bringhurst et al. 1961
Cavendish	I[1], MR[2]	[1]**UNH result**; [2]GRIN; [50]Jamieson et al.1991
Earlibelle	MS	(Scott et al. 1979)
Earlidawn	VS[1], I[2]	[1]GRIN, Maas 1984, Varney et al. 1959; [2] Bowen et el 1968, Shaw et al. 1996
Earliglow	T[1],MR[2], MS[3], I[4]	[1] (Galletta et al. 1982), [2]Maas 1984, Maas et al. 1989; [3]Bowen et el 1968; [4]GRIN, Shaw et al. 1996
Elsanta	VS	GRIN, (Daugaard et al. 2000), Labanowski 2003, Olbricht et al. 2009, Sowik et al., 2001
Eros	MS	GRIN
Etna	R	Gagglioli et al. 1989
Evangeline	VS	**UNH result**
Fairfax	I[1], MS[2]	[1]Maas et al. 1989; [2]Varney et al. 1959
Fairland	I	Varney et al. 1959
Glooscap	VS	(Bordelon et al. 2001)
Gorella	VS	Gaggioli et al. 1989

Cultigen	Qualitative Score[z]	Information Sources
Holiday	I	Maas 1984
Honeoye	VS	GRIN (Agriculture 2013),Labanowska et al. 2003, Maas et al. 1989, Maas and Galletta 1989, (Gaggioli et al. 1989), (Jamieson et al. 1989), Maas 1984
Howard_17	MS[1], VR/MR[2]	[1]Wilhelm 1955a; [2]USDA/Kellogg, Bringhurst et al. 1961
Jerseybelle	MS[1], VS[2]	[1]Maas et al. 1989, Maas 1984; [2]GRIN, Varney et al. 1959, Varney et al., 1960
Juspa	MR	Darrow, 1966
Lassen	MS[1], VS[2]	[1]Bringhurst et al. 1966, Shaw et al. 1996; [2]GRIN, Bringhurst et al.1961, Wilhelm, 1955b
Laurel	VS	**UNH result**
Marlate	VS	Maas 1984
M903-3	VR	**UNH result**
MDUS_1972	VR	Varney et al. 1959
MDUS_2321	MS	Varney et al. 1959
MDUS_2359	MS	Varney et al. 1959
MDUS_2650	VR	Varney et al. 1959
MDUS_683	MR[1],VR[2], MS[3]	[1]Varney et al. 1960; [2]Maas et al. 1989, [3]VR/MS Eastern/California isolates, Maas and Galletta 1989
Micmac	MR[1], I[2]	[1]Maas et al. 1989; [2]Maas 1984
Midland	VS	Varney et al. 1959, Maas 1984
Mira	VS	**UNH result**
Missionary	MS	Varney et al. 1959, Wilhelm 1955a
NC_1768	MR	Varney et al. 1959
Nich_Ohmer	I	[1]
Parker	MR	Shaw et al. 1996
Pocahontas	I	Varney et al. 1959, Maas et al. 1989
Raritan	MR[1], MS[2]	[1]Maas et al. 1989; [2]GRIN, Maas 1984
Redcoat	VS	GRIN, Maas 1984

Cultigen	Qualitative Score[z]	Information Sources
Redglow	I[1],MS[2]	[1]Varney et al. 1959, Bowen et el 1968; [2]Maas 1984
Redheart	I	Maas 1984
Redstar	VS[1], I[2]	[1]Varney et al. 1959;[2]Maas 1984
Royal Sovereign	R	Hancock et al., 1991
Scott	MR[1], I to MR[2]	[1]GRIN, Maas et al. 1989; [2](Galletta et al. 1980), Maas 1984
Selkirk	MS	(Dale et al. 1993)
Senga_Sengana	VR/T[1], MS[2], VS[3]	[1](Labanowska et al. 2004) (T) Olbricht et al. 2009; [2]combined with nematodes Potter and Dale 1991; [3] (Sowik et al. 2001)
Shasta	MR[1], MS[2], VS[3]	[1](Wilhelm 1955)[2]GRIN, Bringhurst et al. 1966, Maas 1984; [3]Bringhurst et al. 1961
Sierra	VR[1], MR[2]	[1][(Wilhelm 1955)Maas & Galletta 1989; [2]GRIN, Amenduni et al 2004, Bringhurst et al 1966, Maas 1984, Wilhelm 1955b
Solana	MS[1], VS[2]	[1]Bringhurst et al. 1966; [2]Bringhurst et al. 1961
Sparkle	I[1], MS[2]	[1]Maas et al. 1989; [2]GRIN, Maas 1984, Varney et al. 1959, **UNH result**
Stelemaster	I	Maas 1984
Sunrise	VR[1], MR[2]	[1]Maas 1984; [2]Maas et al. 1989
Surecrop	VR[1], MR[2]	[1]Bowen et el 1968, Maas 1984, Varney et al. 1959; [2]GRIN, Galletta et al. 1982, Maas et al. 1989
Temple	MR	Varney et al. 1959
Tenn_Beauty	MR	(Babadoost 2001)
Tenn_Shipper	MR	Varney et al. 1959
Tioga	MS[1], VS[2]	[1]Maas 1984; [2]GRIN, (Bringhurst et al. 1980)
Tristar	VR[1], T[2], MR[3]	[1]Draper et al. 1981, **UNH result**; [2]GRIN; [3]Galletta et al. 1982, Maas et al. 1989
Veestar	MR	GRIN
Wendy	I	**UNH result**

[z]Scores (VS = Very Susceptible, MS = Moderately Susceptible, I = Intermediate, MR = Moderately Resistant, VR = Very Resistant, T = Tolerant, U = Unknown). Note: the term "tolerant" has been used in differing ways by various authors. The superscript following the qualitative rating corresponds to the superscript preceding the cited literature in the same row.

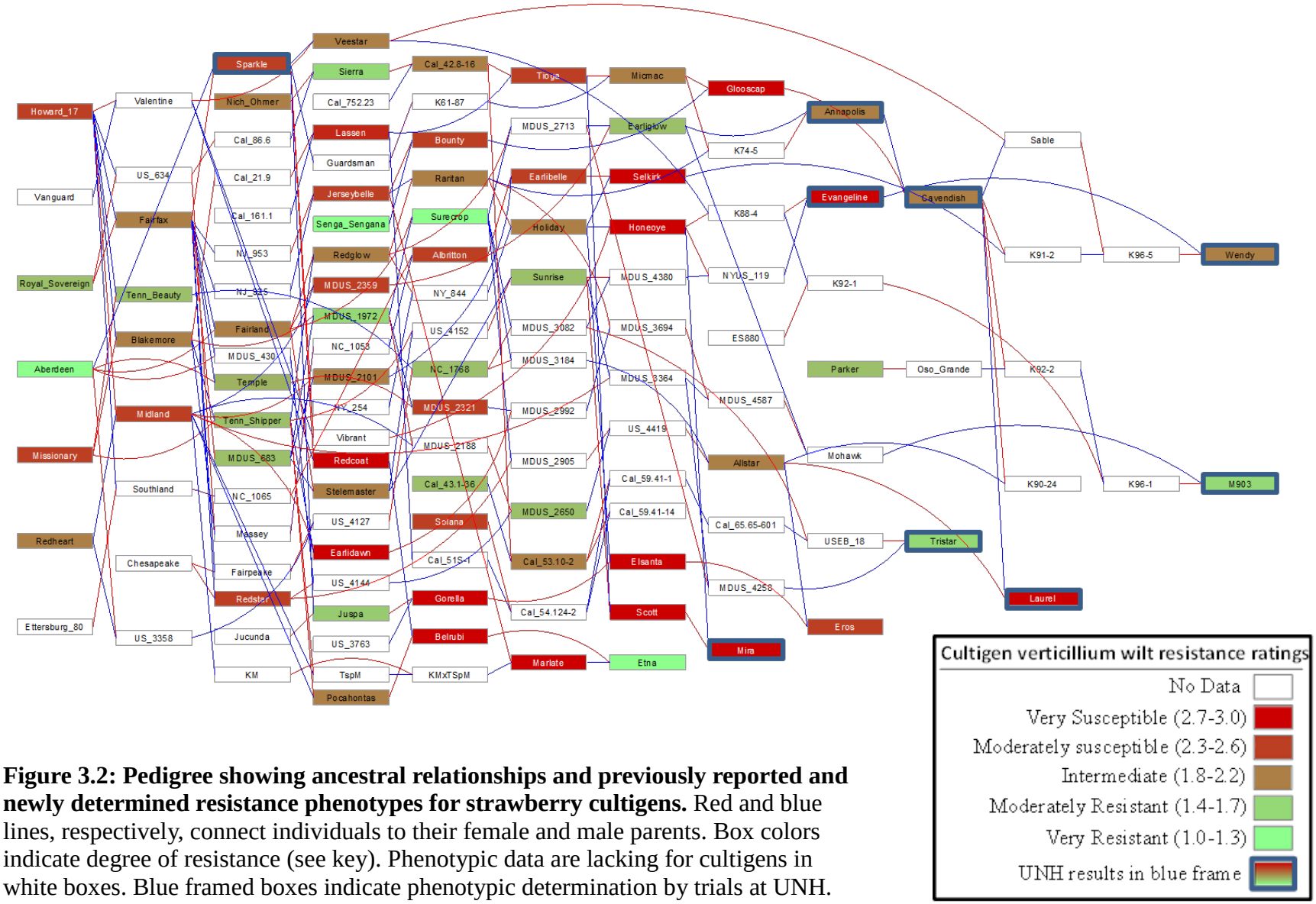


Figure 3.2: Pedigree showing ancestral relationships and previously reported and newly determined resistance phenotypes for strawberry cultigens. Red and blue lines, respectively, connect individuals to their female and male parents. Box colors indicate degree of resistance (see key). Phenotypic data are lacking for cultigens in white boxes. Blue framed boxes indicate phenotypic determination by trials at UNH.

Discussion

Phenotypic assessment provides guidance to the collection and archiving of plant germplasm, and generates knowledge resources of value to breeders and geneticists interested in understanding and manipulating specific traits. The trait of interest to the present study is resistance/susceptibility to the destructive fungal disease, verticillium wilt. This report advances knowledge about the occurrence and inheritance of wilt resistance and susceptibility in wild and cultivated strawberry germplasm in the following ways. First, we present new disease resistance/susceptibility data for 50 Fragaria germplasm accessions representing three levels of ploidy. We also summarize and synthesize pre-existing knowledge and resistance ratings from diverse publicly available but in some cases obscure sources. Finally, we define and informatively display pedigree relationships among a selected group of resistant and susceptible strawberry cultigens, thereby graphically documenting both the extent of, and the gaps in, present knowledge about verticillium susceptibility in a coherent assemblage of important strawberry germplasm.

In the performance of our verticillium wilt resistance/susceptibility screenings, we employed a five point categorical rating scale that, on a single plant basis, ranged from “healthy” to “dead”. We also employed a parallel scale for classifying genotypes based upon their mean ratings, ranging from very resistant (VR) to very susceptible (VS).

In our screenings of diploid germplasm, broad variability in disease responses was observed among the sixteen *Fragaria vesca* accessions, ranging from moderately resistant to very susceptible. The evident biodiversity within *F. vesca* provides an attractive opportunity for association genetics studies within this species, which among strawberry species is currently

unique in having an available reference genome sequence (Shulaev et al. 2011). Among the other diploids tested, all ratings fell within the intermediate to very resistant range. As in our own study, (Olbricht et al. 2009) detected variation for verticillium wilt resistance/susceptibility both within and between *Fragaria* species. Among ten diploid species tested by (Olbricht et al. 2009), susceptibility was reported in at least one representative each of five diploid species, including the only identified *F. vesca* accession included in their study. Perhaps importantly, consistent "tolerance," where the pathogen was internally present but the host plant was asymptomatic, was found only in *F. iinumae* (Olbricht et al. 2009), while in our own study the only tested representative of *F. iinumae* ranked among the most resistant of our diploid accessions (Table 3.1). Like *F. vesca*, *F. iinumae* is of particular interest because of its status as an ancestral subgenome donor to the octoploid species (Folta et al. 2006).

At the octoploid level, the opportunity to identify sources of resistance for exploitation in breeding programs is of particular interest. Although a panel of octoploid cultivars was included in our study, as later discussed, we emphasized the analysis of wild octoploid germplasm belonging to the USDA supercore collection (Hancock et al. 2001). Upon incorporation into the GRIN database, our results will add further value to the supercore collection by expanding the knowledge resources associated with its members.

Among the wild polyploids, high levels of susceptibility were found in at least one representative of each of the two octoploid species, *F. chiloensis* and *F. virginiana*, and in the only representative of decaploid *F. cascadensis*. Moderate to elevated levels of resistance also occurred in each of the wild octoploid species; however, of the wild octoploids only *F. virginiana* subsp. *virginiana* accession Montreal River 10 (CFRA1699) was rated as very resistant. CFRA1699 has also been determined to possess a number of favorable horticultural

traits, including resistance to common foliar diseases, and has been used extensively in the *F.* ×*ananassa* reconstruction project (Hancock et al. 2001, Hancock et al. 2010, Stegmeir et al. 2010). Another accession, LH50-4 (CFRA1697), used extensively in the *F.* ×*ananassa* reconstruction project due to its day-neutrality trait, cold hardiness, fruit color, and resistance to root knot nematode (Hancock et al. 2001, Hancock et al. 2010, Stegmeir et al. 2010), was rated as very susceptible to verticillium wilt in our study.

Several studies of verticillium resistance in wild octoploid *Fragaria* germplasm have appeared, mostly in pre-1970's literature (McKeen et al. 1955, Wilhelm 1955, Wilhelm 1955, vanAdrichem et al. 1958, Bringhurst et al. 1966). These early reports document, with varying degrees of precision, the sites of origin (collection) of the studied materials, and thus point subsequent investigators to potentially valuable sites for future collections.

In a multi-inoculation greenhouse trial (Wilhelm 1955), no resistance was found among two *F. virginiana* clones and 39 seedlings, but the source or origin of the *F. virginiana* accessions was not provided. In contrast, Varney et al. (Varney et al. 1959) found the so called "Sheldon" clone of *F. virginiana* to be very resistant. In a multi-inoculation greenhouse trial, Newton and van Adrichem (Newton et al. 1958) found no resistance in 49 evaluated Ontario *F. virginiana* seedlings, while we rated an Ontario accession, CFRA1699, as very resistant.

Of the two ancestral octoploid species, great attention has been given to the occurrence and transmission of verticillium resistance in *F. chiloensis*. Newton and van Adrichem (Newton et al. 1958) found 8 resistant out of 40 evaluated Oregon coast *F. chiloensis* seedlings. (Wilhelm 1955) found no resistance in *F. chiloensis* from Ambato, Peru. However, we found Peruvian *F. chiloensis* CFRA372, an accession used in *the F.* ×*ananassa* reconstruction project for its fruit qualities and resistance to root lesion nematodes (Hancock et al. 2010), to be moderately

resistant to verticillium wilt. Additional *F. chiloensis* accessions CFRA24, CFRA1088, CFRA1691, and CFRA34 are also involved in the *F.* ×*ananassa* reconstruction project (Hancock et al. 2010), and we found these accessions moderately to very susceptible to verticillium wilt. In a field and greenhouse study of 1009 *F. chiloensis* clones from 14 sites along the California coast from Santa Maria to just north of San Francisco, Bringhurst et al. (1966) found that where multiple clones were sampled per site, a range of resistance and susceptibility was detected within sites, suggesting the possibility of segregation for resistance/susceptibility among seedling-derived plants within sites. For instance, from their Bodega Bay site, Bringhurst et al. (1966) found one resistant *F. chiloensis* clone and two susceptible clones, in comparison to 12 resistant clones previously reported by Wilhelm (1955).

Bringhurst et al. (1966) found the entire range of resistance to susceptibility among six clones from Pigeon Point, the collection site of FRA357, which was categorized as moderately resistant in our study. Similarly, Bringhurst et al. (1966) found intermediate to extreme susceptibility at the Scotts Creek site, the collection site for CFRA1692, which was used extensively in horticultural trait evaluations and in the *F.* ×*ananassa* reconstruction project (Hancock et al. 2010, Stegmeir et al. 2010), but for which we do not have verticillium wilt resistance data. We found *F. chiloensis* accessions CFRA34 (Redwoods Creek Park) and CFRA1691 (Jessie M. Honeyman Memorial State Park, Oregon) both to be very susceptible to verticillium wilt; however as the findings of Bringhurst et al. (1966) suggest, a more in-depth collection from these sites might recover resistant individuals as well. Future collections including numerous clones for screening would be prudent, as was done by (Bringhurst et al. 1966), for there is apparent diversity for resistance within individual sites.

Upon finding that one *F. chiloensis* genotype was highly resistant to verticillium wilt, (Maas et al. 1989) recommended that efforts should be increased to evaluate *F. chiloensis* clones as a potential source of resistance for use in strawberry breeding. Previously, (vanAdrichem et al. 1958) suggested that *F. chiloensis* might have been the introgressive source of verticillium resistance already employed in some breeding programs. Screenings of progenies derived from cultivar × *F. chiloensis* crosses (Olbricht et al. 2006), including crosses involving susceptible 'Elsanta', identified two wild accessions, *F. chiloensis* ssp. *lucida* E2/1 (California) and *F. chiloensis* ssp. *pacifica* 'Yaquina' (Oregon) as potential sources of resistance. In contrast, when 'Elsanta' was crossed with the *F. chiloensis* cultivar 'Culture' (Chile), over one third of the progeny plants succumbed to wilt.

For about half of the cultigens that we assayed in the present study, our literature survey uncovered results of prior wilt resistance testing (Table 3.2). Although the prior studies varied in relation to environment (field or greenhouse) and to methodological aspects such as inoculation techniques, *Verticillium* isolates, and inoculum concentrations, our results from specific cultivars were generally consistent with those previously reported (Table 3.2). For instance, we rated 'Tristar' as very resistant, while it has previously been rated as very resistant, tolerant, and moderately resistant (See Table 3.3 and citations therein). We rated 'Annapolis' as intermediate, and it was also rated as such by (Maas et al. 1989). We rated 'Cavendish' as intermediate, while it has elsewhere been rated as moderately resistant (Jamieson et al. 1991). Thus, we have reason to be confident that our results provide an accurate and useful description of the tested germplasm.

Upon gathering information about ancestors of cultigens employed in the present study, some disagreements among prior studies were evident in the literature. Different ratings were

found for ‘Howard17’ (Table 3.3), which is suspected of having two different clones (Bringhurst et al. 1961). Disagreements among studies may also stem from differing experimental conditions. Resistance to different sources of *Verticillium dahliae* isolates resulted in different resistance ratings (Maas et al. 1989, Gordon et al. 2006), and susceptibility to wilt was synergistically increased when coincident with infection by the nematode *Pratylenchus penetrans* (Muller 1973, Potter et al. 1991).

The pedigree diagram (Figure 3.2) depicts information available to us about the ancestries of nine of the ten strawberry cultigens tested, tracing back as many as 12 generations from the most recent ‘Wendy’ release. All but two of these (‘Sparkle’ and ‘Tristar’) are products of the Nova Scotia breeding program. Notably, verticillium wilt resistance ratings are presently available for only 67 out of the 130 cultigens in the pedigree. Of the 63 cultigens with no available ratings, only 12 are named cultivars. The available ratings span a spectrum from very resistant to very susceptible; suggesting that considerable insight into the genetic basis of verticillium wilt resistance/susceptibility could be distilled from the described germplasm, provided that the missing resistance ratings could be filled in.

We observed that resistance can appear in progeny (e. g. ‘Etna’) of a cross between two susceptible parents (e.g. ‘Belrubi’ and ‘Marlate’). Thus, the possible existence of dominant genetic factors for susceptibility must be considered, as must the possibility that resistance could be “introduced” into a susceptible breeding line simply by providing opportunity for resistance to emerge through progeny segregation, even with self-pollination of susceptible types (vanAdrichem et al. 1958).

We anticipate that useful insights will be gained through examination of breeding pedigrees, such as that depicted in Figure 3.2. However, the power of the pedigree approach can

be maximized only when phenotype information is available for all pedigree members. ‘Tristar’ is described in its release note as resistant to verticillium wilt, leaf blight, powdery mildew, and red stele root rot, as well as tolerant to leaf blight (Draper et al. 1981). We confirmed its wilt resistance in the present study. Although, the day-neutrality trait of ‘Tristar’ is attributed to introgression from *F. virginiana* ssp. *glauca* via CA65.65-601 (Draper et al. 1981), the source(s) of wilt resistance is/are unclear, as there were multiple opportunities for either resistance or susceptibility to be transmitted from cultigens in its pedigree, both with and without known verticillium wilt resistance (Figure 3.2). Overall, the high level of progeny segregation and the lack of any consistent pattern of resistance transmission in the pedigree suggest high levels of heterozygosity. It is likely that verticillium wilt resistance is a polygenic trait in the cultivated strawberry. Thus, an abundance of opportunities exist to breed for increased resistance.

CONCLUSIONS

Recurrent themes unite the research reported in the foregoing chapters. One of these is the abundance of diversity available in *Fragaria* germplasm, and the development of new germplasm resources for genetic research and breeding. A second theme is the validation and application of high-throughput genotyping platforms. The Axiom IStraw90® strawberry SNP array was validated as an effective tool for genotyping at both the diploid and octoploid levels in strawberry. Genotyping-by-Sequencing was shown to be a valuable and complementary marker technology, enabling the identification of markers in genomic regions that were under-represented on the IStraw90 Array. The abundant potential for gain from selection with respect to many traits, including fruit and ornamental qualities and diseases resistance, was demonstrated in octoploid germplasm, providing the basis for expansion of breeding activities aimed at developing locally adapted varieties at the New Hampshire Agricultural Experiment Station. As tangible research products, the first linkage maps of the ancestral diploid *Fragaria iinumae* were constructed, markers associated with a trait of horticultural interest – NW flower color – were identified, and population development was initiated toward the goal of marker-assisted breeding for verticillium resistance. Finally, several attractive directions for further research progress were defined. A set of candidate genes on chromosome five were identified in relation to the NW flower color trait. The trait instability with respect to NW flower color deserves further exploration and explanation. Potential genomic rearrangements between diploids *F. iinumae* and *F. vesca* warrant further investigation.

Looking ahead, the *F. iinumae* linkage map, as described in Chapter I, will be used in an effort to generate a de novo assembly of the *F. iinumae* genome to provide a second *Fragaria* reference genome. The linkage map and reference sequence are anticipated to be used in the future for various genetic studies, including identification of subgenomes in octoploid strawberry.

As described in Chapter II, a Closed Pedigree Set of four generations segregating for NW versus W flower color and for hues of NW was developed from previously identified octoploid germplasm (Mahoney 2007, Mahoney et al. 2009) as sources of unique and favorable fruit pelargonidin and cyanidin contents, or of NW flower color. Selections with the sought after red flower color were achieved in the Closed Pedigree Set, and dominance of NW over W was determined. The upper end of the range of anthocyanin floral content of the Closed Pedigree Set exceeded that of the NW founder, indicating that the white-flowered founders contributed determinants of floral anthocyanin content and hue. Factors impacting selection against the NW flower trait in the initial generations and then favoring the NW flower trait are evident. Using a pedigree-based approach, 35 Array SNP markers co-segregating with flower color were identified: 28 of which are syntenous with PC5 of FvH4, and span a homoeologue of chromosome 5. Potential candidate genes related to anthocyanin biosynthesis and located on PC5 of FvH4 were identified, the most intriguing being two regulatory genes, *FaMYB1* and *JAF13.* In the second phase of the program, and taking advantage of selections in Phase 1, select members were crossed with commercial cultivars to develop hybrids with attractive flowers and sizable and delicious fruit. Ten members of the Phase 2 LM49 family were selected by Pleasant View Gardens for evaluation.

In Chapter III, the final chapter, using a pedigree based approach and phenotypic data on verticillium wilt disease resistance, potential sources of disease resistance and susceptibility were identified and parents were selected for crosses of resistant × susceptibility for the next phase of genotyping on the Array, for identification of QTLs for resistance.

My post-doctoral research plans are to continue breeding strawberry, including both ornamental and production varieties and to advance marker-assisted breeding in strawberry, utilizing the Array, a break-through technology. An additional 104 members of the Closed Pedigree Set progeny have now been genotyped on the Array, and the data await analysis. A selected progeny individual LMJ6 derived from the three founders has been crossed with two locally popular cultivars, for the purpose of introgressing flower color, hue, and fruit pigment genes into a cultivated strawberry with acceptable fruit size and quality.

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APPENDICES

APPENDIX A

ARRAY AND GBS MARKER DATA FOR THE 21 F2D MAP

TABLE A: *F. iinumae* 21F2D mapped markers and *F. vesca* reference information. In the table heading, the Marker ID for the Array are 8 digits long and begin with 89, and the GBS markers are the remaining markers. The Type indicates the type of marker on the Array or is simply referred to as GBS for the GBS data. The quality ratings of the genotyping for the Array markers are provided in the Class column, and for the mapped markers included PHR (poly high resolution), CRBT (call rate below threshold), Other, and NoCls (the mSnps, where qualities were not categorized). The SNP nucleotides are provided for the Array markers in the Allele columns. The SNP nucleotides are also provided in the Query sequence column in [brackets] for the Array and as the degenerate code for the GBS markers. The location of the markers on the *F. vesca* "Hawaii 4" H4_v1.1 reference map, version pseudochromosome (PC); and position in base-pair designation (Start) and for GBS data only (Finish). Referring to the PC column: for the GBS markers that could not be located on the mapped FvH4 version 1.1 pseudochromosomes, thirteen were located on unmapped FvH4 v1.1 PC0; one marker (3^{z}) could only be located on *F. vesca* pseudo- chromosome v.1.0 PC3; twenty-three markers could only be found on *F. vesca* reference v1.1 scaffold database (SCF^{y} refers to scf0513160 and SCF^{x} refers to scf051358b); and forty markers could not be located in any of the FvH4 databases, and these are designated as 'No good hits' abbreviated 'NGH'.

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1	1	1015	0.00	89865109	F1Dsnp	PHR	A	C	1	322,779	+	CGAGATTTGGTCAAATTACAAAAGCCTCCAGAGCC[A/C]GATTTTAGTGCTGAAGATGCAGATTGATGTATGAT
2	1	1015	0.00	89865115	F1Dsnp	PHR	T	C	1	334,311	+	AGCTGTATCAACTAGAACCACTTCAGAGCCATTGA[C/T]TTTGGCTTCCTGAATTGCTTCCTTTGCAACAACAG
3	1	1015	0.00	89809150	F1Dsnp	PHR	A	G	1	379,204	+	TCATCAAGCTGTTTACCAATAGTGGTAAAAAAATG[A/G]CATATGGCCTCCACGTTTTCCTCAGCAGGACAAAT
4	1	1015	0.00	89809153	F1Dsnp	PHR	T	G	1	387,693	+	CGCGGAGAGGATCGATCAAGAAGATGAGTGCAGGA[G/T]CGCCCCATTTGATGCAAAACATGTTACAGAACACA
5	1	1015	0.00	89809155	F1Dsnp	PHR	T	C	1	404,575	+	TTCGATGGACTAACACCTCTAGAAGGAGGAGTAGA[C/T]GGTCTTGAAGACCGAGATGGACTGGCACCTCTTGA
6	1	1015	0.00	89809158	F1Dsnp	PHR	T	C	1	426,920	+	CATCTCTCAATTCCTCATCATTGAATATTCCAAGG[C/T]GCCTTCGGATTTTTGACCTGTACATGAGGGGGTAA
7	1	1015	0.00	27_261427	GBS				1	472,184		TCTGGGCAACAATATCTTTGTTTGTAAATCTCACAACAAACCGGTACTTGGGTGTGTTGTATTT
8	1	1015	0.00	TP3561	GBS				1	472,285	472,222	TGCAGCATAGTTTGTGAGACCAAAATCAAGCCCATAGTGTGGCAGCTCATGAGCATAGGCAGAT
9	1	1015	0.00	89865135	F1Dsnp	PHR	T	C	1	502,090	+	TCCCAAAAAGGTCGCCGGAGTAAGCTCAGATAGAG[C/T]GTTCAAGGCGGTAGAAGGCGAGAACATCGGAAGCA
10	1	1015	0.00	89809175	F1Dsnp	PHR	T	C	1	511,002	+	ACAGAATCTGCTTCAACAAGAAACTCTAGCAGCTC[C/T]TGTTCAAGTGCAGGATTAACTTTTTTCATCACTTT
11	1	1015	0.00	89809178	F1Dsnp	PHR	A	G	1	524,821	+	AATGGTACTAGTGCTCCTCATAACGATGATCATG[A/G]TGCTGATGATGCCCGCAGCAGCTACCCAGAACTGA
12	1	1015	0.00	89865142	F1Dsnp	CRBT	A	G	1	528,172	+	CAAGGAGCGTTCATGACTGAACCGTCAGCTACGGC[A/G]ACAATGCTATTGCCGTGCTTGCCACCACTAGGAAT
13	1	1015	0.00	TP2819	GBS				1	541,851	541,797	TGCAGCAACCTCCCGTTATCTTATTTTCTTTTGTTAGTGAACATTAAAATATCCGAGATCGGAA
14	1	1015	0.00	89865148	F1Dsnp	PHR	A	G	1	565,729	+	CCCCAGATTCCAGGACTTTAGCGACTCCATAACCA[A/G]TTACAGTCTGCAACATTCCAAATTTTCTTAAATTA
15	1	1015	0.00	89865155	F1Dsnp	PHR	A	C	1	608,172	+	AATACAAATTGGCGATCGAAGTTAGAAAGTAATGG[A/C]ACCTAAGCTTGTATCTGCTATGTCTGTTGTTATAG
16	1	1015	0.00	89865157	F1Dsnp	PHR	A	C	1	627,615	+	GACACAGAGGCCTGAACAGGAGGAGTTGTACTATC[A/C]CTTTTGTTAGAATTTTCTTCCACATTCCTGTCGAC
17	1	1015	0.00	89809190	F1Dsnp	PHR	A	G	1	629,685	+	GGCGCTTTTGCAGTTAATGGGAATGTAAATCCAGC[A/G]GCAGAGGCCAACGTAAGCAGATTAATATGTATTAG
18	1	1015	0.00	89865160	F1Dsnp	PHR	T	C	1	642,993	+	AAACTTAAAGCTGGTTATGATTCAGAGGTGCGCCT[C/T]GGCTGGGCATCTCTTTGGGTAAGTTCTTACAGATT
19	1	1015	0.00	89865173	F1Dsnp	PHR	T	G	1	673,183	+	TATCTTGCAGGGTTGTCTTCCCTCCCTTGTTAGTA[G/T]CACTACTCAAACAAAGCGTTTGGTTATCGTTGGAT
20	1	1015	0.00	89865174	F1Dsnp	PHR	A	G	1	674,239	+	TCAAGTTCTGGAATTCAGATTGAAGTTGGAGAGAG[A/G]GCCAATCGATATTCATTCAGTGAGTAATATTCATC
21	1	1015	0.00	89818669	snp	PHR	T	C	1	694,006	+	GTTACCAAGTATTTGTCCTTCAAAGCTGTGGACGG[C/T]GGCTTTGTCTATAATAAAGGAAAAGTAAAAGTTGT
22	1	1015	0.00	89865177	F1Dsnp	PHR	A	C	1	694,266	+	TAATGAAAGTGATCCCAGAACACACGAGGGAATGG[A/C]CTTAACAAGAGTGACAACTAGAGAACTGATAGCGT
23	1	1015	0.00	89865186	F1Dsnp	PHR	A	C	1	724,699	+	AATCCGTAAGCTCTTTTGGCAGAGTCAAGGGTGTT[A/C]GAAAGGAGCATTGAGATTACAACAGGTCCTACTCC
24	1	1017	2.44	89865096	F1Dsnp	PHR	A	C	1	257,573	+	ACTCAAGAACCTCAATCTATCTCATAACCAGATTT[A/C]TGGGTCCTTGCCTAACAACATTGGCAACTTTGGCC
25	1	1017	2.44	89809134	F1Dsnp	PHR	A	G	1	257,626	+	ACATTGGCAACTTTGGCCTACTTGAAAGCTTTGAT[A/G]TTTCAAGCAACAATTTTTCTGGTGAGATTCCTGCA
26	1	1017	2.44	89809135	F1Dsnp	PHR	A	G	1	258,777	+	GTGGCAGATGTTAAGCAAGCAACGTCAGTCCTTGT[A/G]GTGATTTTTGAGAAGCCATTGCTGAACTTCACATT
27	1	1017	2.44	27_459772	GBS				1	260,168		TGCAAAATGTGGTCCATTACATGATTACATCRCTAACTGCCGGCAGCGCTTAGGCGGTGAGGCC
28	1	1017	2.44	TP2303	GBS				1	260,373	260,312	TGCAGATGAGTTTGGGACGTTGGTATGAAAGTAAACTATACATTTCCTGAACACGGGTTCTTGC
29	1	1014	4.88	TP8568	GBS				1	86,462	86,399	TGCAGTCTTCCGCAATGCAGATTACTACAGCATAAACTATCCGTTCCAGGCTGTTTCGAGCAGC
30	1	1014	4.88	89865024	F1Dsnp	PHR	A	G	1	150,896	+	TCAATTGACCCAGTATCCACACCAATGAGGTCTAA[A/G]GTTTTCTCATAAGGTAGTCTTATCTGCTTCTGGAA
31	1	1014	4.88	89865032	F1Dsnp	PHR	T	G	1	163,207	+	ATGCACGATGGATCAGGCTGGAAGATGCAGGCTAT[G/T]CTGTTGGAGCTCGAGTTCTGGAGCTTCTTTGCCAT
32	1	1014	4.88	89865033	F1Dsnp	PHR	T	C	1	166,732	+	TCAGTTCCACAGGTGGGCAGGTTCCCATTCTCGTC[C/T]GAAAACGTGAGACCCAGCTGAATCAACTTCAACAG
33	1	1014	4.88	89809081	F1Dsnp	PHR	T	C	1	176,173	+	GAAGAAGGGGTCAGGATTCTTGGTGAAGGGAAGTT[C/T]TTGATGTCTGATAGTTTTCCTGGAAATGAAAGAAC
34	1	1014	4.88	89865105	F1Dsnp	PHR	T	C	1	3,133,380	+	TTATTCAACATTCCTTGAATTTTAGCCCGAATTGC[C/T]CTCTCCCTCTCAAGTTCAGCATATACTTCCTCCAG
35	1	1014	4.88	89865106	F1Dsnp	PHR	T	C	1	3,134,735	+	CCTCGTTTCCCAGGCCCATTCTTCCTCCTTTTGCT[C/T]TCTTTTGTTATTGGCACTACATCTTCAGATTGTGT
36	1	1014	4.88	89865107	F1Dsnp	PHR	A	G	1	3,136,384	+	CCTTCGAACATCATCGTTGCGACTCCTCCTATGTT[A/G]GTCATTATTTTCTTCTCTTTGTATGCACACAAGGT
37	1	1014	4.88	27_769439	GBS				1	3,166,304		ATGGTCGCTGAGAAGCGTTTTCAGAGCACTTTCTGCAGATTCTCTTAGCATATATAGTGATTTC
38	1	1014	4.88	27_769359	GBS				1	3,166,384		TTCCTAAACTTTTCTTGCCGGATATCAGAAAYATGAGTATATCTCAGAATTTACGAAGGTTAAC
39	1	1014	4.88	89865108	F1Dsnp	PHR	A	G	1	3,200,753	+	ATGTTTCAGTTAGCAACAACTCTAGGAATTTTCAC[A/G]GCAAACATGATAAACTATGGAACTTCAAAGCTCGA
40	1	1014	4.88	89809148	F1Dsnp	PHR	T	C	1	3,215,933	+	ATGCTGCTGATAGACCTCCAAAGCCAGATTCGCTG[C/T]TTTCTAAATTTGTGGATGGGAATGACATGTTTCGC
41	1	1014	4.88	89865110	F1Dsnp	PHR	A	C	1	3,251,653	+	AATTCTGCAAATCCAGATGGCACCAACTTTGTCAT[A/C]ACAGATCTACCATGAGCGAGATGAAGATCAAGTTC
42	1	1014	4.88	89865111	F1Dsnp	PHR	T	C	1	3,293,847	+	ACCTGAAGCCTTTTCGTTCCCTCATCTGTGCTCAA[C/T]CCTTGTTTCGAGCATTTCAGCTGCTCGAACACTTC
43	1	1014	4.88	89865112	F1Dsnp	PHR	A	G	1	3,306,582	+	TTCTTTCCTTTTGACAGATAAGTTTCCCAGACCTC[A/G]AAGACTATGATTCTGATCAAGCATGGCCTGTGATA
44	1	1014	4.88	89865113	F1Dsnp	PHR	T	G	1	3,307,043	+	AGTTTTAATCGTGATTGTATCATTGAATGGGGTTC[G/T]CTGCTATGTTTTTGGCAATTAATGAATCGATACAA
45	1	1018	7.32	89809145	F1Dsnp	PHR	T	C	1	2,988,279	+	AAGCATTGAAGCAAGAGAATTTGCAATGTCAGTAG[C/T]AGCTTCAGATTGGCTATTGTTGTTAGCATCAACTG
46	1	1018	7.32	89809146	F1Dsnp	PHR	A	C	1	2,998,810	+	TCTTTAAATTCCTTGTATGTGATTTGTATGTTGTT[A/C]AGACGTGGGGCGTTGTTAATATCGTCAACACGATC
47	1	1018	7.32	89809147	F1Dsnp	PHR	T	C	1	3,050,241	+	CATCCACTAAAACACCGCCTTCAGCGGATTTAAAG[C/T]AGTCCTGAGCCATTTTAAACTGTGTGCAAGAAATA
48	1	1018	7.32	89779666	snp	PHR	A	G	1	3,055,187	+	CCAAACAGAGCATAACAGCAGCAATGACAATGAGA[A/G]CCAGTCTTCTGTGAAACATAGCAAAACATAAATGT
49	1	1018	7.32	TP9162	GBS				1	3,101,068	3,101,127	TGCAGTTAATTGTTGATCTTTACACATCATAAACTTGCTTAAAACTTATACACATCATGATGAT
50	1	1018	7.32	89865104	F1Dsnp	PHR	A	G	1	3,104,710	+	AGAGGCATGTGCTCATGTGGTTCATTCTTGATGAC[A/G]GAAGAGTCTAGTGCTCGGGCAAGTATATCGAGAAT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
51	1	1013	9.76	89809136	F1Dsnp	PHR	A	G	1	2,640,812	+	TTATGCAGCCCTCCAAGCAATCCTTCATAATCTGT[A/G]TCTCCACATTCTCCAGCAACCACCACCATCTTTGA
52	1	1013	9.76	89809137	F1Dsnp	PHR	A	C	1	2,655,388	+	TTGAGGTGTCTCAAACTCTGCACATGTAAAGTCGG[A/C]TGCCATCTCTTCAGGTGTCTCCTCAGGATCCATTC
53	1	1013	9.76	89865098	F1Dsnp	PHR	A	G	1	2,661,683	+	GTGCAGGCATTTAAAAAGTTAAATGAAGGACGTAT[A/G]ATGGAATTGATTGATCCTGCAATAGAGGAAGCTGT
54	1	1013	9.76	89865099	F1Dsnp	PHR	A	G	1	2,692,757	+	GCATTAACTGAGAACTTGAAATTTCGGCCCAGCCG[A/G]GACTCAGACCGTAAATTTCCACCCAACACCATATC
55	1	1013	9.76	89809138	F1Dsnp	PHR	A	G	1	2,692,886	+	TCTCTACCTCGTAAAGTAGTTTCCAGAGAGCCACC[A/G]TATGCGACTTGTTCACGATCCACCTTCAATTTGCT
56	1	1013	9.76	89809139	F1Dsnp	PHR	A	G	1	2,693,978	+	TTCTCAACAAAAAGTACTGGGTTTTCAAGTCTGGA[A/G]TCTGACACCGCCTGATGTATATAGTGCTGCACCAT
57	1	1013	9.76	89865100	F1Dsnp	PHR	A	G	1	2,699,623	+	CTGTCATCTACTTCATTTTCCACTCCGCTTGGAAC[A/G]ATAGGATGATGTAGAAGAGATGAGAGGAGATGGGG
58	1	1013	9.76	89809140	F1Dsnp	CRBT	A	G	1	2,853,416	+	GAGCATTGCCCATTATACGGAAGATAGAAGTGTTA[A/G]GCTCTAAGCTGATGGAATTGTTAAACACTCGTCGA
59	1	1013	9.76	89874765	snp	Other	A	G	1	2,853,417	+	AGCATTGCCCATTATACGGAAGATAGAAGTGTTAA[A/G]CTCTAAGCTGATGGAATTGTTAAACACTCGTCGAA
60	1	1013	9.76	89865102	F1Dsnp	PHR	T	C	1	2,853,418	+	GCATTGCCCATTATACGGAAGATAGAAGTGTTAAG[C/T]TCTAAGCTGATGGAATTGTTAAACACTCGTCGAAC
61	1	1013	9.76	89809141	F1Dsnp	PHR	A	G	1	2,853,748	+	TACTATAAAGTTGACAACTATCATACAACTTATTC[A/G]GAATCCATAACCCCTGTGGCGGTGCCTTTTAAGCC
62	1	1013	9.76	89809142	F1Dsnp	PHR	T	C	1	2,855,173	+	ATTGAGTAGCCAACTTATAAGAGAGCTTTTCTTCA[C/T]GTGAAGGAGTACCTTTTCCACGAGAAGTTGATGCA
63	1	1013	9.76	89809143	F1Dsnp	PHR	T	C	1	2,865,401	+	GAGAACACTGCAGGGGACAGCTTTGATTTGTATTA[C/T]GGGTTGTTTGTGTATAACAAGAATGCGCTGGATAT
64	1	1013	9.76	54_230768	GBS				1	2,865,432		CCAGCGCATTCTTATTATACACAAACAAACCGTAATACAAATCAAAGCTGTCCCCTGCAGTATT
65	1	1013	9.76	54_230708	GBS				1	2,865,490		GACTCCCGAAAAGCTGCGCCTTCAAAGCCTCRAAAGCCGAGTCCAGCCTCTCCAGCATATCCAG
66	1	1013	9.76	TP6704	GBS				1	2,958,568	2,958,505	TGCAGGCTCTCCATTTTGACAGTTGTGACGGTCTTCGGTTGAGTAATATTACGCATATTAATAG
67	1	1013	9.76	89865103	F1Dsnp	PHR	A	G	1	2,966,726	+	TGATTGTTGATTTCTTCCTCTTCTTTGGTGTGGCT[A/G]TTCTGACTGTTGTACAAGCTTCTCAAGTAAGTCTT
68	1	1012	14.76	89809119	F1Dsnp	PHR	T	C	1	2,224,076	+	AATCTGCAGAGGATTTGTGATGGGATTTACTTGAA[C/T]CGTGTTAGGGATATGGTCACTGTGTTTGAGGCTGC
69	1	1012	14.76	TP9668	GBS				1	2,228,764	2,228,821	TGCAGTTTACTCTTTTGATAGCATCCGCATCGGAGGATTTGAGCTGACCTATTGATTCAATTCA
70	1	1012	14.76	89865088	F1Dsnp	PHR	T	G	1	2,230,477	+	GCAAAAGATGGATCAGCAAACTTCACAACAATTAG[G/T]GATGCCATCAAGGCTGCACCAAATTATAGCTCGAA
71	1	1012	14.76	89809120	F1Dsnp	PHR	A	G	1	2,230,510	+	AGTGATGCCATCAAGGCTGCACCAAATTATAGCTC[A/G]AAGAGAATCAACATCAAGGTGATGGCCGGAGTATA
72	1	1012	14.76	54_738214	GBS				1	2,253,639		CATGAAGAACTCCATGCAGCAGCACAGTTTGMGCCATGATCGCTCAATTCAAGTCTCAATCTTT
73	1	1012	14.76	89809121	F1Dsnp	PHR	T	C	1	2,276,679	+	GTCAGTGAGAGAGGTTTTTGGGTCATGGGTAATGC[C/T]CAAGCTCTGAAGAGTCTGATCTCATTAACAATCAC
74	1	1012	14.76	89809122	F1Dsnp	PHR	A	G	1	2,290,052	+	GTAATCATCTCAAATGCATTCATTAATAAAGGACC[A/G]CTGTCTTTATTATCTGTTCTTTCTTCTGCATATTG
75	1	1012	14.76	89865089	F1Dsnp	PHR	T	C	1	2,291,727	+	AGTTTGGGGTTCCACATGTTGTGAAAAGAAGACCA[C/T]CCCCCTGCTCAGGATATAGGCAAAACAGGAACGCC
76	1	1012	14.76	89865090	F1Dsnp	PHR	A	G	1	2,291,878	+	TTAGATAAGGCTTACTTGCTGGGGCAATGCACTCA[A/G]TCCAAAATCAGAAACTTTCAAATTTCCATAAGCAT
77	1	1012	14.76	89809123	F1Dsnp	PHR	T	C	1	2,292,985	+	CCGTGATACTTACCGGGAAATGCGAATATTCCGGT[C/T]GCCGGAGAAGCGAGGCACGTGCGAAGGGGAACCTT
78	1	1012	14.76	89809124	F1Dsnp	PHR	T	C	1	2,310,240	+	GAAATTATTCAATCAAAGGCTGTTGAGCATCCTAC[C/T]ATGGGGCACGGAAAGGAAAAACTAAGCACTACTGC
79	1	1012	14.76	89809125	F1Dsnp	PHR	A	G	1	2,311,555	+	TCTCAAGTGGGTGTTCATCCACAGTCTAGTCAGTT[A/G]GCAAGGACAATTTTGGAGCACCTTGACAGAAATTC
80	1	1012	14.76	89865091	F1Dsnp	PHR	T	C	1	2,334,880	+	TGTTCATGAGTCGGGCACGAAGATTGAAGCAGAAG[C/T]GACTGAAAATGGCAGCAACGGCAATGAGGCTGTGA
81	1	1012	14.76	89806427	ins	PHR	-	ATCG	1	2,382,500	+	TCCCATCTGAAATTGAAATGCTGCACACAAATAAC[-/ATCG]ATCAGTATCACCATGTTCATCACACATACACATAT
82	1	1012	14.76	89809128	F1Dsnp	PHR	T	G	1	2,391,480	+	AAGCTAGCCATCAACGTGACTTCAACCACCTCTGC[G/T]CCGGCTCCTGCTCCTGGTCCAGCTACTCCTAGAGG
83	1	1012	14.76	54_537633	GBS				1	2,410,529		TGGAGACATGTGTACACAAAATTCTGATGACAATGAATCCTTGGATATCGTTATTTGGATTTGG
84	1	1012	14.76	89809130	F1Dsnp	PHR	A	C	1	2,414,774	+	ACCTTGAAGGAGGATTCAATGGTCTTCTTCGAGAG[A/C]GCGGAGAAGGCCATCACTTGATTAATTGAAGAGGA
85	1	1012	14.76	TP7557	GBS				1	2,418,552	2,418,615	TGCAGGTTCGGATACGAACAACCTTGCTGTTTTGAACTCGCGTATGTATTTGATCGGTGGAGAC
86	1	1012	14.76	54_571711	GBS				1	2,418,839		CGGCAACTTGTCCCATTTATCGACACCGGAAYGGAGTCGGTAAAGCGTAGGCCCGACCGAGTAA
87	1	1012	14.76	89865094	F1Dsnp	PHR	A	G	1	2,419,298	+	TGTTTCAGATAAGAAATGACAACGAGCACCACCTG[A/G]CTGTGCTGTGGGAATCTCTTGTCGAGAATAATTGT
88	1	1012	14.76	89809131	F1Dsnp	CRBT	T	C	1	2,511,683	+	GGGGTGGATGGTCACATTATCCTTCACATAAACCA[C/T]CTCGGCGCCTTCGTGCTCGCTCGACGAGCTGTGCC
89	1	1012	14.76	89809132	F1Dsnp	PHR	A	G	1	2,559,249	+	CAGAATCTTCAGCCGGAGTTCAACTTCAACATGAT[A/G]ACCTTTGATACTGTCCAAGGAGATTGCATTGCAGC
90	1	1012	14.76	89865095	F1Dsnp	PHR	T	C	1	2,570,049	+	CAGTTTCAACAAAGTTTATGGTGAAGAAGCTCCAA[C/T]GTTTATCAAGATTGTTGATGATGGAATTCATGAGC
91	1	1012	14.76	TP8672	GBS				NGH			TGCAGTGACGGGAATGGAACCCAAGATCTTCATCCTGCTGTTCTTTAAACTCCAAAACAAGTCG
92	1	1019	17.20	89803202	del	PHR	-	AAGG	1	2,132,886	+	CAAAACCTGAAATTCTGAATCAAGTTAAACATCTT[-/AAGG]TATTTCTCTGCCATAATGTAATGACTTCAACATTT
93	1	1019	17.20	89809118	F1Dsnp	PHR	A	G	1	2,142,368	+	CCTTATTGTACATACTCATCAATGAATTAGAAACC[A/G]TAACATAAGAAATAAACCCAGACGAAACAGCAAAG
94	1	1019	17.20	54_805565	GBS				1	2,174,426		AGAGAGCCAGCCGGGATTTGAAACTTTCCGATGGACCTTTCCATGGTAGATGCTTGTTCTACTG
95	1	1020	19.67	TP6555	GBS				1	1,843,794	1,843,765	TGCAGGCCGAGACGGAATTGTTCCACTGGAGCCGAGATCGGAAGAGCGTTCAGCAGGAATGCCG
96	1	1020	19.67	89865073	F1Dsnp	PHR	T	C	1	1,951,989	+	AATGTGCAATCATTATGTTCGACGTCACTGCAAGG[C/T]TGACATACAAGAATGTTCCTACATGGCATCGTGAT
97	1	1020	19.67	TP8061	GBS				1	1,953,128	1,953,175	TGCAGTAGTTGCGTTGTGCTGATGGGCTTATGGGATTGGGGTCTTCCCTGCACACAAAAAAGAT
98	1	1020	19.67	24_141007	GBS				1	1,953,214		GTTCTATACTTCAATATCTAAGTTGGTTATTCCTTGCTCGTCCCTCCCCATCCATCTTTTTTGT
99	1	1020	19.67	TP2272	GBS				1	2,066,321	2,066,258	TGCAGATGAACTCTCTCCACCGATCACCTGTACTCCGTCCACCACCGTCTCCACGCCACTCCAA
100	1	1020	19.67	89865085	F1Dsnp	PHR	T	C	1	2,073,083	+	CTCCCATGTTTATACCGGGGCCATTTGCAATTGCC[C/T]ATCACCTCATATCTTCTTGGGTTTATCAGGATGCA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
101	1	1020	19.67	437_79157	GBS				1	2,126,333		TACTCTTCCATGTGGATCTAGGTATTTTTGTCGCACTGTTCCGGTAGTCGCATTCAATCCTTTG
102	1	1020	19.67	437_81224	GBS				1	2,132,104	2,132,166	ACCRACATAAGGCAAAAACCTGCAGAAAAGCAAAAATAAAATAAAATACAATACATCTAGAAAA
103	1	1020	19.67	TP64	GBS				1	2,132,123	2,132,186	TGCAGAAAAGCAAAAATAAAATAAAATACAATACATCTAGAAAATGAAAGCTCACTCGTTTAGC
104	1	1001	22.16	TP8738	GBS				1	1,684,122	1,684,087	TGCAGTGATGTGCATACGTAGTATTTGCCACAGCCGAGATCGGAAGAGCGGTTCAGCAGGAATG
105	1	1001	22.16	89865041	F1Dsnp	PHR	T	C	1	1,687,831	+	GGACACCTGGAGAGTTTTGCAAACCCAAGTGAGTT[C/T]TGGTATGTGAAAAGAGATGCCCAAGATGATGAGAA
106	1	1001	22.16	89809074	F1Dsnp	PHR	T	C	1	1,695,697	+	CGTAGAACTGACCACTTTCCTTTCCCTAACCAACC[C/T]TGCCCATGCCACCCTCCACCTCCATTTTCAATGCC
107	1	1001	22.16	89865044	F1Dsnp	PHR	A	C	1	1,698,663	+	ACTAATCCCCAGCACTGAGACTGAATCGGCAAGCT[A/C]GATATTAACCGAGCCGAAGCGATTGCACTGTGCAG
108	1	1001	22.16	89865048	F1Dsnp	PHR	T	G	1	1,729,811	+	TTGTTTGTTGGGACTGGTATGGGTCTGGGCCCTCC[G/T]GTTGCTTCTCTTTACGTAACTGAGGTAATCAGCAT
109	1	1001	22.16	89809079	F1Dsnp	PHR	A	C	1	1,733,772	+	GTCTATGGCAAACCAAACCTGTTCAAAAGTGCTAC[A/C]GGGTGAGCCGCGAGTTTCAAACCTTGCTGAAAACT
110	1	1001	22.16	89865060	F1Dsnp	PHR	A	G	1	1,844,826	+	CAATGGAGGTTCTAGGAAAAATCAAGCACGATAAT[A/G]TAGTTCCGTTGAGGGCTTTCTACTTCTCCAAAGAT
111	1	1001	22.16	89874267	snp	PHR	T	C	1	1,875,320	+	AGAGTAACCACCCTTTGGAAGACCCACAAAGCCTC[C/T]TGTTTGGCACTCTTACTTGAAAATCAAGGATCTTG
112	1	1001	22.16	89809093	F1Dsnp	PHR	A	G	1	1,890,538	+	TTGAATGAAAAAGATGCAGCCACTTGGACTTCAAT[A/G]ATCTGCGCGCTTGCAATGAATGGAATGACAAGCAA
113	1	1001	22.16	89865072	F1Dsnp	PHR	A	C	1	1,935,713	+	AAGTCCAGCTGTTCTTGGCCGCACATTGAAACACC[A/C]CTGAACGCCATTGCAAACTTGGTTTTTGTCTCTTG
114	1	1002	24.65	89865025	F1Dsnp	PHR	A	C	1	1,545,889	+	CCTGATGCTAGTGACCCTATTAGAGAAAACACATT[A/C]AGGGTTCCCACCAAGATTTCCTGTTGAGTTCGTGT
115	1	1002	24.65	89865029	F1Dsnp	PHR	A	C	1	1,584,059	+	AGTCTCTACAGTTCTCATGGAAGCTCTGACTTTGA[A/C]TCAAGGCCCTATGACACAAAGCAACGCAACCTGGA
116	1	1002	24.65	TP842	GBS				1	1,619,274	1,619,211	TGCAGAATGAAAGTTGAAGTAAATGACTGTAGCACAAACCTGGTCATCAGCATGATGTGCCGTT
117	1	1002	24.65	89865030	F1Dsnp	PHR	A	C	1	1,622,654	+	TGAGTTAGTTGGTAGGAGAAGCTTCAGTTTGATGA[A/C]TTTGTCCAAGTTTTCATACCTGTAAACATAATGTT
118	1	1002	24.65	89865031	F1Dsnp	PHR	A	C	1	1,626,383	+	ATCCAAATGACGGCCAAGCTCTTGACGAATAGCAA[A/C]GTACGTGAGATCAGGACCAGGCATGGAAGCTGTGG
119	1	1003	27.11	89865143	F1Dsnp	PHR	A	G	1	5,335,635	+	ATATATTGCCTCTATCTCCTTTCCATTCTTCACTA[A/G]CTCATCAATAACATCTGTACAAATCACACAGTATT
120	1	1003	27.11	89809179	F1Dsnp	PHR	T	C	1	5,370,367	+	ATTTGATGGAACGGACAACATAAGTGATCCGGTCT[C/T]CGTCTCTAGCGTCGTGTTCTTCGTCGAAACAAATG
121	1	1003	27.11	89865144	F1Dsnp	PHR	T	C	1	5,387,469	+	ACTCTATTATGGATTTCCCAGGTGCTTCTTGGGGA[C/T]ATGGGAGCTGGGAAAACAAGTTTGGTATTGAGATT
122	1	1003	27.11	24_587529	GBS				1	5,388,077		TATGGGTTTACAATGAGCATGTGACAAGTGCYCATTCTGCTTTCAAAGCTTAAAATATCAAAGA
123	1	1003	27.11	24_587450	GBS				1	5,388,159		TATCATTTGACAGATAAAGTCTAAGCAACTCGTATTGCAGATGATCAGTGACATAGTCTTTATC
124	1	1003	27.11	TP3747	GBS				1	5,388,239	5,388,176	TGCAGCCAAAAACAATATGCATAGAACTAATCACACCTGAAAGATATATTACTCATATTGCAGA
125	1	1004	29.55	89809177	F1Dsnp	PHR	A	G	1	5,190,089	+	AGTTGGTGCTGTTTCATATATGGACATTAATGGGT[A/G]TAGCTACAAAAGGGATGTCTTGTTTTGCTATGATT
126	1	1004	29.55	89865139	F1Dsnp	PHR	T	C	1	5,192,472	+	GCACGCACACCTTCAGCAAAGTCATTACGCAGGGA[C/T]GATCTTAAGGCAATGCGGTATTCAGTTTTCATGAC
127	1	1004	29.55	24_767979	GBS				1	5,233,132		TCCAGGGGTCGCAACTGGAGCACCAACAGGGRGAAATGTTGACGAGCTCGTAACTGGTGCAACT
128	1	1004	29.55	89865140	F1Dsnp	PHR	A	G	1	5,262,221	+	CCTCCAATTGTGTCCGGCAGCGGCCCCAAGAACTG[A/G]TTGTAGCTCACGTCGAACACCGTCAAGTTCTTCAG
129	1	1004	29.55	89865141	F1Dsnp	PHR	A	G	1	5,262,824	+	CCGGTGTAGCTGCACACATCAGATCCGACCCAGTC[A/G]CCAGTGAGATTGAAAGGGTCAGAGAGAATAGCCTT
130	1	1005	31.99	89809156	F1Dsnp	PHR	A	G	1	4,160,087	+	TGGAAGATTCTCATGGTGTTTTCTGCAAGAAACGT[A/G]CAGCACTTAAAGGTGCCTTATAGTACTTGGAGACA
131	1	1005	31.99	156_201589	GBS				1	4,239,440		CCTTGAGTTCCTCTGGCTCTCTTGGCTTCCCRAAATGGCGCCATGGAAGCTGCCTTTTGAATTC
132	1	1005	31.99	89809157	F1Dsnp	PHR	T	C	1	4,253,847	+	GGCAATGTGATTGGAAGTGGTGGATCAGGGAAGGT[C/T]TATCGTGTACCTGCGAATCGTACAGGTGATGTTGT
133	1	1005	31.99	89809159	F1Dsnp	PHR	T	C	1	4,357,017	+	CCACCTTCTTTGCAAGATCCTCCAAGCTCTTCACA[C/T]CTGCCAGAGATGTGAAAGATTGCGACTTTCCTTGA
134	1	1005	31.99	89865121	F1Dsnp	PHR	A	C	1	4,361,293	+	TCAAGAATTGTCTTAACTTGTCTGATCACATCTGC[A/C]AGAGATCCACGATCCATGTATTCTAATACAAGAGA
135	1	1005	31.99	89867502	SNPinIns	PHR	A	G	1	4,363,096	+	ATCAGTTTCTACTATCCAAGAACATAAATTTGGGG[A/G]AAATTACATGAAAGATTGAATCTTTGGGTACTTAC
136	1	1005	31.99	TP9660	GBS				1	4,381,667	4,381,604	TGCAGTTTAAGGCTGAGGAGATTGCTGGTATCATGAAAGATTTCGATGAACCTGGACACCTTGC
137	1	1005	31.99	89865122	F1Dsnp	PHR	T	C	1	4,420,159	+	CATTCATACCTCTGACTTCATCGAAGCTACTTTGA[C/T]ACCATTCGGCAGAGTAGTAATCTTTGGCTTCTCCG
138	1	1005	31.99	89809160	F1Dsnp	PHR	A	C	1	4,421,994	+	ACGCCAAGCCAAAAGATGCGTCAAGGAAGAGAAAT[A/C]CGAGAAGCTCAAAATCAAAAAGGCCATGGAGAAAG
139	1	1005	31.99	89809161	F1Dsnp	PHR	A	C	1	4,431,808	+	ATCTGAAAAGCTAGAGAGATGGAGTAGTTGCACCA[A/C]CAATGCTTGGGGCGCTTGTTGCACCAGAAGAAGTT
140	1	1005	31.99	89809162	F1Dsnp	PHR	T	C	1	4,449,646	+	GTAGAAATGTATATTACCTCACAAAAAATACCATA[C/T]AACCCTCTGGGACAGGCCCTTCCAGTGATAGTCCC
141	1	1005	31.99	89865123	F1Dsnp	PHR	T	C	1	4,450,701	+	CATGCCCACCAACAGTTGAGATTGTAGAAGAATCA[C/T]CAAGTGCTAATGTCTGAACGAATAAAAGAATAGTA
142	1	1005	31.99	89809164	F1Dsnp	PHR	T	C	1	4,452,302	+	TTTATGGATCTGTAGCTTACATTGATACTAAAAAA[C/T]AGAGACAAAACCAGGTGTTGCGCTTCAATAACATC
143	1	1005	31.99	89865124	F1Dsnp	PHR	T	C	1	4,452,308	+	GATCTGTAGCTTACATTGATACTAAAAAATAGAGA[C/T]AAAACCAGGTGTTGCGCTTCAATAACATCTCCTGC
144	1	1005	31.99	89809165	F1Dsnp	PHR	A	G	1	4,511,933	+	AGCTTTGTTACGAGGAATTTGAAACCAGTAAGCTT[A/G]TCAGAGCTGAACTTGACCGGCTGGGCATCCCTTAC
145	1	1005	31.99	89809166	F1Dsnp	PHR	T	C	1	4,515,015	+	GAAGTAACATTGGTCATGAGGGATATGATGTCTTC[C/T]ACTACTAATACCTATTCGTTATCATCATCAAAAAA
146	1	1005	31.99	26_49562	GBS				1	4,518,977		CCATGGCGGCTTTCCTTGCCCTAGCAGCAGCRGCCGCTGCCGCGGCTTTCCTTGCCGCAGCAGT
147	1	1005	31.99	26_49634	GBS				1	4,519,062		GCATCTTTGCAGCAGCAGCAGCAGCAAAAGCCTTGTTTTTCGACATAAAAGACTTGTCGTAATC
148	1	1005	31.99	89809167	F1Dsnp	PHR	A	G	1	4,521,805	+	GAGCCAAAGCAATTTGAAAACATGGGTGTCTGATA[A/G]GTTAATAGCATTGCTCGGATACTCTAAGCCGGTAG
149	1	1005	31.99	89809168	F1Dsnp	PHR	T	C	1	4,523,086	+	TCATCAGGTTCTTGTTATTGTCGGCGAAACTGGAT[C/T]TGGAAAAACTACACAGATTCCTCAGTATCTACATG
150	1	1005	31.99	89809169	F1Dsnp	PHR	T	C	1	4,523,115	+	CTGGATCTGGAAAAACTACACAGATTCCTCAGTAT[C/T]TACATGAGGCAGGATACACAAAGCATGGAAAGATT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
151	1	1005	31.99	89865125	F1Dsnp	PHR	T	G	1	4,526,648	+	CAGACATATTTGGTAAAATCAACAAAGGGTGACTT[G/T]TTGATTGTTGAGAGATTGTTGGGACCAGAGGAAAC
152	1	1005	31.99	89809170	F1Dsnp	PHR	T	C	1	4,530,696	+	TTCAAAGAGAGAAGGAACCGGAAGCAGCAGCCACA[C/T]AAAATCACTATGAAGAGGAAGAGATCAGACGGGTT
153	1	1005	31.99	89809171	F1Dsnp	PHR	T	C	1	4,536,230	+	ATTCAGCTCCAATTTTTATAGTCCCAGGAAAGCTG[C/T]ACGATGTTGATGTCTTCTACACGAAAGAACCAGAA
154	1	1005	31.99	TP3555	GBS				1	4,542,509	4,542,572	TGCAGCATAGAGGTAAGAGTTGAACCAAACATGAGGATGAATAATAGAATAAAAACTATGACGA
155	1	1005	31.99	26_87196	GBS				1	4,545,982		TTTTTGTAAACATGAACATCAATTGACAGAAGTAATATTAAGATTCATTCCTGTACTAACCCCG
156	1	1005	31.99	89865126	F1Dsnp	PHR	T	C	1	4,585,730	+	GGACTTCCCCATTGCTTCACTATCTTGCAATCCTG[C/T]CAATTCAGCCATCTTTGCATTCCATCCATTGATGA
157	1	1005	31.99	89875209	snp	PHR	T	G	1	4,587,384	+	CTGTAGCAAATGACCTTGAAGGTTGCTTCATCAAC[G/T]GCAAGCATGCAGCCAAAAGACTGAACAAGAGCGCC
158	1	1005	31.99	89865127	F1Dsnp	PHR	T	C	1	4,597,798	+	GGCTGCCGGGTGAGAGGGTGGACTGGCCCAGTGTT[C/T]CTAAACTTAACTTTATCTTCAGACATGTGAATCAG
159	1	1005	31.99	89865128	F1Dsnp	PHR	T	C	1	4,601,616	+	ACTGGCCGGACAACATGATCACCGCCTAGGTCTCT[C/T]TGCAGAGCCTTTGCCATTTTCCTCCGTGCATGTGA
160	1	1005	31.99	89865129	F1Dsnp	PHR	T	C	1	4,650,169	+	ATCTTGTTGTACCTTTTTTGTTGCGAAGGACATTG[C/T]GACTGGGAAATCTATTCTGTTTTCTCCTAGATTAC
161	1	1005	31.99	26_190726	GBS				1	4,653,888		AAGGTAAACGTCTATGCAGAATGTGGTATTCGAAGGGCCGCCGTTCTCTCAGCAAGCCAAGACT
162	1	1005	31.99	89865130	F1Dsnp	PHR	T	G	1	4,655,559	+	ATGGCCGACGACGAGCCTGCGGAGGTCTCCAATGA[G/T]AAGACCAGCGCCGACTATTACTTCGACTCCTATTC
163	1	1005	31.99	89809172	F1Dsnp	PHR	T	C	1	4,707,977	+	AAGAACACCGATGAAAGTGATCTCATCTGGCACGG[C/T]GCCTTCGTCTAACATTATCGAAAAAGCTTCCAGAG
164	1	1005	31.99	89865131	F1Dsnp	PHR	T	C	1	4,708,378	+	AACCAGTAATGATGACTGTCCAAGAGAAGAGATCT[C/T]GATTACTCAATCTACTGAAAGCTATAACAGCATCA
165	1	1005	31.99	156_201543	GBS				1	5,495,263		ACCAGCTCAACGGCTCTGTCCCTGCAGAAATWGGTAACCTCTCCAACCTTGAGTTCCTCTGGCT
166	1	1005	31.99	89866187	F1Dsnp	PHR	T	C	5	21,776,724	+	CAGTCCATCATTCCCGCTCCAGTTTCTTCCCTTAG[C/T]TGTTTAACCAAAGCAGCAGAAATAGCTACAGTTGG
167	1	1005	31.99	89810224	F1Dsnp	PHR	T	G	5	21,827,716	+	AGGTGAATAGCCAAACATAACAGGCAAGTTTCCAG[G/T]ATTCATGGGTTGAGGCCCTGATCGCTCACTATTTG
168	1	1005	31.99	89866188	F1Dsnp	PHR	T	C	5	21,840,876	+	GGCAATAGAAACCACGGCGTTATTCCACACGTGAT[C/T]GTGAACTTCAATCTGCAAAACTGGAGATTGAGAAT
169	1	1005	31.99	89810225	F1Dsnp	PHR	T	G	5	21,897,620	+	CTAGAATCATGTTTTGACCTCAATGAAGAGACATC[G/T]ATTATTGAAGAGCTTGATGAGGTTTTAGAAGTCAT
170	1	1005	31.99	89866189	F1Dsnp	PHR	T	G	5	21,912,930	+	AGGAGAATGCATACATTGTCAGGTTTTTGATATCA[G/T]TCACTGATGTTATCTTGTTATTAGATACATCCAAG
171	1	1005	31.99	89866190	F1Dsnp	PHR	A	G	5	21,931,536	+	GCCTCAAGTACCTCTGCGTTAGGCTCATTAGCAGG[A/G]CATAATGCTGCTTCTGCTTCATTGAGAAGATTCAT
172	1	1005	31.99	89800803	snp	PHR	A	G	7	14,783,143	+	GAAGCAACCAGAAAAAAATCTTGAAGGAGAAGCTC[A/G]AAAAACTTACCAAAGCAAATGAAGAGCTCCTTGAA
173	1	1005	31.99	TP2513	GBS				NGH			TGCAGATTCGATGTAGTTGATTTTGTGTTCCACCCCGAGATCGGAAGAGCGGTTCAGCAGGAAT
174	1	1006	36.99	89809173	F1Dsnp	PHR	A	G	1	4,745,646	+	CTATCAGCTTGTCCAAGATAAACCGGGACTATCCT[A/G]TCCGCTTCAACCCCACGGCCCAAACCACTCCGCGA
175	1	1006	36.99	89780009	snp	PHR	A	G	1	4,749,550	+	TCTAATATTAATCTCTTCCCACTTTGTCTTCACAG[A/G]TTAAGATCAGGATAAAAATCCTCTCTGGCTCACCA
176	1	1006	36.99	89865132	F1Dsnp	PHR	T	C	1	4,750,472	+	CGAGAGCCAGATGTTGGAGTCCTGAACTATAGGCT[C/T]GATTTGAACTTGAGTAGAAGTGTACGTGAAGCAAT
177	1	1006	36.99	TP546	GBS				1	4,784,454	4,784,406	TGCAGAAGAGCAGGACCAACCTCTTCCACACCCCCAAATCACTTATTTTTCCATACGACTTTTT
178	1	1006	36.99	89809174	F1Dsnp	PHR	T	C	1	4,792,206	+	GCATAACTCAATCTGTTCTTTTGCTTGTGAAACGA[C/T]AGCTACGTTCGCGGATGGCAATGGTTCTGTAGGTA
179	1	1006	36.99	89865133	F1Dsnp	PHR	T	G	1	4,800,284	+	GTACTTGTGATAATGAAATCGGTCTGGTTCATGGC[G/T]ATGAGATCAGCTGTGAACTGGCAAGAGAAGTGGTA
180	1	1006	36.99	89865145	F1Dsnp	PHR	A	G	1	5,466,831	+	AAATTTACACAGAAAATTGTGTATATGATGAAGGC[A/G]GAAAGGTTGTTCCAAACTCAAGGAGGTCCTATAAT
181	1	1006	36.99	89865146	F1Dsnp	PHR	T	C	1	5,476,415	+	CTCCAATACTACTCGTCCTTGATGCCTCCACTGCT[C/T]CAATCTACTGCAGAGATCCATCACCACCACATCAT
182	1	1006	36.99	89809180	F1Dsnp	PHR	A	G	1	5,550,107	+	TTGATCTCAGCAACTAACTCTGCCACCATAGAGTC[A/G]GTGCCAGAAGGCTCAGAGGCTCTGGGAGGAACATC
183	1	1006	36.99	TP2350	GBS				1	5,568,665	5,568,602	TGCAGATGCGTATTCATGGACAATATGTCCCCAGTCTGAAGCTGTGGAGTTGATGGACTGGCTG
184	1	1006	36.99	89809181	F1Dsnp	PHR	T	G	1	5,593,948	+	AAGTTTTTGTTGGGGTTTCAAAAGAGGAAAATGAA[G/T]TGGAGAAGATGATAACTTCAAAAAGCTTTGAACAT
185	1	1006	36.99	89809182	F1Dsnp	PHR	T	C	1	5,595,634	+	GGGGGTACACTTCTCTCTAGAAACAAAGATTTCAT[C/T]GTCTTTTACAGGGGTAATGACTTCTTGCCACCTGT
186	1	1006	36.99	89865147	F1Dsnp	PHR	A	G	1	5,595,887	+	CGATTGAAGATGTCGATAAAATGACAAGAGATTCA[A/G]ATTTGGAAAAACGTGCATCTCTAGTTAGATACCTT
187	1	1006	36.99	89809183	F1Dsnp	PHR	A	G	1	5,642,742	+	TTGGATGTAGAGCCTATAATCCAACAGAAAGAAAT[A/G]GAGACTTCTGTGTCTGCTGGTGGTGCAGAGGAATC
188	1	1006	36.99	89865149	F1Dsnp	PHR	T	G	1	5,669,859	+	CGCTTAGTAATCTGAAGAGCTTTCCTGCCATCCAA[G/T]GTAAGATCCGAGGGACGAGCACCCTTTGTAAGCAG
189	1	1006	36.99	89809184	F1Dsnp	PHR	A	C	1	5,713,782	+	TTATGTTGAGGATTCACCAGGTCAAGTACTGGCTT[A/C]AATTGCTCTCCTACATGAAAGTAAGTGAGATAAGT
190	1	1006	36.99	26_580720	GBS				1	5,732,094		TGATCAAACCCCGGTAGCTGTGAAGGTTCTTCGCGCTGATGCAGTCGAGAAAAAAGAGGAGTTT
191	1	1006	36.99	89865150	F1Dsnp	PHR	T	C	1	5,769,504	+	TTAGAGACGATCCGAACTCCTTCCCTATTGACCAG[C/T]AGATCCCCATCCATAAAGGTACCACTTTGAGTCCT
192	1	1006	36.99	89865151	F1Dsnp	PHR	T	C	1	5,785,620	+	AATTCCTCTGACATTAGCCTATGTTTGGTCCTTAG[C/T]TGTGTCTTCGCCTTGCCCTGAATGGAAGTCCTCAA
193	1	1006	36.99	89865152	F1Dsnp	PHR	A	G	1	5,794,926	+	CACCACTGTTCCAACTCAGCCAATCCGGCTTTTAC[A/G]AACTCCCCATTACTGAATGAACAACACTCCCGCCG
194	1	1006	36.99	71_367836	GBS				1	5,814,837		ATAAGATCTCCATGGCGCAATTGGTCCAGCCGATTGCGAATGGCGCTTTCGTGCTGAGCATTGA
195	1	1006	36.99	89865153	F1Dsnp	PHR	A	G	1	5,815,502	+	CCGTGGTGGTGAGCACTGCTCATGGTTTGAAGTTC[A/G]CACAGTCTAAGGTTGATTATCACTCGAAGGACATT
196	1	1006	36.99	89865154	F1Dsnp	PHR	A	G	1	5,825,063	+	GTGCTCGTTGAAACTGTTGAGCCTATTTCTAGTAA[A/G]CTAACAGTAGAGAATGAGTGTGAAGAGGATGACTT
197	1	1006	36.99	TP56	GBS				1	5,941,875	5,941,823	TGCAGAAAACTGTCAGTCATTATATGCAGGCAAAGCTTGCATGGAAGTGGAATGGTCCAGAGTC
198	1	1006	36.99	71_501478	GBS				1	5,977,584		AAGAGAGCTCTTAACGCTAACCGTTGAAGCATGCAGACCTTATACATCCCGGGATTCAGGTACA
199	1	1006	36.99	TP894	GBS				1	5,997,446	5,997,506	TGCAGAATTAATGTCTTAGGAGTTGGGAGGAACATTTCAAGTTCAACATTTCACTCAATTCTTG
200	1	1006	36.99	89809186	F1Dsnp	PHR	A	G	1	6,036,492	+	AACAATCCCATTTCAAAGAGGTGGAAAATTCTCTT[A/G]CCGGATGGGTCTCATGGCACTTATCCTCAGCCTAG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
201	1	1006	36.99	89809187	F1Dsnp	PHR	T	G	1	6,081,866	+	AGAAGGAAGTTTAGCAGACAAGAAAAAGGGAAGGA[G/T]AAGTTGATTGGAGGAGCTTTGTTACCGAATGATTT
202	1	1006	36.99	89809189	F1Dsnp	PHR	A	G	1	6,244,623	+	GACGATCTGAAATTCTTGCAGACTCTTATGTGGCG[A/G]TTGAGGGCCTCCTCAGTAGAGATGAGCCTATCTGA
203	1	1006	36.99	TP3567	GBS				1	6,249,480	6,249,417	TGCAGCATATGATGCTAGTTAGTACGTGGTCTGCTGCAAATATGTCACAAACAAGAAGATGAAA
204	1	1006	36.99	1115_6059	GBS				1	6,272,422		TCCGGTAATTTGCCTCGGAATCTCCCAGATACACTCAATGGACTCTCAAATGATAGGTCTGGAA
205	1	1006	36.99	89809191	F1Dsnp	PHR	T	C	1	6,297,896	+	CTTCCCAGTGTAAAGTGCTTGGAACAAGAACCCTA[C/T]AAAGGCCAACATTGCAAGACGTCCATTCTTGATCT
206	1	1006	36.99	89865159	F1Dsnp	PHR	A	G	1	6,376,332	+	GAAACCCTGAAGGAACTTGTGGATCATTTAAGGAA[A/G]GCACCTGTGACAGCAAAACTGCTTTGTCCATCCTT
207	1	1006	36.99	596_44334	GBS				NGH			GAGTGTGAGCCATATATATCTAGCTCCCTCTGTGTCTTTTCCATTTGCCTGTGAGTGTAAGCAA
208	1	1007	39.43	89865161	F1Dsnp	PHR	T	C	1	6,432,459	+	CACGCCGGCCAGTGACCGTTTGGGTATCCATATAA[C/T]CTGAATTACTATCATCAGTTTCTTCATCACCGAAA
209	1	1007	39.43	89865162	F1Dsnp	PHR	T	C	1	6,433,311	+	GCATCCAGCCCACATTTCTTGACAAGCATTTCTAG[C/T]AGAAGCTTAATCTGAAAACAGTTCAGGTTTCACCA
210	1	1007	39.43	89865163	F1Dsnp	PHR	A	G	1	6,455,944	+	ATCCCTGAGTTTCCACACAACAAAGGCCCTCAAGC[A/G]TTTCAAGGTCAGGTTCTGCATTCTCTTGATTACTG
211	1	1007	39.43	89865164	F1Dsnp	PHR	A	G	1	6,475,342	+	ACCCTTTCGGCGGAAAACAGTCCCTTATCTAGTCG[A/G]GGAACCCTTTCACCAGCAATTAGTAGGAGGCTCAC
212	1	1007	39.43	89865165	F1Dsnp	PHR	T	C	1	6,499,266	+	CATTATCCATATAGCCATTGTTGGCGCTTCTGCTT[C/T]TACTGGTAGACGGTTTGAGAAGGTAAAATAATTGA
213	1	1007	39.43	89809193	F1Dsnp	PHR	A	G	1	6,511,455	+	AACCTGGACCTGCTGGAAGTTCTGTTGGAGATGCA[A/G]CTGCTCAGAAGGTTGAGGCACATAAACCTGTTGAT
214	1	1007	39.43	89865166	F1Dsnp	PHR	T	C	1	6,546,914	+	GGGACCAATGTGGATAAATTACATGAAGAAATTAT[C/T]GAAGATGGCCAACATTTGAAGCATTTGATTGGAAT
215	1	1007	39.43	89865167	F1Dsnp	PHR	T	C	1	6,553,210	+	CATGGCAAGGGCCAACTCATTGTTTTGCCTCGAAA[C/T]GAGTTCAACCATCCAGAGCTGAAGAAAAGCACAGA
216	1	1007	39.43	89809194	F1Dsnp	PHR	T	C	1	6,559,843	+	TGTTCGGTCTCAACATCATTAGCCACTCTTCCCTT[C/T]TCATTAACACCACGTTTTAGATACCTATTCGAGTA
217	1	1007	39.43	89809195	F1Dsnp	PHR	T	C	1	6,586,870	+	GGGAGACTGCCTTACAAAGTCAAAATGAGCAATCT[C/T]CTAATAATCCTGAAACCAATGATGCTAGTACTAAC
218	1	1007	39.43	89809196	F1Dsnp	PHR	A	G	1	6,602,612	+	CAGAAGTGTTTGACAGGTGGTTAAGTGTATTGTGC[A/G]AATCTTTGGTTCTTGAGTCTGAGAAGTTCTACTGT
219	1	1007	39.43	89865168	F1Dsnp	PHR	A	G	1	6,602,768	+	TCTGTGCGCAGTGTAAGGTTTCCTGGCATGCGGGG[A/G]TCGACTGCGCAGAATTTCAGAACTTGAATGAAAAT
220	1	1007	39.43	89865169	F1Dsnp	PHR	A	G	1	6,602,878	+	CACGAGCAAAAATGGAGGAGGTGTACAAATTGCCA[A/G]TACTATGTTGAAAAATCTGATGGTTGCTCTTACAT
221	1	1007	39.43	TP2888	GBS				1	6,604,913	6,604,865	TGCAGCAAGCAATTCAAAATAAATAGAATATCAGAACAAATTTAAACCGAGATCGGAAGAGCGG
222	1	1007	39.43	89809197	F1Dsnp	PHR	A	G	1	6,612,677	+	ATGTCCATCGCTCTTGCCAATGCCATACTGACCGA[A/G]AAGGAATCTTCACCGCCTCCTGATTCTGCCGAGAA
223	1	1007	39.43	89809198	F1Dsnp	PHR	A	G	1	6,650,322	+	TCTTGGTAACCGCTGAAGGCACACTTGTACAATGC[A/G]GCAAGGTCTGCATTTACTCTCAATGCAACTGCTTG
224	1	1007	39.43	89809199	F1Dsnp	PHR	T	C	1	6,684,665	+	GATATGTAGTTCGAGACATTCTGATACACCCACGT[C/T]TCAGCAATTGTAACAGTACTTGCGAGTGCTGCCAG
225	1	1007	39.43	89865172	F1Dsnp	PHR	T	G	1	6,695,701	+	TCTTTATGATAGCTTCACTTTCAGACTTGGTATCA[G/T]AAGACACCGTTCTTCTGGGAAGAGCCAGATTAAGA
226	1	1007	39.43	166_52041	GBS				1	6,821,960		AAACAGAACCTATCTGCAATGCAGCATCAATTTTCCTGTTATATGGCATCAGAGMATATGCGGA
227	1	1007	39.43	TP7773	GBS				1	6,822,063	6,822,001	TGCAGTAAGCTTCTTCTAATCCTTTTGATTAATTGGTCCTTTCCGCATATGCTCTGATGCCATA
228	1	1007	39.43	89865175	F1Dsnp	PHR	T	C	1	6,837,648	+	AAGTTTTACATGGTGTGGATCCAATACGACGGCGG[C/T]TCACATAACCTGTCGGTGTTCATGGCCAACCAGAC
229	1	1007	39.43	166_74474	GBS				1	6,843,027		ACGCCGGCCAAAAAAAGCAAGAACGTTTTGCGCTAGGATTTCCATACATTGCTTTTGATTGTCG
230	1	1007	39.43	166_74589	GBS				1	6,843,147		TTCCACTCTTGTACTGCGTTGGATAAGAAACGTGTTTAAACTGCAGAAGACGATTTGAGTTGAA
231	1	1007	39.43	89865176	F1Dsnp	PHR	A	G	1	6,843,575	+	CTCTCTTGGTGGCCGCTCATCCTGGATATCTTCCA[A/G]ATCTTCATCTTCTCCTCTCTTTCCAGCCTGTTCTT
232	1	1007	39.43	89809202	F1Dsnp	PHR	A	G	1	6,936,429	+	TTTCTTCACTGGGAGTGGATGAGTAGACAGTTCTT[A/G]GTGTTTGCGGAGTTGCTAGAGACAAGTTCAGCAGC
233	1	1007	39.43	89809203	F1Dsnp	PHR	A	G	1	6,938,771	+	CTTGCTTTAGGTGCTTCTGGCCCTGCTTTAATCGG[A/G]GAAAGCTTCATAATACCTGTTACTGTCACATCCAA
234	1	1007	39.43	TP8167	GBS				1	7,010,713	7,010,733	TGCAGTATTTAATTTGTATGAAATTATAGCTTTAACCATGAGCAAATTAACTCCCATTGATTTG
235	1	1007	39.43	89865178	F1Dsnp	PHR	A	G	1	7,018,515	+	CCCAAGTCTAATGCTTACCCAACAATCACTTTTGC[A/G]ATTGCAAGCTTGAAATTGGCATGGAAGCAAGATTG
236	1	1007	39.43	89865179	F1Dsnp	PHR	T	C	1	7,050,762	+	GTGGAACAAAAGACAGATAAGATCCCCTCAGATCC[C/T]GCTTCAAATAAGATGCATGGCATGTTAGTCATGCT
237	1	1007	39.43	89809204	F1Dsnp	PHR	T	C	1	7,088,458	+	CACACTGACTTAAAACCAGAAAATATTCTTCTTTT[C/T]AACACCATTGATCCCACCAAAGATCCCATCAGGTC
238	1	1007	39.43	89865180	F1Dsnp	PHR	A	G	1	7,121,636	+	AAGCAGAAAAAGCGTCAGGGTGCTGCCTCCATGTC[A/G]AAGAAATTTTACATCAAAATTAATGAAGATGAAAT
239	1	1007	39.43	89865181	F1Dsnp	PHR	A	G	1	7,123,098	+	GGGGGCATAAACATCGGAAGGAAAATGCTGATGCT[A/G]AGAGAATTGATAGAGCAAATGCAGAAGAGAGGAAG
240	1	1007	39.43	89809205	F1Dsnp	PHR	A	G	1	7,123,707	+	ACTACAGTGAAGAACTACACATTTTGCCTGTAGAT[A/G]GCATAGAAGGGAAATGTGAAGTCAGAAGGAGGAGT
241	1	1007	39.43	89865183	F1Dsnp	PHR	T	C	1	7,123,763	+	GTCAGAAGGAGGAGTGATCTTCCAGAATGTAATGC[C/T]CCTGCATTGTTTCAGCATATATTCTTCTGTGAGCA
242	1	1007	39.43	89809206	F1Dsnp	PHR	A	G	1	7,128,595	+	ACAGGCGACACTGCTGTGATGTGCATAATGCCTCA[A/G]CCAACATGTGAAAGTAGAAGGTAGTATCTCTAAAA
243	1	1007	39.43	89780491	snp	PHR	A	G	1	7,130,008	+	TCTCGACTTCTTGTTTCTGGAGATCAGAGTGGAAC[A/G]GTGAAGTACCATCTTTGTTCTGTTTATTGATTATT
244	1	1007	39.43	89809207	F1Dsnp	PHR	A	G	1	7,131,300	+	TGTCTTTGACAACGGAGACTGCAGTAAGGGGATTC[A/G]TGTATACCACATCAAAACCAAATTCACATGCTGGC
245	1	1007	39.43	TP7248	GBS				1	7,140,069	7,140,118	TGCAGGTATATCACGGCCAACTTTTGGAACTGGAACTGACACCAAGACCGAGATCGGAAGAGCG
246	1	1007	39.43	89865184	F1Dsnp	PHR	A	G	1	7,140,109	+	GTATATCACGGCCAACTTTTGGAACTGGAACTGAC[A/G]CCAAGACCGGAATATTGGATTCCAGCACTCTTAAG
247	1	1007	39.43	TP8014	GBS				1	7,182,877	7,182,939	TGCAGTAGGAGCCACTGGCAAATTCTAAGCATCTCCCTCACCACCTCGGCTGACTTCAGCAGTT
248	1	1007	39.43	908_1530	GBS				1	7,192,260		CAGTATCACCACTCTGATTTGGCTGCAGTAGGAGCCACTGGCAAATTCTAAGCATCTCCCTCAC
249	1	1007	39.43	908_1604	GBS				1	7,192,337		GACTTCAGCAGTTCATCAGACTCCGTCAACAKTGCACCACCTACACATGCAATGTAGACATGGA
250	1	1007	39.43	89809209	F1Dsnp	PHR	T	C	1	7,209,527	+	TGTTCCTTAAGGGCGTCAATGTTGCCTTGTGTTGC[C/T]GCCATGAAGATGTTTAGATCCATGCCCTTCAATAT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
251	1	1007	39.43	TP1808	GBS				1	7,244,423	7,244,381	TGCAGAGGTGGATTTTGGAGTTGGATAACTATGACAGAGGAGAAAGCTGAAGGTGCGCCGAAGC
252	1	1007	39.43	89809211	F1Dsnp	PHR	A	G	1	7,248,102	+	TTTGTTAACTGAGTCCTGGTTGGGTTCCCACCTTG[A/G]GGGGTGAAAAGAGCTGCTAATGGATTTGAACTATC
253	1	1007	39.43	89865187	F1Dsnp	PHR	T	C	1	7,279,395	+	AACGCCTGCTCTAAACATTCATGCGCCAAGATGCT[C/T]GCATACAAGAAGCTACTCAAAATTGGCTCCTTCTC
254	1	1007	39.43	89809212	F1Dsnp	PHR	A	G	1	7,289,854	+	CCTGAGTGGGACTCTCTGCCTTCAGATGAGAGATC[A/G]AAGCTTAAAGCTCGACAAGGGGTGCAGCATGTTTG
255	1	1007	39.43	TP4225	GBS				1	7,290,196	7,290,133	TGCAGCCTCAAGAACTGCTGGATGGCTAAACAGAACTGTTTCAACCTCAACTGTGCTTATGTTC
256	1	1007	39.43	34_83680	GBS				1	7,290,239		GCATTTGTGAAATTGAAGGAGGGCTTTGATGTGGATGCACAAGAACTAATTGAGTTCTGCCGCT
257	1	1007	39.43	89809213	F1Dsnp	PHR	T	C	1	7,303,557	+	GTGTAATTCACTGAAATGGGATCACATTCATTGTG[C/T]GGTCGTCGAATCTCAAAGTCTGGTTCTGCTTTCGT
258	1	1007	39.43	TP9330	GBS				1	7,334,543	7,334,482	TGCAGTTCCTAGCCTATTGGTCCAAATATACCATATAATTAGGATTCTAGCTCATTGTTTAATT
259	1	1007	39.43	89865188	F1Dsnp	PHR	A	G	1	7,346,169	+	TGATTGAGAATCTCTCTATCAAAGCCCCTAGTGGT[A/G]AAGCGAAGTTGAAACTCATGAAGGAAATAGCCAAG
260	1	1007	39.43	TP1497	GBS				1	7,347,967	7,347,920	TGCAGAGAGTGAAAAGGGTACCATTTGGAGGAGTTGAAGCCCCGCCGAGATCGGAAGAGCGGTT
261	1	1007	39.43	89865189	F1Dsnp	PHR	A	G	1	7,373,762	+	GGGTGCTGCCCCGTCCAGAGAAAACTCAGTGAAAC[A/G]GGTGGGTGTTTGGAGGCCATGAATGCTTATTCTCA
262	1	1007	39.43	89865190	F1Dsnp	PHR	A	C	1	7,379,742	+	CGAAACGCATGGAACGTCTTCAACTTAAGTTCCAG[A/C]ACCATTTGAAGGTGTGTGTCAGTTGTTTTATTTCC
263	1	1007	39.43	89809214	F1Dsnp	PHR	T	G	1	7,400,728	+	CTTGGATTTATACCTGAAAGCTTTTCTTGTATACC[G/T]TCGGCTCTCCCTTTCACCAGAGATCCAATACCATA
264	1	1007	39.43	89809215	F1Dsnp	PHR	A	C	1	7,436,239	+	AAGACATTGCAGCCATCAAGATCCAAGCATTTTTC[A/C]GAGGCCAACTTGTATATAACATAAACCCAACACTA
265	1	1007	39.43	89809216	F1Dsnp	PHR	A	G	1	7,441,907	+	TCGGCTAATTGCAGCAATCTCTTATGTGTAAGCAC[A/G]TCCTCTGCCCTCTCCACATTCACATCCAATGCGTA
266	1	1007	39.43	34_249169	GBS				1	7,445,118		AAGTGCATGTTTGACCGCAGATAGTTCACCCAAACACAAACGCAGTTTTTCAAGCACTCATTTT
267	1	1007	39.43	34_259282	GBS				1	7,454,828		AGGGGGAGAGGGTGTGGAGTTTGGTTGAGAACTTGAGAGAGGTGGGTGGTGAGAGCTTGTGGGG
268	1	1007	39.43	TP9171	GBS				1	7,490,895	7,490,958	TGCAGTTACAGTTAGGGAGTATGATCAGCTAATCAGCTTTGAGCTTTCCTCCAGAAATCATCTT
269	1	1007	39.43	89809217	F1Dsnp	PHR	A	G	1	7,497,752	+	AAACTTTACTATTCTTGGAGCAGCTCAGGAAGCAA[A/G]CATCGGTATAGCCTTCCGCGTAGCGTTGAAGATCT
270	1	1007	39.43	34_306841	GBS				1	7,498,271		CATGCCTAGAAAAGCTACGCATCTCAACAAAGTATAGGCCTCCATTGCTAATCTCTCTCTTGGT
271	1	1007	39.43	34_330691	GBS				1	7,518,817		AATAAGTTTTAAGTTTGCATCCATCACCTTTTCTGCAGTAAGGATTTGTTTCCTTTCCGTAGGT
272	1	1008	41.90	TP7302	GBS				1	1,495,367	1,495,307	TGCAGGTCCAGAACTAAAGCTCTGTTGTAAAATGGAAAAGGGCCACCGCTGCACATAGTAGAGA
273	1	1008	41.90	89865191	F1Dsnp	PHR	A	G	1	7,558,326	+	GGTTGAAGTTCATGCACAGAAATTGCTGGATCCGC[A/G]CTTAAAATTGGCCTTTTGAAAGGTTCACGCAGGCG
274	1	1008	41.90	89780597	snp	PHR	T	C	1	7,581,979	+	TTTCGAGGTCAGCAAATATGACCCTAAAGGATCAT[C/T]GACTAGCAAGATAGTCCGTTGCAACAACAGGTTGT
275	1	1008	41.90	89865192	F1Dsnp	PHR	A	G	1	7,594,552	+	GCACATACCTTAACATACCTCCAATCCAAGTTAAC[A/G]ACAGCAAGCCTGTGAGTTTCCTTCTCGATTTGCGG
276	1	1008	41.90	89865193	F1Dsnp	PHR	T	C	1	7,596,970	+	GTTGCTATATCTGACCCTGAGTTTATAATCTGCCG[C/T]TTAACAGAGTAGTTGTCGAAGATCCCCTCCATTTG
277	1	1008	41.90	89865194	F1Dsnp	PHR	A	G	1	7,616,207	+	AATCTGGAAATGAAATGCTATCAGCTCATATCCAA[A/G]GTATTTCACTCGATGAGAAGACTACTAACAACAAC
278	1	1008	41.90	89809219	F1Dsnp	PHR	T	C	1	7,648,387	+	ATACGAAGCCCACATACTCCAAAAGCACCAAGACA[C/T]GGTCCCAGGCCACCATCTCGCCTCAAAGTTTCAGA
279	1	1008	41.90	89809220	F1Dsnp	PHR	A	G	1	7,915,470	+	AAACAGAAACGTACCTCCTTAAATATACCATCTTC[A/G]GTCTTATCCCAAAATGGACGTCGCCCACAAAGCAA
280	1	1008	41.90	TP3364	GBS				1	7,990,429	7,990,368	TGCAGCAGCCGTTTCCTCTGAACACTAACTGGCCTGGGGCCGATAAGTACGGTGTCCAGCCGAG
281	1	1008	41.90	89809221	F1Dsnp	PHR	T	C	1	8,012,387	+	GCTCGTGTACAAAACCATCCAGCTGTCATAGTTCC[C/T]CGTTTGCCTGCTGGGATTAACTTGCCTAAGCCTGG
282	1	1008	41.90	89865195	F1Dsnp	PHR	T	G	1	8,031,255	+	GGATCTGAAGAAGACGAAGGCTTCCTCACTAAAAT[G/T]TCAGTCAAGCTACCCTCACTTGGAGGTGAAGTCAA
283	1	1008	41.90	89809222	F1Dsnp	PHR	T	C	1	8,078,480	+	GTAAGCGAACCAGCTATCAAGCAGTTAAATGTTGA[C/T]GTGTTTGGGAAAACCCTTCTCTCTATCATCATGTT
284	1	1008	41.90	89809223	F1Dsnp	PHR	T	C	1	8,083,491	+	GATGGGCATGTAAAGATGGATAATAAGTTAATTGA[C/T]TTGAACATGAAGCCTAATCGGATGCATGGACAAGC
285	1	1008	41.90	TP1719	GBS				1	8,090,960	8,091,023	TGCAGAGGAGATGAGGGTTGCTTTCATGAATGCCGAGGTAGTTAGAGGCTAAGACTCTGAACCC
286	1	1008	41.90	89809224	F1Dsnp	PHR	A	G	1	8,097,953	+	TATGCTATCACTTCTACCAATTCTCGGAAATTTCA[A/G]AAGCATTGTTATCTGGCTTCTGCCTCTTTGATTTT
287	1	1008	41.90	89865197	F1Dsnp	PHR	T	C	1	8,102,315	+	AGCCTGAGCCAACACATAGGGGATGTACGAGTCCA[C/T]CACCTTGTCCTTGTGTTTCTTGTGGAATGTTAGCT
288	1	1008	41.90	TP8047	GBS				1	8,102,378	8,102,315	TGCAGTAGTGATCGGAGTCCTCGCATTGAGCTAACATTCCACAAGAAACACAAGGACAAGGTGA
289	1	1008	41.90	21_477967	GBS				1	8,126,080		TTCAAATTCAGCGAAACATGTCGAACTTAAAMTCACAATTCCATAATTCAAATCCCTAAACATA
290	1	1008	41.90	89865198	F1Dsnp	PHR	A	G	1	8,126,593	+	CAGCCGAGGTGAAAGAGATTGTTCAAGCGGCGGGT[A/G]TGCCTTTGGAAGATCAGCGAGAGATTCGTGGTGAT
291	1	1008	41.90	TP7746	GBS				1	8,131,905	8,131,863	TGCAGTAACTCATTTCAGTCAGAATTCTTGGCTTAGTGAGAAAATGTCAGCAATCAATGTGCAC
292	1	1009	44.36	89865199	F1Dsnp	PHR	A	G	1	8,230,715	+	TCTTCTTCATCGTCAGGGCAATTGCTACCAATATG[A/G]TTTTCACTTTCGACATTTGAATCTGTCAATTTGGA
293	1	1009	44.36	89809225	F1Dsnp	PHR	A	G	1	8,241,120	+	GATTTAGCATATGCTGTGGCCAGATTCATACAGAA[A/G]GGAGGATCATTTGTTAACTATTACATGGTCAGTGT
294	1	1009	44.36	89809226	F1Dsnp	PHR	T	C	1	8,291,074	+	GCCACAGAAGAGAAGGTCATCCCTGAACAACCTGA[C/T]GAGAAAATTCATCAACAAACAAACAAGAACAGCGG
295	1	1009	44.36	89865200	F1Dsnp	PHR	T	G	1	8,308,919	+	CCAACGCTTTTGATCTGTTGGGGGAGGACTCATCA[G/T]ATGTGAAGAGAGTGGTTGCCATCGTCGATGCGAAC
296	1	1009	44.36	89809227	F1Dsnp	PHR	T	C	1	8,330,430	+	GAGCTTAAGCTTTTTCATCCAATTTGCTTGCTTAG[C/T]GTCGTCCTTGCTTGTATCCGTTACCCTAGTTCATG
297	1	1009	44.36	89809228	F1Dsnp	PHR	A	G	1	8,330,933	+	TGGCGTCGGAGCCGATGGTTGGCCCTATAATGATT[A/G]CCTCCAACATCCAGGCAGTTGCAAGCGACTCCCTG
298	1	1009	44.36	TP9086	GBS				1	8,331,942	8,331,905	TGCAGTGTGTTACATACAAGTCGTTAACAGTGTCACCGAGATCGGAAGAGCGGTTCAGCAGGAA
299	1	1009	44.36	TP9863	GBS				1	8,336,304	8,336,241	TGCAGTTTTTTACATACAAGTCACTAACAGATTCACCAGCATTTCTACCGAGGCTTCCGATGCT
300	1	1009	44.36	89809229	F1Dsnp	PHR	T	C	1	8,348,868	+	AATCATTCTCAAGGTTGAACTTTTTAACCATATCA[C/T]CCCACGTAGCTTCAAATTCTGCTTCGGCGACACAC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
301	1	1009	44.36	89865201	F1Dsnp	PHR	A	G	1	8,349,616	+	TGCACGAACAGTTGATATATGCCGACTTGATCTTA[A/G]AAACTGCCTCTCTTCTGGCTTAGCAAACTCGTGGT
302	1	1009	44.36	89865202	F1Dsnp	PHR	T	C	1	8,357,707	+	CCAGTTGTACCATGAGTCTTGTGCCCCGTTCCGGT[C/T]GTTTCATGAGTTCCGTACCCTGTTATAGTGTCATG
303	1	1009	44.36	89780759	snp	PHR	A	G	1	8,403,998	+	AAGAGGATCAATTCATAAGAGCAGACACTGACCTC[A/G]GCATCCAGCTTGATAAACTTGGTGTCAAGATGCTT
304	1	1009	44.36	89865203	F1Dsnp	PHR	A	G	1	8,438,298	+	CCACCTTGTCGTAGGCCTCGTTGAGCTCCATGCCG[A/G]TGACCTTGTTGATGACAAGAGTGAGATTGTCATTT
305	1	1009	44.36	89809230	F1Dsnp	PHR	A	G	1	8,465,043	+	CTAGGGGTTTTGCTGACCTTTAGACGTTCGTTGAT[A/G]GAACTGATCTTGGTTTGGAGGTAGACCTGCGCCGC
306	1	1009	44.36	89865204	F1Dsnp	PHR	A	G	1	8,501,721	+	GTTAGAAGATGCAGTGAGGAAAGAGGGTTCGTTTC[A/G]ATTGGACAGGTTGGAGATGTTTGAATTAGAGAGGG
307	1	1009	44.36	21_154151	GBS				4	9,484,136		AATCCTTCCGGTTGCTGCATATAAATCTCCTYGTCTAACTCACCATTTAGGAATGCCGTTTTGA
308	1	1010	46.80	TP5751	GBS				0	4,602,671	4,602,734	TGCAGCTTTGCGGTAATAAGCTGACCAACAATGGCTTGCAGAAAATCCTTGATTGTTGTCCGAA
309	1	1010	46.80	TP9138	GBS				0	5,368,067	5,368,130	TGCAGTTAACATGGAGGAATAAATACAGTATCACATACATAACAAGCACCACAGAAATAATTGA
310	1	1010	46.80	89865206	F1Dsnp	PHR	T	C	1	8,604,381	+	GTGGCTTTTAATATCTGGATCATCATAGCCGCCGC[C/T]GCCAGTCCACAATACCAGTTTTTGAACCCTTTGAA
311	1	1010	46.80	89809232	F1Dsnp	PHR	A	G	1	8,604,428	+	ATACCAGTTTTTGAACCCTTTGAAGCATGAAGTCA[A/G]AGCCATAACTACGTACATAGCTGAAGAGACAGCTA
312	1	1010	46.80	89809234	F1Dsnp	PHR	A	G	1	8,607,710	+	TGTAGTACTAGCAGAAGGCACCTCAGTCATAATCC[A/G]AAGCTCACGAGGTAATTCGTGTTCACCTCCTAGAA
313	1	1010	46.80	89809235	F1Dsnp	PHR	T	C	1	8,649,154	+	AGAACGCTATCTCCTTCCCTGACATAGATAGTTGG[C/T]CCCGGAAACCTCCCGTTTACGGTAACAATGGGTTT
314	1	1010	46.80	28_37203	GBS				1	8,667,173		ATTGCAGTATTATGAAGCCGGTGATCGAATTYCCATCAAGATGCAACATACTGACAACCCAGAA
315	1	1010	46.80	89809236	F1Dsnp	PHR	T	G	1	8,680,231	+	TTTGTGACGAGCGCTAAGAAGTCACTCAATAAAGA[G/T]ACTCAAGATATTGCTGATATATACCTTGAAGGCGC
316	1	1010	46.80	89865207	F1Dsnp	PHR	A	C	1	8,680,723	+	AACTTAGAAGCAGGTTTTCAAGCCATTCAACAAGG[A/C]CAACAAACTCAAGGTCAAGAGATGGTTGTAGATGC
317	1	1010	46.80	89809237	F1Dsnp	PHR	A	C	1	8,680,753	+	CAAGGACAACAAACTCAAGGTCAAGAGATGGTTGT[A/C]GATGCTACTGTTGCTCTTAAGATAGATAAATCTTT
318	1	1010	46.80	89809238	F1Dsnp	PHR	A	G	1	8,681,857	+	CTAGGAATACAAGTGGCACTCAAGATTAATTATCT[A/G]CAGTAGTACTCTAAACTCAGCGGGATTGCCCAAGC
319	1	1010	46.80	89809239	F1Dsnp	PHR	A	C	1	8,687,259	+	CCAACTATGCCCGTGACAATTGGGATCAGTCAATA[A/C]GAATGCCTACTGAGAGAGCTGGCAATGCTGCCCAA
320	1	1010	46.80	89809240	F1Dsnp	PHR	A	C	1	8,732,200	+	TGTACTGATTGGCTTGCAGTGCCTTTTTCGAACTC[A/C]TTTGAACAATTACGACGCTGTGATTCTTCTTCATA
321	1	1010	46.80	28_95895	GBS				1	8,735,173		TACTCTTCTCGTCTATATCTGCAGTCTAAAAYCCAAACCCAAACCCAAAACCCAAATCAATGTT
322	1	1010	46.80	89865209	F1Dsnp	PHR	T	G	1	8,749,215	+	TAGGGGAGATCCTCTGCCCACGGCTTTCATACTTT[G/T]GGAGTCTTTGAAGCAAACAAAATGCACTATTGTAC
323	1	1010	46.80	89809241	F1Dsnp	PHR	T	C	1	8,831,887	+	CCTTTCTTTCTTGTTACCATGATAGATTATAGCCT[C/T]AATTGAAGGCGTAAACCTAATGGGAAAAGAAGGAA
324	1	1011	49.32	TP7501	GBS				0	2,367,661	2,367,721	TGCAGGTGGTTAGTGGCTCTCCTACAAGAATTTTTCTTTTAATCCCATGCCAGTTTTTCACTTG
325	1	1011	49.32	TP9847	GBS				0	2,462,024	2,462,076	TGCAGTTTTTAACTTTTTATGAGTCAATTTAATTTGAAACAAAATACAAGAAAAGCAAAACCAG
326	1	1011	49.32	89865000	F1Dsnp	PHR	A	G	1	1,048,825	+	TCACCCTCGTCGGCGTCTTGTCCATGTTCGCTGCC[A/G]GCATGCCTATTTTCTTACGCCAAGCTTATATGGTT
327	1	1011	49.32	TP8478	GBS				1	8,735,201	8,735,249	TGCAGTCTAAAACCCAAACCCAAACCCAAAACCCAAATCAATGTTTCTGAAACTCCCATACAAT
328	1	1011	49.32	89809242	F1Dsnp	PHR	T	C	1	9,014,403	+	TTAAGTTTGCCTTCAACACGTTACCAGCATGGTCT[C/T]GAGCTGATAGCAACCGCTAAGAAAATCGTTGTCCC
329	1	1011	49.32	89780852	snp	PHR	A	C	1	9,204,844	+	CAGTCACCTAATGCATCGTTAAAATCATCCATTAA[A/C]TTCCTCCTCCTAACACCTCCACTTTCCTTCTCCAT
330	1	1011	49.32	89809243	F1Dsnp	PHR	T	C	1	9,290,112	+	ATCGTGGAATACCATGCTAGTTGCCTTTTCAGGTA[C/T]TTGCTATTCTACCAAGTTTCTTAACTTATTAAACG
331	1	1011	49.32	89809245	F1Dsnp	PHR	T	G	1	9,416,869	+	TTGCTGAAGAAAGAGACGAATGTTATCACGGAAGG[G/T]ACCCAATGGGAGAATTGGGTAACCGGGTTCCCCAA
332	1	1011	49.32	89809246	F1Dsnp	PHR	T	C	1	9,564,250	+	AGAGAAATGTCAAAGCAACCCATATCATAAAGTTC[C/T]TTGGCCACATAAGCTACTTGAGATGGGGGAACAGC
333	1	1011	49.32	TP4026	GBS				1	9,573,293	9,573,355	TGCAGCCCATCCCTGAGACCGACTTCTACTATCTAGACAAACTCGGGAATGTTTCCTAATGCCG
334	1	1011	49.32	89809247	F1Dsnp	PHR	T	C	1	9,698,406	+	AACAATCAAAGGCCAACAATCATACCCAAAATACA[C/T]GAGGAACCTTTATCCATTTGTTGTTTTTGAAATTA
335	1	1011	49.32	89809033	F1Dsnp	PHR	T	C	1	10,093,882	+	CTGCTTCAAAATGGCTTCTGCAGCAGCAGCCATGA[C/T]GCGATCAGACTCCATAGCTGAAAGCATGCCCGACG
336	1	1011	49.32	89809034	F1Dsnp	PHR	A	G	1	10,097,301	+	TGCACTTATACTTACTGGAGGCAGTTGAACAAAGA[A/G]CAGAAACAGGCAAAGCAAAGATACATCCAGATGTT
337	1	1011	49.32	89809035	F1Dsnp	PHR	T	C	1	10,104,258	+	ACAAATTTGGAGCTTCTTGAGCACTATGGCTTTCT[C/T]TTAAATGAAAATCCAAATGACAAAGCTTATGTTCC
338	1	1011	49.32	89864996	F1Dsnp	PHR	T	C	1	10,138,326	+	CAGAGGGTGATGGTTTGCCTTTTGGAGCTAGGGGT[C/T]GAGTTTGAGATTGTGCCTGTTGATCTTCAAGCAGG
339	1	1011	49.32	89864997	F1Dsnp	PHR	T	C	1	10,155,878	+	CAAACAAAACCACCTTCACTTTTAATTGCATAAGC[C/T]ACCATGTCATCGATGAGACGATGTTCATACCTTTC
340	1	1011	49.32	89865001	F1Dsnp	PHR	A	G	1	10,597,997	+	ACTGTCCTTTGAGGCAAAGACCCATCTTCCTCGTC[A/G]TCATCAAATTCCAATAAATAACTGCACCAGATATT
341	1	1011	49.32	89809036	F1Dsnp	PHR	T	C	1	10,682,216	+	ACCCTGACTAGCAAGTTGTGACACGATGCTAGATT[C/T]TCCCTTGCCAAGGCCGAGAACTCCATCTATAGGAT
342	1	1011	49.32	50_76574	GBS				1	10,684,346		GCTCCTTGTGTTAGATGTACTGAGGTAAGTAWTCTACAGTTCATTGTTACAGTTGATGATTACA
343	1	1011	49.32	89809037	F1Dsnp	PHR	A	G	1	10,731,506	+	TTCTGTTATACAGCAAGAGGAGGATTTTGTTACTC[A/G]GATGATGACATATTTGATTTTCGCACAGGCAATAG
344	1	1011	49.32	89809038	F1Dsnp	PHR	T	C	1	10,765,178	+	GCCTATGGTTACTATTTTCACATGGCTACAGCAGA[C/T]GGGCTTGTTAACCGAGGTGATGGAAGGGATAGGCC
345	1	1011	49.32	89809039	F1Dsnp	PHR	T	C	1	10,766,533	+	CCTGTTGCTCGTCCATTGTGGATGGAGTTTCCTTC[C/T]GAGGAGGCTACTTTCACAAATGATGAGGCTCTTAT
346	1	1011	49.32	89865003	F1Dsnp	PHR	A	G	1	10,794,396	+	TCAGCTTGTTCTCTTTGGACTTGAAGGTCTCGCTC[A/G]TTCTTTTCCGCAAGTGCTTTCACCTAAAACAGAAA
347	1	1011	49.32	89778396	snp	PHR	A	G	1	10,795,766	+	TTGCATGTTCATCAAAGTTACTATGACTCTTTCCC[A/G]TGGCAAAATCGTCAAGATTGTCAACGGAAGAAACA
348	1	1011	49.32	89809040	F1Dsnp	PHR	A	G	1	10,815,248	+	ATAGAGTTGTGCTGCATCCAGATGCAATCTTCAAT[A/G]TTTCTAGTGCACAGGCAGCTGATATAATCGCATTT
349	1	1011	49.32	372_174713	GBS				1	11,086,602		TTTTATGATGATAACGATCTAGCTCTGTTCGTTGCTGTTGTTTTCCAGTGCCGGCAGACGTCGC
350	1	1011	49.32	89809041	F1Dsnp	PHR	A	G	1	11,087,061	+	ATTTGCAAATGCCATTCAAAGCTCGCAGCAGCAAC[A/G]GCAAAACATGGCATTGCTGCAGCCTGCCTGCTCCA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
351	1	1011	49.32	89865005	F1Dsnp	PHR	T	C	1	11,589,012	+	TCCCAGTTACAAAAGGTCCAAGAGAAGCAATCAGC[C/T]TTTCAGGGTTTCCAATATCTTCAATGGATGCATTA
352	1	1011	49.32	89865006	F1Dsnp	PHR	A	C	1	11,633,965	+	GAAGATCAAATACTTTGATACAATTCCAGTCACAA[A/C]TTCAATCTGTGTGTTAAAATCAGGATTTTTGTTTG
353	1	1011	49.32	89809042	F1Dsnp	PHR	T	C	1	11,654,251	+	TCCATTGTTTGGATATTAAAGAGGTTCGCACGGCG[C/T]CTAGTGTGGAGAAGAAAGAAAGGATGTGGAGGAGG
354	1	1011	49.32	89809043	F1Dsnp	PHR	T	C	1	11,797,246	+	GAAAAGGGAAAGTACCTGGAAGAGAAGGAATATAA[C/T]GACCATAAAAACTCCTATAACCATTGAAGTGCTGT
355	1	1011	49.32	TP852	GBS				1	11,879,840	11,879,901	TGCAGAATGCAGACATATATATGATACGAATCTGTTTTAAATTTAGGGTAAAGTAGGTTTGGTG
356	1	1011	49.32	89809044	F1Dsnp	PHR	A	G	1	12,348,127	+	GGTCGCCCTGTACTTGTTGGAACAACTAGTGTTGA[A/G]CAGAGTGACTCATTGTCTGAGCAGTTGCAAGAAGT
357	1	1011	49.32	167_209325	GBS				1	12,376,423		CTACTTTGGTTAAGAAAAACCTCTACAAAAGMTTGTTTTTACACAAGGACGACAAGGCATGCCC
358	1	1011	49.32	89809046	F1Dsnp	PHR	T	C	1	13,006,868	+	TTATTTCTTTCTGCTTCTGTTATTTCATTTTCCAC[C/T]GCAACAAGACTTTTATTTGGAGCAGTGTCAATTAC
359	1	1011	49.32	89809047	F1Dsnp	PHR	T	C	1	13,008,847	+	TCTTGTTTACCTTTGTTAACATCCCATATGATGCA[C/T]GAATTATCAACTGAACCGGAGATGAGAAATAAACC
360	1	1011	49.32	89809048	F1Dsnp	PHR	T	C	1	13,028,586	+	GAAGCTGGAGCAAGAGGTTCCCAACAAGAGCGAGT[C/T]GGCGGAGCTACGACTCTCTTGGCTTCGCTCTCAAG
361	1	1011	49.32	89809049	F1Dsnp	PHR	T	C	1	13,039,962	+	CCTGCTTCACCAGCAATAGCTTTGGCCAGCAGTGT[C/T]TTTCCTGTTCCGGGAGGTCCATGGAGAAGCACACC
362	1	1011	49.32	89865019	F1Dsnp	PHR	A	C	1	13,837,202	+	TTCAGGAAGCACTTAACGGCACGACTAGGACTAGG[A/C]AGAAACCCGAATTTTCTAATGGATGGATTCCAGAG
363	1	1011	49.32	89809053	F1Dsnp	Other	A	G	1	13,837,337	+	GTTCCGACCACTTTGGAACCCCTATTTTTGGTCCA[A/G]CAACTATTCTTATTGTTGTCAATCGGATGCAGGAG
364	1	1011	49.32	89809054	F1Dsnp	PHR	A	G	1	13,841,860	+	TAGCGGTGCGGTTAAAGAGGCACTGGATCAGCTCA[A/G]GGAAGCTGGTTGGGCTAAGAAATGGAGTTCTCAGC
365	1	1011	49.32	89809055	F1Dsnp	PHR	T	C	1	13,847,621	+	TTTCCTTTGAAAGGAGAGAAATCAGTAAAGGATGC[C/T]CTGGCATTAGCCAAGAGGATTTCGCTGTCATATAT
366	1	1011	49.32	TP3182	GBS				1	14,025,900	14,025,857	TGCAGCACTCTTTTGTAGAACAAATTGAAAATGTGCTGTTCTACTATATATGGACCAGTCATTG
367	1	1011	49.32	89809057	F1Dsnp	PHR	T	C	1	14,161,889	+	TTTCCACATCCCAGACATTACATAGAAAACATCTG[C/T]TTTTGCAGCTTTTGATTTCATGCTGAAAAGTTCAA
368	1	1011	49.32	89865021	F1Dsnp	PHR	A	G	1	14,187,360	+	AATACTGGGAATTGACGTATCGGGTTTCTGCATTG[A/G]CGAAAAGATATTACAAGGAAAACAATAGTAGTAAC
369	1	1011	49.32	TP1276	GBS				1	14,190,974	14,191,037	TGCAGACTCTGCATTGTAGGAAGCGGTGCAATAGTCCCGTATGCCCCAAGCAACGAACCCCCCG
370	1	1011	49.32	TP1282	GBS				1	14,640,508	14,640,574	TGCAGACTCTTGCAGATGAGAGTGGAGTGATCAGCCACAAGGTCCCTAGCTCTGTTTCTTTGGT
371	1	1011	49.32	89809059	F1Dsnp	PHR	A	G	1	14,984,733	+	CACACCGCTCTGCTTCCTCATGTAGATAATGAAGC[A/G]CCGAGGCCAAGCCTAGAGCTATTCTATACCTAAAC
372	1	1011	49.32	89809060	F1Dsnp	PHR	T	C	1	14,988,571	+	ATGTTTTCCAAAGCTAAAGAATTGTTTGAAGAAAC[C/T]AAGGCTGCTAAATCTGATTCTGACCCTTCGCTGGA
373	1	1011	49.32	89809061	F1Dsnp	PHR	T	C	1	15,072,119	+	AGGCTGGACTATGCTGGAATTGCAGCCCTTATATC[C/T]ACCTCATTCTACCCTCTTGTTTACTACTCCTTCAT
374	1	1011	49.32	TP7819	GBS				1	15,150,085	15,150,143	TGCAGTAATGTTGCAGCCGAGCTCAACGAGGACCGCGGATATCTCAGACATTAACCCCGAGATC
375	1	1011	49.32	89809062	F1Dsnp	PHR	T	G	1	15,157,586	+	ATCAAATTCGACTGGTTCTCCAAGGAAGGATCAAT[G/T]TGGTATGAAGATGAATGATGTTCCAAGATGGGTGG
376	1	1011	49.32	89873705	snp	PHR	A	G	1	15,475,046	+	ATGCTGCCCACAGGTGACACGACAACAGCGGTTCC[A/G]GTACAAAAGACTTCATCAGCTTCAAGTAATTCATC
377	1	1011	49.32	89865026	F1Dsnp	PHR	A	G	1	15,552,189	+	AAGAGAGCAAGAAGTGCTGGAGGGGGAGATTGATC[A/G]AGTTGATTTGCAGATCAAGGATCATGACATGAAGA
378	1	1011	49.32	89809063	F1Dsnp	PHR	T	C	1	15,552,226	+	GTTGATTTGCAGATCAAGGATCATGACATGAAGAT[C/T]GATCGCATGAAAAAAGAGAGAGCCAAAATTACAGA
379	1	1011	49.32	89865027	F1Dsnp	PHR	T	C	1	15,644,792	+	AGTAATGGCAGATTGTTGAGGGGAGTCTGTGACTG[C/T]TGTTGTCTCTCCTACTTGCTTTGAGCCTGGTGGAA
380	1	1011	49.32	89809064	F1Dsnp	PHR	A	G	1	15,726,840	+	CTCCATCATCTTCATCATCTTCTTCAAACTTGTCA[A/G]CACTTCTAAGGAAGATCCCTACAAAAAATAGCACA
381	1	1011	49.32	89809065	F1Dsnp	PHR	A	G	1	15,729,766	+	CTAGTTTCAATAGATTCCAAAAGCATTGTGGAGCC[A/G]GTAGGAGGTAAACCTAAAGTTACAAATTTTGTCAC
382	1	1011	49.32	89865028	F1Dsnp	PHR	T	C	1	15,732,228	+	TGGCAAATTCCGCTCTCATCACAAATCCCAATGCT[C/T]CCATTGACCCCATTGCTTGCTATTGCTCCTCGATC
383	1	1011	49.32	89809066	F1Dsnp	PHR	A	G	1	15,737,571	+	TCCATTTCCGTACATATGTGCACAATGTGAAAGCC[A/G]TTCCTGATAATAAGAAATATGAAATTGACAACATC
384	1	1011	49.32	89809067	F1Dsnp	PHR	T	C	1	15,740,547	+	ACTGTTTTGATAACATACTGGGCTTATAAGGTTCT[C/T]GTACATCCTTTCTTTGCTGTAGTGGCTGCTTCAGA
385	1	1011	49.32	56_554487	GBS				1	15,749,675		TTAACATCAGCACTAAGCAATATAATGAATAGATGGAAAACGTTAGCCAACAAGTTACTTACAG
386	1	1011	49.32	89809068	F1Dsnp	PHR	A	C	1	15,850,299	+	GGACTCCTAGACGATCTTCGAGGTTGGTTGGTAAG[A/C]AAAATGTGGTTGAGAAACAAACTGATAAGGCAAAT
387	1	1011	49.32	89809069	F1Dsnp	PHR	T	C	1	15,871,188	+	GACTTAATTTTTTTTGTCATTGCAGTTTCTGAAGG[C/T]CAGGACAGTTCCTTTACTGGCTTGAAAAAGAAAAA
388	1	1011	49.32	89809071	F1Dsnp	PHR	A	G	1	16,729,658	+	TAAACATCTACTTTAACTGTTACAGGGATTTTCCT[A/G]TGCCACTCAGGTGCCACATACCCTTTAGTTCCTCG
389	1	1011	49.32	89865036	F1Dsnp	PHR	A	G	1	16,734,310	+	TCCTCTACAATAACAACCTTGTCTCTTGATTTAGA[A/G]CCACATCCAATAGAAACCTGCCTTCTTTTTACACC
390	1	1011	49.32	89809072	F1Dsnp	PHR	A	C	1	16,734,810	+	CCTGGGATGGGATTTCAACTTTATTCTTAGAGAAA[A/C]TGACAAACCAACCCACATTGTTGCCGTTGTAAGTC
391	1	1011	49.32	89865038	F1Dsnp	PHR	T	C	1	16,750,828	+	AATCTGGTCATTGAGGGTCTTCCAAGCACCAGCTT[C/T]GAAGCAAAGCTCAAGAATGTCAGTGGCAGCCTTCT
392	1	1011	49.32	89865039	F1Dsnp	PHR	A	G	1	16,823,806	+	TTGTGACTCAGTTCCTTTGGATATGTGTTTGTACC[A/G]TCTTGTTGCTGTTGTGGAGCACTTTGGAAGAGCCG
393	1	1011	49.32	89865040	F1Dsnp	PHR	T	C	1	16,859,469	+	ACCAGGCATTTTCTTCACCCCTTGATCTGCCATTC[C/T]CTTCCTAACCATTTCAGCTTCCTTCCATTGCCCAC
394	1	1011	49.32	89865042	F1Dsnp	PHR	A	G	1	16,958,656	+	AGGAGAAGAACGGCTTTTAGTTTACGAGTACATGA[A/G]GTATGGGAGTTTAGATGATGTTTTACATGACCAGA
395	1	1011	49.32	89865043	F1Dsnp	PHR	A	G	1	16,959,215	+	GCCTGTTTGGATGATAGGCCGTGGCGCCGCCCTAC[A/G]ATGATTCAAGTCATGGCAATGTTCAAGGAGATCCA
396	1	1011	49.32	89809075	F1Dsnp	PHR	A	G	1	16,980,681	+	GAAGATGCATGGTGATCATCAGAACCAAGTGAAGA[A/G]GGTAAGGAACTCAAGGCTTTGACAGATTGTTGACA
397	1	1011	49.32	483_4019	GBS				1	16,990,499		CTCAAATAGCAGGTATTATTTCAGAAATAAGCTAATTCATGCGAAATATCACCACCAATACCAG
398	1	1011	49.32	89865045	F1Dsnp	PHR	A	G	1	17,032,709	+	TTTGACAAAAGGGTCTGCATTTCATGCAGTTGGCC[A/G]TGAAAGTGATATAATGGAGTCTCTCGCTCGAGCTC
399	1	1011	49.32	89809076	F1Dsnp	PHR	T	G	1	17,036,612	+	TGTCTCCAGTAAAAGTACCATCTGAAATTTTACTT[G/T]TGGATTCCGCACTGAAGCTTGCTGCTATGTCAACT
400	1	1011	49.32	89865047	F1Dsnp	PHR	T	C	1	17,044,547	+	AGAATAGAAGATGCTGAAATGAGGCGAACTTTCAA[C/T]ATGGGTATTGGGATGGTTCTTGTTGTGAGTAGAGA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
401	1	1011	49.32	TP6373	GBS				1	17,204,841	17,204,778	TGCAGGCAATAGGTGAAGAAATCTCTTTTGGAAGTAATGTAAGTAACTAATTTCTTAGCGTCAT
402	1	1011	49.32	89809077	F1Dsnp	PHR	T	C	1	17,260,352	+	CCCAGCAATTCAACCATACAAGCATAGTGATCCCT[C/T]GTCAACTCAATAATGTGATTATTCCTAATGGTAGA
403	1	1011	49.32	89809080	F1Dsnp	PHR	A	C	1	17,589,670	+	CTTCCCTTATTCTTCTGTATGAATACAAATAAGTA[A/C]CATAGAACAGGGCTGCAACCATGACAAATATTCCA
404	1	1011	49.32	TP1174	GBS				1	17,647,307	17,647,245	TGCAGACGAATCAGACAAGTCGGAAGCAATCAAAAACGACGGCGCCGCATCCTTATAACCATCC
405	1	1011	49.32	89865050	F1Dsnp	PHR	T	C	1	17,666,974	+	GTTTGGGCAAACATTTGCGAAGTGTGACGGATCTC[C/T]ACAAACAAAACACCTCCTACCAGAATTGGGATCAC
406	1	1011	49.32	89809082	F1Dsnp	PHR	T	C	1	17,831,364	+	AATGGAACCTTTGATGTGTATAAAGCCTCAAGAGA[C/T]GATACTCGGTGTGCGCAGTATTGCATGTGGAAAAT
407	1	1011	49.32	TP2187	GBS				1	17,874,773	17,874,710	TGCAGATCCCAGCAACTGCATCGATGATCATCTAAATTATGGACAGTATGTTGGGATGATTTCT
408	1	1011	49.32	822_9971	GBS				1	17,875,191		TTGGTAACGAATTGCTTTCACGAGCAATCCTTAGGGAAAGATGGGGTAGCAATTTCTGCCATGT
409	1	1011	49.32	89865052	F1Dsnp	PHR	A	G	1	17,895,741	+	AAAGATTGGGAATGTTTGCTGTTCCAGATGGAAAG[A/G]ATGAGAAGACCGAACTGGAAGTGTACAACTTTACA
410	1	1011	49.32	89779184	snp	PHR	A	G	1	17,909,404	+	ACCTCTTGGGAGATTTTGTTGATTATGACAAGACA[A/G]ATCAGAATACAAGAAAGCGAAGGTCATAATTTGTT
411	1	1011	49.32	89865053	F1Dsnp	PHR	A	G	1	18,035,784	+	ATTCTGAGTAAAGTCTATAGCATATTCCAGGTCCC[A/G]TTCTTCCAGCACGCCCAGTTCTTTGATTCGCAGAA
412	1	1011	49.32	89865055	F1Dsnp	PHR	T	C	1	18,101,696	+	GTGTACCATGATATTGCTTCCAGACTCGACATCCG[C/T]GCCATTGAAATTCCTAGCCAAGGGAATGACATGCT
413	1	1011	49.32	89809083	F1Dsnp	PHR	T	C	1	18,102,003	+	TCAACTTCGGTTTGAAATTTAAATCGCTTCCAGCT[C/T]CCGAAAAAATCAATTATGCGGTCAAAGAAATTGCT
414	1	1011	49.32	89779211	snp	PHR	A	G	1	18,103,288	+	GGATAGCCAAAACTTTCTCAAGTTGTTTTCTAACT[A/G]TACAGCGCCACAAGAATTCTGCAAAGGCAACCATT
415	1	1011	49.32	89865056	F1Dsnp	PHR	T	C	1	18,178,798	+	TTTCCTTTTAACTTTTAACAGGAGTTCAGGGGATA[C/T]GTCTTCAAAATCATGGGAGGCTGTGACAAGCAAGG
416	1	1011	49.32	89809084	F1Dsnp	PHR	A	G	1	18,179,254	+	GCATCCAAGATCCGCAAGCTATTTAACCTCACCAA[A/G]GATGATGATGTGAGGAAGTACGTCAACACATACCG
417	1	1011	49.32	89809085	F1Dsnp	PHR	T	C	1	18,180,773	+	GGTCTCCGGTCACGTTTTGGTCCACATTCAAAGGA[C/T]AGAGCTTGTCTAGCTTTTCTCTAAACTTGGGTTCA
418	1	1011	49.32	89809086	F1Dsnp	PHR	T	C	1	18,194,185	+	TGGAGCTTTCTTCATTGCAGTCCTCCACAAGCATT[C/T]CCCTTTGCCAGGTGACATCTATCATCCAAGTCATT
419	1	1011	49.32	89809087	F1Dsnp	PHR	T	C	1	18,307,020	+	TTACAACATCAAAGTCCTTGTTAATAGTTCTAAGG[C/T]AGTGATCTGAAGGGTTTCTCAGAGTTGGACATGGG
420	1	1011	49.32	89865057	F1Dsnp	PHR	A	G	1	18,318,033	+	ACATTCAGCCCTGAGAAGTTCTTGACAAACTTTTC[A/G]TCAATTTTTACACTGTAGCACCCTACCACATTTAG
421	1	1011	49.32	89865058	F1Dsnp	PHR	T	C	1	18,318,080	+	ACTGTAGCACCCTACCACATTTAGCAAATGGAGCT[C/T]AGGGCAGCTCAATAGTATCTGAAGCACAGGTTCTG
422	1	1011	49.32	89809088	F1Dsnp	PHR	A	C	1	18,318,133	+	TCTGAAGCACAGGTTCTGTACTAATACGCATAAAG[A/C]GTAGCTCAAGATGCTTGAGTTTTGGCATTGTGGCT
423	1	1011	49.32	89809089	F1Dsnp	PHR	A	G	1	18,319,505	+	ATACTGCATTGATATTGTTGTACTTACTGGTCCGC[A/G]ATAAATGAAAAACTCTGATCATTGAGAGCCCCAGA
424	1	1011	49.32	89809090	F1Dsnp	PHR	A	G	1	18,319,790	+	GCATCAGGTATAAGCTCCTCCCAATTCCTAAACTC[A/G]TAGTCCACCTCCATTCAATTCCCTTCTAGCAACAA
425	1	1011	49.32	89865059	F1Dsnp	PHR	A	G	1	18,398,913	+	CTTGAAAAATGTCAGGCTCAAAGACATTCCTTACC[A/G]TCCTAACAAAATAATGTTCGATTTCATGGGATCAG
426	1	1011	49.32	89809091	F1Dsnp	PHR	A	G	1	18,483,273	+	AATCACTGGTTATTTTTTGATGACGAAAATGTGGA[A/G]ATGATTGATGAGTCTGCTGTGCAAACTTTCTTTGG
427	1	1011	49.32	89865062	F1Dsnp	PHR	A	G	1	18,798,740	+	GACCATTGTTTTTTTTTTTGGAAAGTAGGAGGACC[A/G]TTGTTAGGCCAGATATGAGAGTACTGACACACCAT
428	1	1011	49.32	TP163	GBS				1	18,927,594	18,927,613	TGCAGAAACGGTAGTGACTGCCGATTATGGAGGCTCATTAGGCTGGGATGACAGTAATCCATCA
429	1	1011	49.32	89809105	F1Dsnp	PHR	A	C	1	19,826,044	+	GTATTGAGTGACTTGTCCAAGCTCTTTGTCATGGT[A/C]TATAGTGATTCCAATGATATTACTGGCAATACACT
430	1	1011	49.32	89809112	F1Dsnp	PHR	A	G	1	20,082,332	+	CTATGGAGAAGCAGGATCACTTGATGAAGATGGAG[A/G]GCAATACTAGATCCTCATCATTTCACGAAACTACA
431	1	1011	49.32	89865083	F1Dsnp	PHR	T	C	1	20,383,331	+	TCAGAACTAACACGCACTGATATCCTAAAGTGTAT[C/T]CAGTCTGAGAAAGTCAGATTTCGTGGCGTTAATCT
432	1	1011	49.32	89865084	F1Dsnp	PHR	A	G	1	20,578,889	+	CCAGAGACCAGATTCCTTTTTACAACCCAAAGATG[A/G]TCCAAGTCGAGGTATTGGCAAGGAAGTTCGAGCCT
433	1	1011	49.32	89809116	F1Dsnp	PHR	A	G	1	20,703,990	+	ATTCCACTAAGCGGGCCTCATTCCATTCTTGGGAG[A/G]GCGGTTGTTGTGCATGCTGATCCTGATGATCTTGG
434	1	1011	49.32	89809117	F1Dsnp	PHR	T	C	1	20,908,548	+	AGGGGTTTTCTGATGCTAGAATCTTGAATTTCTGA[C/T]TCTATTTTAGGAACGACATCTTGAAAAACGTGCAA
435	1	1011	49.32	152_299703	GBS				3	26,021,299		GCTTCCAGGCGGCGCAACGGCAAGCGGGACTRCTCCAAAAATGGAGAGGACAGCTGTGGGAGTC
436	1	1011	49.32	TP7308	GBS				3	28,134,485	28,134,545	TGCAGGTCCCGTGGAAGTTGACCTACGAAACTGGGCAGATCCTGATTTCACATTTGATGTGTCT
437	1	1011	49.32	TP395	GBS				4	7,798,292	7,798,236	TGCAGAACCAAAACTCCAGCATTTGATTTCTTCCCAGAGACAGAGGCCTCGTCGCTCGTCGCAC
438	1	1011	49.32	89810039	F1Dsnp	PHR	T	C	4	25,834,837	+	CCCGCATTTAATACCATTGAAAATAAAACATCTTT[C/T]CCTAGAATCATAACGTTCTAAGAGAGCCGATAGAA
439	1	1011	49.32	TP5138	GBS				6	34,722,496	34,722,559	TGCAGCTCGCGCGACTGGTCCAAGGCCATCCGAGTCCTCGACTCGCTCCTCTCCAACTCCTCTT
440	1	1011	49.32	89866612	F1Dsnp	PHR	T	G	6	34,729,049	+	ATTATGTCTCCCAGCATCGTATGGCAGGATTGGCT[G/T]CTATTGAAGTTGCACAGAAGGTCTCCAAGGCGTGG
441	1	1011	49.32	89810642	F1Dsnp	PHR	A	C	6	34,749,591	+	TCTATTCATATCCAGAAACTCGACATGGTTGGAAG[A/C]TTTTTGCGACTACACACCCTTAATCTCGACTTTTG
442	1	1011	49.32	89810643	F1Dsnp	PHR	A	G	6	34,753,668	+	CAGCAAAGATTATATTTCAGCAATTATCCTCTACC[A/G]GCATTTCTATGGTTTCTGAAGTAACTAAGTAGCGT
443	1	1011	49.32	89866613	F1Dsnp	PHR	A	G	6	34,763,485	+	GTGCTAACTTCTAATTCCTGAGCTATGAATTCACC[A/G]AGTTCTGTAATGTGGGGCTCCAGATCTGAGTAGCT
444	1	1011	49.32	89866614	F1Dsnp	PHR	A	G	6	34,767,753	+	CAACTTAAATCTACCTGTGCATCTCCATTGCTGTC[A/G]CCTTGTGAATTTCTCCTCAGTTCTTTCAAATATGT
445	1	1011	49.32	89810646	F1Dsnp	PHR	A	G	6	34,879,956	+	CATATATTTGATGTGGACTGTGCAACCCAAACACT[A/G]GCTGAAATATCCGAGGAGATCAATTGTTTCGATGA
446	1	1011	49.32	89810647	F1Dsnp	PHR	A	G	6	34,975,356	+	GTTCTGCTTCATAAATTGTGGACAATCAGAAGAGG[A/G]TAATGTTCAGGCAAGCCATGTTCCAGTTCCAGAAG
447	1	1011	49.32	89810649	F1Dsnp	PHR	A	C	6	35,026,616	+	TCTTTGCAGCTATTGAATTTGAGTAAAAACAAGTT[A/C]GAGAGTATACCAAATGAAATCGGCCAGCTATCCTC
448	1	1011	49.32	89866615	F1Dsnp	PHR	A	C	6	35,096,980	+	CTGTCATCAATGTAATTTGCACTCTTTCCCACATA[A/C]GGCAACGAATTAAAGGTGTGCCAACCAACCAACTT
449	1	1011	49.32	89810650	F1Dsnp	PHR	A	C	6	35,331,271	+	GCGGCTGGTAATTATATCAAGGGAGCGTCCTATTT[A/C]GGCTACGCCTCCGGCACAGCTAAAGGCATGGCTCC
450	1	1011	49.32	TP4439	GBS				6	35,363,809	35,363,872	TGCAGCGAGTAATCCTAGAGCAGCCTCTGCTGTAAGGATGAACTGGGCCTCTAGCTTTGAAGCA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
451	1	1011	49.32	89808459	ins	PHR	-	TCA	6	35,364,014	+	TACGACCGTAACCATTCTCTACATCCATCTCGTCC[-/TCA]TCATCGTCCTCGCCATCCTCCTCATTGAATTGTTG
452	1	1011	49.32	89810651	F1Dsnp	PHR	T	G	6	35,380,095	+	TTTCAGCGCAGATGGCTCATATTTCTGTCAATTGT[G/T]GTGCAAAAGCTGCTGCAGTTTGTATCGAAGCCAAT
453	1	1011	49.32	TP5669	GBS				6	35,380,186	35,380,246	TGCAGCTTGCATGGACTGCTCCTAAATCTTTCGCAAGGTATTTAATTTCTATTGCTTCCTAGCT
454	1	1011	49.32	89810652	F1Dsnp	PHR	A	G	6	35,386,207	+	GTTTGGTGAGTTCATGGAGGAAAAGTTGCAAGAAC[A/G]TAATGTTCGATATTATAGATTTGTTTATGGTAATG
455	1	1011	49.32	89810653	F1Dsnp	PHR	T	C	6	35,399,999	+	TCAAATAGTAGAACCTCTAGTTTTCGCATTGCTGC[C/T]TCAGCTTTTGCTTTCTGCAAGTTCTCCCATGCATT
456	1	1011	49.32	37_608547	GBS				6	35,453,073		TATTTTTGTGCTCTACTAAAAGAGTGTTCATYGATCCAGCAGTAAACATGACCGGTAATATTGG
457	1	1011	49.32	TP3261	GBS				6	35,455,395	35,455,457	TGCAGCAGAGTAAAGACAGTCCAATGAAGCTTTGCAATTATAAAAGGTCGAGTGCTCCGACCGA
458	1	1011	49.32	89810654	F1Dsnp	PHR	A	C	6	35,488,070	+	AACAACTTCTCAAGCTTCGTTCGCCAGCTTAACAC[A/C]TATGTAAGTAAACTAGCTAGCTAAGCCAACTTACT
459	1	1011	49.32	89866616	F1Dsnp	PHR	A	G	6	35,594,792	+	TGGGGATTTTCAGGGATATGATGGATACCAGCATG[A/G]TCTACCCTGATTTGGATTCTCTTTCTATTGCAATT
460	1	1011	49.32	89810655	F1Dsnp	PHR	T	C	6	35,596,705	+	AAACGAAAACGTCTAAGGCCTGGAAAAGTTTCACC[C/T]CGTCGCCCTGTTCCAGATCATATACCAAGGCCTCC
461	1	1011	49.32	89810656	F1Dsnp	PHR	T	C	6	35,599,779	+	TTCTTATTTCTTGCAGGAAACAATGATAGTGGACG[C/T]ATGGTGTTAAATCAGACCTTCACAATAGGTAATGC
462	1	1011	49.32	89866619	F1Dsnp	PHR	A	G	6	35,675,722	+	GACAGCAGGAGTTCAAGCATCTGTTTTGAATAAGC[A/G]TAATTCTGCACTTCCATATTCCTCTTGATAGCAGT
463	1	1011	49.32	89866620	F1Dsnp	PHR	A	G	6	35,738,857	+	CATAAGCTCGTTTCAAGTCAGATGAGTATACAAGT[A/G]AGATTTTAGGATCCTTGGATAATCTATTGGCCACC
464	1	1011	49.32	TP765	GBS				6	35,831,048	35,831,111	TGCAGAATATAAAGGGAAAATCATAACATAGGAAGGGAAAATCATAACAGAATGTCATGTCACT
465	1	1011	49.32	89866622	F1Dsnp	PHR	T	C	6	35,831,748	+	GTACTTTCAGACAGACGATTAAATAAGCTTCCATT[C/T]GGCATGAACTCATAAACTAAGAGCAATTCCTTTTT
466	1	1011	49.32	89810658	F1Dsnp	PHR	T	G	6	35,832,300	+	TCTGTAGCATTGGCCAACTCGGAGAATTGGTAGAC[G/T]ATCAAGTTGGATGCCTCCAAAACTCGACTTGTTCC
467	1	1011	49.32	89810661	F1Dsnp	PHR	T	C	6	35,913,282	+	CTTCGCGCCCACCATCATTTCTGTTAAAATATACT[C/T]TATTTCTTCATCTGGGAGTCCCAATTCTAGATTAT
468	1	1011	49.32	89866666	F1Dsnp	PHR	A	G	6	37,665,707	+	TGGGAAGGAAGTCTTGATTAAAACGGTGTTACAAA[A/G]TATCCCAAACTATGTGATGAGCTGCTTTGAGTTAC
469	1	1011	49.32	162_132285	GBS				7	606,053		TTTGTGACCACACACCAAATTCTATGGATGTMGAGAAAAGTTTGATCCCAGGTCCCAGTTAGTC
470	1	1011	49.32	TP6132	GBS				7	665,018	665,081	TGCAGGAGCATGTCTGGACTACGTATGAAACTTAGTACTTTGCGCCAGTAACAAGTTTTTCATA
471	1	1011	49.32	89872141	codon	PHR	A	G	7	3,735,094	+	TCTCGAACTCGTCCCGAAATTTGCCGGGACGAGTT[A/G]GGATTTCAATCTCAAAACGTGAGGCCCGTCCCGTT
472	2	2013	0.00	TP506	GBS				3	29,749,323	29,749,304	TGCAGAAGAAATAAGTAAGGAATACATACTCAACTTCTTACTTGACCAAAGGAAATGTTCACTT
473	2	2013	0.00	103_234224	GBS				4	21,220,469		TGGTTTGGTTGTTGTTGGTGAGGGGTTTGGCRGTGGAGAAAACGCAGGTCGTGTGCTCCTACTG
474	2	2013	0.00	TP1139	GBS				7	14,486,208	14,486,164	TGCAGACCGATCGTAGCTCCTATTCAAGGCTTTAGCAAGAGCAAAACCTGCCTCTCTCTTTTTT
475	2	2008	2.49	101_228760	GBS				2	2,720,511		CCTATGGCGTCGACCCTAGCCTTGCCATGCARCTCCCTGCTAAGTGCAACCTTGCCCGGTCCGT
476	2	2008	2.49	89865418	F1Dsnp	PHR	A	G	2	2,727,011	+	GAACAAATTTTCCTCACCTTCAGATGACCTCTTTC[A/G]TGGAAAACCCACTTGCTAAGTTCAGTCACAAACTG
477	2	2008	2.49	89809446	F1Dsnp	PHR	T	C	2	2,752,315	+	TGATATTTGTGATTGCGACTTCTATATTTCCACCA[C/T]TCGCCACGTTTGTACTTAAAGCAAGAAGAGACTCA
478	2	2008	2.49	89809447	F1Dsnp	PHR	T	C	2	2,792,997	+	CATCAAGGCCCAGTAGTGGTCTCTGTAGCATTTCG[C/T]CAATTGCTTCAGGTTCTGCGAGCGGCGGCGGAGGA
479	2	2008	2.49	89865419	F1Dsnp	PHR	A	G	2	2,819,495	+	TGCTCTAGTGAGAGGCTAAGCTGTGGGTTTTGTGA[A/G]GGTGTTGTAGTCGATGCTTGGGTTTCTTGTGATGA
480	2	2008	2.49	TP7533	GBS				2	2,835,319	2,835,259	TGCAGGTTAATTACATACATAATGCATCCTGAGAGATAATCAGGGAAAATCTCTTGTTCCTTAA
481	2	2008	2.49	TP3228	GBS				2	3,372,312	3,372,278	TGCAGCAGAATCTGAACGGCCGAATCGTCGAGCCGAGATCGGAAGAGCGTTCAGCAGGAATGCC
482	2	2008	2.49	89865425	F1Dsnp	PHR	A	G	2	4,064,546	+	CGCGCCAAGACTGTTATCGAAAACTCCGAGGCTGT[A/G]CCCTGTATCAGGTAATCCAATCCTCTACTTTTCTT
483	2	2008	2.49	89809453	F1Dsnp	PHR	T	C	2	4,065,249	+	AGGAATTTGGCCTTAGTACTGAGGATGTTGGCAAA[C/T]TGATAGCATTTAGGCCCCAGCTGATGGGTTGTGGA
484	2	2008	2.49	89865426	F1Dsnp	PHR	T	C	2	4,066,744	+	AAGGTTATAGCTTTAGGGCCAGAGCTCTTGGGATG[C/T]AACATTGTGCACAAGCTTGAGGTTAACGTAAAATA
485	2	2008	2.49	89809454	F1Dsnp	PHR	T	C	2	4,113,139	+	AAGTCAGCAATCCAAGCAGTTATAAAGCTTCCTTC[C/T]GGCGAGCTTGTCACTGGTATGGTTTTATATAACTT
486	2	2008	2.49	TP2558	GBS				2	4,122,791	4,122,836	TGCAGATTGCCGAGGAGGAAAATCTAGAAATTGATGCAAAATTCCGAGATCGGAAGAGCGGTTC
487	2	2008	2.49	TP1383	GBS				2	4,122,794	4,122,731	TGCAGAGAACCATATATTATTATTGTCATGACTCACCAAACACTAATTTCGAGATCTCCAAACA
488	2	2008	2.49	89865427	F1Dsnp	PHR	T	C	2	4,125,584	+	TTTTGCATAAAACCTCTGGTCACTCCACAACAACA[C/T]CCTATTCAAAGGAATGCTCACATTCCTCTCCTTCA
489	2	2008	2.49	89865428	F1Dsnp	PHR	T	C	2	4,167,758	+	CCGTCATAACACTCTGCGGCCACCTCTACTGTTGG[C/T]CTTGTTTGCTCAAATGGCTGTTCAATACGCATTAT
490	2	2008	2.49	89809456	F1Dsnp	PHR	A	G	2	4,174,110	+	CATGGCATCTGTGTACTTCATCTTGACGAGGCTCA[A/G]CAGGATCATTGTTATCGGCCGAGTTGTTTGTGTTG
491	2	2008	2.49	89865429	F1Dsnp	PHR	T	G	2	4,174,432	+	CTTGCATATAAATTCACAGTCAATGTCGTCTTTGT[G/T]GTTGTAACCATAACGATCACCAGTAGACCATCTTT
492	2	2008	2.49	89809458	F1Dsnp	PHR	T	C	2	4,196,385	+	TCATTGGTAATCCAAATCCTCTCATCAGGAAATTG[C/T]TTTCTGGCCTCGTAAGCAATCTGCACGGCGCGCTC
493	2	2008	2.49	89809459	F1Dsnp	PHR	T	C	2	4,196,731	+	GGTGAGATTCTTCCGGAACACCTTGGCGTCGAAAT[C/T]GGACTCCACGGCGGCCGAGGAGGAGGAGTCGCCGG
494	2	2008	2.49	89809460	F1Dsnp	PHR	T	C	2	4,202,099	+	ACTCACTAAATCGCTTCTACTTTGATGTCACTCCC[C/T]TTGATACACAACTCAATGATGAACTTCACAAAGAA
495	2	2008	2.49	89809461	F1Dsnp	PHR	A	G	2	4,246,798	+	CCAGAAAAAATCCTTTGGATGCCTCAGATTCGGTA[A/G]AAGTTTCCTCCACACCGGTAGAAGCTGTATCACAA
496	2	2008	2.49	89809462	F1Dsnp	PHR	A	G	2	4,282,440	+	AATGTTTTATTTGCTGGCTACAAGCTCCCTCACCC[A/G]CTTCAGTACAAGATCATTGTCAGGGTTAGTTATCC
497	2	2008	2.49	89809463	F1Dsnp	PHR	A	G	2	4,289,418	+	ACCTTATAAAGGACATTACAGTGTTAGAACTAGAA[A/G]TAGTCCTATTGGAGCGCTATCTTCTATCCTTGTAC
498	2	2008	2.49	89865432	F1Dsnp	PHR	T	G	2	4,290,184	+	GAAAAGTGGAGTTCCCGGCGTACGAAAATTCCTTT[G/T]TTCAATTCACAGTTTGACAAGCCTAGCCACATTGA
499	2	2008	2.49	89865433	F1Dsnp	PHR	T	G	2	4,299,773	+	GAAGACAACTCGGAAGAGGTCACGGCACGGCTTTC[G/T]AAGAGGTTTGTTTCTCAACAATCCATCTTTCTGAA
500	2	2008	2.49	89865434	F1Dsnp	CRBT	A	C	2	4,301,603	+	GGCTTACAAGCAACTTGAAGAACTCTGGGAGGATG[A/C]TAAAAGCTTGGGATTTGATTTGTCTTGGTTAGCTC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
501	2	2008	2.49	89809464	F1Dsnp	PHR	A	G	2	4,317,995	+	AAGTCAGATAAGAAGAGTTCACTAGACTCTGCAGC[A/G]CTTGCCATGCTTCTTGATCTCAGAAGGCAGGGTAA
502	2	2008	2.49	560_51187	GBS				2	4,434,414		AGAAACACAATGCCTAAAGATAACTTCACAAAAAACCATACAATCAAGCTAAGGTATCCATCAT
503	2	2008	2.49	TP702	GBS				2	4,434,433	4,434,370	TGCAGAAGTCACAAACAAGAAACACAATGCCTAAAGATAACTTCACAAAAAACCATACAATCAA
504	2	2008	2.49	89865435	F1Dsnp	PHR	A	G	2	4,661,648	+	ATTTTTCATCCCTCCTAATCTTCCTCTTCTCCTCC[A/G]AAGGCTGAGCAAAGAACTTCCTCGCCGTAGTCTCA
505	2	2008	2.49	89809467	F1Dsnp	PHR	A	G	2	4,681,065	+	CTCGAACATGAGTTTAAGCCTCCTGAAGACCTTGG[A/G]CACAATTCCACATAACCTGTTAGAGTTAAGGTGGA
506	2	2008	2.49	89865436	F1Dsnp	PHR	T	G	2	4,764,295	+	GATCCTCCACCAACTTCCAAGGATATTCCATCTAG[G/T]AGGTCTCAAGGTCGAAAGAGGGCATTCCAGAAATA
507	2	2008	2.49	89809468	F1Dsnp	PHR	A	C	2	4,782,656	+	GCCGTAAAGAAAAAGGTTGGGAGCCCACTGGTAAT[A/C]TGTATAGGAAGGTTAGCACTATCAACTATCAACCT
508	2	2008	2.49	89865437	F1Dsnp	PHR	A	G	2	4,785,274	+	ATTGGTTGTTTTTGTAGGTTGAGAGATGTGGCTCC[A/G]GTGAGTTATGTGGAAACTACTCCCAAAAAGGAGAG
509	2	2008	2.49	89809469	F1Dsnp	PHR	T	G	2	4,807,592	+	AGAATTGGCAAAAGTTGCAGCTGAAGCATTAATGA[G/T]ACTTGAACCTGAAAGCTCAGCTCCATATGTATTGT
510	2	2008	2.49	685_21611	GBS				2	4,852,500		TTTTTTGTAACCTCTTTCTTTTTTCTTTTTTKGTTCAATGAATTGTCTTGTATCACAAGTTGGT
511	2	2008	2.49	685_21690	GBS				2	4,852,561		AAAATGTTTAGATGCTATGATAGGATTTTCTGTTGAGAACACATTGTCTTTTATCGCTGCAGAA
512	2	2008	2.49	685_21706	GBS				2	4,852,577		ATGATAGGATTTTCTGTTGAGAACACATTGTCTTTTATCGCTGCAGAAAACTGAACTATGGAAA
513	2	2008	2.49	89809471	F1Dsnp	PHR	T	C	2	4,874,000	+	TAATTTCACGAAGAGACTGGCCTCATGAGGTGAAG[C/T]GTAAAGTTCTTATGGATCTTATGAAGGAGACTCCT
514	2	2008	2.49	89865438	F1Dsnp	PHR	A	C	2	4,879,119	+	TGTCTTCTGCAACCAATGAACTTAGTATTGCATCA[A/C]TGAAAGCAAAGTCAGCTTCAGGTCATGCCTTTTCT
515	2	2008	2.49	89809472	F1Dsnp	PHR	T	G	2	4,884,712	+	CACTGATGTTGGGGTTAGCCAAGCAAGAGGAATGA[G/T]CTCCTCAACGTTGTTGGCTCCAGTGTTCGGCCGAG
516	2	2008	2.49	89865440	F1Dsnp	PHR	T	G	2	4,889,642	+	CACATCTTAGAATCTCTCTAGCATATCTGAGAGCT[G/T]CATCTACAGTATCAGGCTCTAATGCAGTGACTAGG
517	2	2008	2.49	TP3415	GBS				2	6,870,205	6,870,142	TGCAGCAGCTGACTACCAGCATGCACCTCCCTGTAGAACTCACTCCTCAACACGCACAATTCTT
518	2	2008	2.49	89809488	F1Dsnp	PHR	A	G	2	7,439,644	+	CTACTGTCCTTCTGAAATGAGTAGCTTCCAGGCGA[A/G]TCCAGTGTACCGCTCAAAAGGACTAATGGCATCAG
519	2	2008	2.49	399_146964	GBS				2	7,471,255		TTGGATGCATATATTGTAGCTCACTAATATGTACAAAATATGTACAGGTTTATGTACATTCGTC
520	2	2008	2.49	399_146961	GBS				2	7,471,255		TGATTGGATGCATATATTGTAGCTCACTAATATGTACAAAATATGTACAGGTTTATGTACATTC
521	2	2008	2.49	399_146946	GBS				2	7,471,311		ATACACGCTAGTCTATGATTGGATGCATATATTGTAGCTCACTAATATGTACAAAATATGTACA
522	2	2008	2.49	89809489	F1Dsnp	PHR	T	C	2	7,749,650	+	CCTCAGTTTGTTAGGAAAACTGGTTGTGGGCATTA[C/T]TGTAGAAGCAGCATTAGGGGCAGGCTTGTCTTGCC
523	2	2008	2.49	89812904	codon	PHR	T	G	2	8,257,347	+	TAAGAGCCTTGCAATGCGTTGATTCATTTCGACGC[G/T]GGACGACATTATCTCTTTCTTGCTTCAGACAAGGG
524	2	2008	2.49	89865454	F1Dsnp	PHR	T	C	2	8,264,673	+	GAGTTGTCAAAGCTTGACAAGCTTTACTGGCTTTA[C/T]CTCTCAAACTGTAGCATCACAGGTGAAATCCCAAA
525	2	2008	2.49	89809491	F1Dsnp	PHR	A	G	2	8,267,077	+	CCTCGATGAGAATGGTGGTTCAAATGCTGGAAGAG[A/G]CACAACCTTGTCAGCTCACCAGCATAAGCATCACC
526	2	2008	2.49	525_61485	GBS				2	8,569,153		ATAGGTGTTGGAGGTTAACTTACGAAATGTCRAGGGGAAAAATGGAAGGTGCCATCCGCATAGC
527	2	2008	2.49	TP2879	GBS				2	8,598,486	8,598,549	TGCAGCAAGAGCCTTGTTGAGCTCGAGCACAAAGTCCCTGTAGTACCTGACGTACTTGCGGAGA
528	2	2008	2.49	89809495	F1Dsnp	PHR	A	G	2	9,322,916	+	GATTGAATCCATGAAGACACCTTTTGGGTTCGGGG[A/G]TGCAACTAGGGTTTCAAAAAATCCTAACCCTAATT
529	2	2008	2.49	TP4412	GBS				3	6,267,406	6,267,439	TGCAGCGACGGAGCTCGAAGGCGTCGTCCGTCATCCGACCATCTCCCGAGATCGGAAGAGCGGT
530	2	2008	2.49	89865535	F1Dsnp	PHR	T	C	3	20,912,160	+	TGGTTCGTCGGAGCCAAAATCACAGATTTCGTGGC[C/T]GACTTCTGCCCGAGTATCGCAAACGAATTGTGGGT
531	2	2008	2.49	TP8316	GBS				3	20,917,966	20,917,903	TGCAGTCCAATAAAAGCAACGAAACCCAGAAGACATCCGAGTCTGTAAACCACCATGGTGGAGA
532	2	2008	2.49	89809567	F1Dsnp	PHR	A	G	3	20,931,250	+	TCGGAAGGAACTCGAGTAAGAGGCATGCAACCTCC[A/G]GAAAGTTCAAGCAACTTCTCAAGCTGTCCCCTAAG
533	2	2008	2.49	89865539	F1Dsnp	PHR	T	C	3	20,964,971	+	AACCACCCATTCCAATCCCTGCACCCGGAAACCCA[C/T]CACCTTGAGAGAAAGCAGTATTCCTAGAAGGTTCC
534	2	2008	2.49	89809570	F1Dsnp	PHR	A	G	3	21,079,536	+	ATTGGATGATACTTACAGAGAGAAGCTCAAGCAGA[A/G]CTACCACATGGTAGACAAGGGTTACAATTGTTTTC
535	2	2008	2.49	89865541	F1Dsnp	PHR	A	G	3	21,134,981	+	GCTATTATACTGATGGGGAAGAATCTCCGCAGATG[A/G]TGCTATCCAAGACAAGGAGGGATCCAACCAATAAT
536	2	2008	2.49	89809571	F1Dsnp	PHR	A	G	3	21,135,623	+	AAGCCCAAACTAGAAATGGTGAGATGCTTCAGTCT[A/G]TAACACTCCCACACAGTCAAAGCACCATGGTGGGA
537	2	2008	2.49	89809572	F1Dsnp	PHR	T	G	3	21,149,073	+	AGGCGAATTAGCAATGTTCTGAACCATTCCTCTAC[G/T]CTCACGCATATCCCACTGGCAAAGCCTGTTATCAT
538	2	2008	2.49	44_51080	GBS				3	21,231,493		GGAACATTGTTGCCCTTGAAGGACAATGGTGYCAACCAGGGAGGGAAGACTACTCTAAGAGATG
539	2	2008	2.49	89865544	F1Dsnp	PHR	A	G	3	21,578,487	+	TGATTGCTGCAGGCAGAGATACTTGCAAAATACAA[A/G]CCTACAATCAATACAACTTTGCTCTTAGCCGACCT
540	2	2008	2.49	TP4167	GBS				3	26,309,117	26,309,075	TGCAGCCGTACAGAAACTCCATGACAGCTCCCGCGCTAGTTTGTATTTGTTGGTGAGCCAACCT
541	2	2008	2.49	89866267	F1Dsnp	PHR	A	G	5	3,658,198	+	GAAGTAGGACTCTGTGTAAGTGGATATTCGCCGCC[A/G]CCAATGCTAGCACGGAGACATTCCATTAGTGATCC
542	2	2008	2.49	89810302	F1Dsnp	PHR	T	C	5	3,661,750	+	GTCAAGTCCCTCACAAATGTTGAAGCTTTTGTTCT[C/T]ATAGCCAATGACTTGAAGAATGTCATCTCTAAATT
543	2	2008	2.49	89866702	F1Dsnp	PHR	T	C	6	38,743,637	+	AATTCCGTGCAGAGAAATGGACACTACACCGTCGG[C/T]GATTTCATGACCACGAAAGAGTCCTTACACGTCGT
544	2	2008	2.49	89810728	F1Dsnp	PHR	T	G	6	38,794,983	+	ATATCATTGGTCTACAGATGTTGCAGCCAAGTTTG[G/T]GATCCCGAGGATCATCTTTCAAGGAGTTGGTTTCT
545	2	2008	2.49	TP5133	GBS				6	38,970,132	38,970,171	TGCAGCTCGAGGATTAAGGCTTAAAATCCAGAAAATCCGAGATCGGAAGAGCGGTTCAGCAGGA
546	2	2008	2.49	89866706	F1Dsnp	PHR	T	C	6	39,029,189	+	AGCAACCCTTTGATCTCTCCCCCGTTCTTCACGCT[C/T]TCACGCGCCCTCTTCACCATATTCTCATACAGATG
547	2	2008	2.49	89811023	F1Dsnp	PHR	T	C	7	8,055,935	+	AGGCTCAACTATTGAACCTCTCACAATTTCAGACA[C/T]GGTTTCCCTAATTACATTCTTAGCCATACGGTTGG
548	2	2008	2.49	TP8567	GBS				NGH			TGCAGTCTTCATATGATTTGAGAATTGAACAAAGACTCAACTTAACACCACCAACAGTAAACGA
549	2	2001	4.98	89865416	F1Dsnp	PHR	T	C	2	256,606	+	CTTACACTTCTTGATACCTTGGCACTCCATTGGAA[C/T]ATGTCAGCTTGACCATTGTTCTTGGAATATTGATC
550	2	2001	4.98	89865417	F1Dsnp	PHR	A	G	2	269,599	+	GTAGAAGCAGAGCGTGGAAAGAGACGGGGAGTTCA[A/G]TCATTGGGACTAAAACAAAATAGGAATGGATTTGG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
551	2	2001	4.98	89809448	F1Dsnp	PHR	A	C	2	283,249	+	AACAACTTATAGACATGGTGTACAAGCAGTTAGAT[A/C]AAAGCTCTGTATCCAATACAATTGTGCCCAGGTGC
552	2	2001	4.98	179_281458	GBS				2	334,757		TATCTCATTGGTTTTGCCAACGGTGTGTGTGACAAGGTCGCAAACGGGCCGGGTTTGGGATAGC
553	2	2001	4.98	89879858	snp	PHR	T	C	2	431,345	+	ACCATTGATGAGCTTCAACAAGCTTGCAAAGACTT[C/T]GGTCTAGGTGATGTTCATCTTGATGATATGATCAA
554	2	2001	4.98	89809470	F1Dsnp	PHR	A	C	2	482,000	+	CTTGCATGGATTTAGGGTCCCTACTCCCTAGAGTC[A/C]GCAGTAGCAGACCTGCCTGAAGTATCCTCAACACT
555	2	2001	4.98	89803764	del	PHR	-	CGTC	2	483,166	+	CTTTGCCATCGTAAGGAGCGAGAGGGAACATAGAG[-/CGTC]CATAAAACCACAGTCAGCCTCCCTTGAGAAAGTCA
556	2	2001	4.98	89865441	F1Dsnp	PHR	T	C	2	492,329	+	ATGACTGCTCGAAGTTTTGACAGAGATCTAGTTTT[C/T]CCTTCCAACCTTTGGGTGAATCAAGTAGTCGAGTT
557	2	2001	4.98	89812845	codon	PHR	T	G	2	492,332	+	ACTGCTCGAAGTTTTGACAGAGATCTAGTTTTTCC[G/T]TCCAACCTTTGGGTGAATCAAGTAGTCGAGTTTGA
558	2	2001	4.98	89865442	F1Dsnp	PHR	A	G	2	503,651	+	ATTTATAATATGGTTCTTCTTCTTATGCCAGAGTC[A/G]AGTTCAAGCTGGAAGCATAAATCTCAATGGAAGTC
559	2	2001	4.98	89809473	F1Dsnp	PHR	T	C	2	503,679	+	CAGAGTCAAGTTCAAGCTGGAAGCATAAATCTCAA[C/T]GGAAGTCTTACGATTGTAGTGCAGAGACCAGGTGG
560	2	2001	4.98	89809474	F1Dsnp	PHR	A	G	2	508,546	+	TTTATGTTCAAGTGATTCCAGGTAGGAACTTCCTT[A/G]GGAGCTAAAAGAAGACTGCTTTTGCGTGGTGGAAA
561	2	2001	4.98	TP6463	GBS				2	510,727	510,787	TGCAGGCATGGAGTCAACAAGAATCCATTTGAAGAAGTTGAAGCCCATAAAAGTCAATCTGCTG
562	2	2001	4.98	89865451	F1Dsnp	PHR	T	C	2	736,836	+	AGTTTTGGGGCAAAGAAAGCGAAACCAAGTCGTCG[C/T]TGGAAGTTGAAGCTTTGAGGTTAAATTTTCCGGGA
563	2	2001	4.98	89865452	F1Dsnp	PHR	T	G	2	746,622	+	ATGGCAACAATGATCAAGAATCCAACTAAGCAACC[G/T]ATGACAATCCCTGCAATTGCTCCACCCGAAAGCTG
564	2	2001	4.98	89809490	F1Dsnp	PHR	T	C	2	807,471	+	TCATTTGCAACTTAACAGAAGCTTCAGTTCCTGCT[C/T]CAGAAGAAACAAATGAACCACCAAGCTGCCCGAAC
565	2	2001	4.98	TP4876	GBS				2	867,523	867,546	TGCAGCTACTGGTGCGATCTCCTCTTCCACGAGTACTAGTGCAGCTTCCGAGATCGGAAGAGCG
566	2	2001	4.98	89809496	F1Dsnp	PHR	T	C	2	939,242	+	CTATTTCAACATTTACAGCTTCTGTCGGATGCAAC[C/T]CATCAAAATACATATAAGTCGTCCTATCTACACAT
567	2	2001	4.98	89809498	F1Dsnp	PHR	A	G	2	957,027	+	AGGGATAAATTTCGTCAGAAAATGGCTCAGCTACA[A/G]CCTGTGTTCCAGTATGACAATGGGCATCCTGGAGG
568	2	2001	4.98	89809248	F1Dsnp	PHR	A	C	2	1,022,628	+	ACCGGCAAAAGGATAGTAAAACACTAGAGCTTGTG[A/C]TATCGCCTCCCGAATCACTTTCACGCAGTCCTTTC
569	2	2001	4.98	89809251	F1Dsnp	PHR	A	G	2	1,045,829	+	GAAAGGAAAAGAATCATAGAATGGAAGAGCAGAGT[A/G]GTAGTACATCAGTCAAGTCTGGGCAGGAGATGATG
570	2	2001	4.98	89865215	F1Dsnp	PHR	T	C	2	1,065,145	+	TCTCTCCCTCTCTTTCTCTCTCTAGAAATGCATCC[C/T]TATCTTCTCCTCCTGCAGCTCTTAGTAATACTAGC
571	2	2001	4.98	89809256	F1Dsnp	PHR	A	G	2	1,086,805	+	ATACTTATTTGTTACCACAAGTGGGAACAAAGGTG[A/G]AATTGATCGAGTACGGGGCATCAGTTGAAATTGTG
572	2	2001	4.98	TP4871	GBS				2	1,165,179	1,165,116	TGCAGCTACTCGTAACTTTCTTGTGACTACATAAAATGTTTTGAAACCTTAAGAATCAAGTTTG
573	2	2001	4.98	89865227	F1Dsnp	PHR	A	G	2	1,195,575	+	TGGCAACAAGCTTAATTTTTCAGGTGGCAGGCTCA[A/G]AACTTGTTGCAGTAAAGCAGAGTCCACCTCAGGTG
574	2	2001	4.98	89865228	F1Dsnp	PHR	A	G	2	1,199,301	+	TTGACTCCTAGACATTTTGGCTAGATGAAGTGTCA[A/G]AGGATCATTGGCTAATGCAGATTGATTATGCAAAC
575	2	2001	4.98	89865230	F1Dsnp	PHR	T	C	2	1,204,707	+	GAAGCAGATGCTTCAGATGCCTCGTACAGTTGGGT[C/T]TGTGAAGTAGCTGACTGGGTGAAGTCAAAGCTTGC
576	2	2001	4.98	89809271	F1Dsnp	PHR	A	G	2	1,205,169	+	GCAAAGTAAGGAGTTACCAACCTGAGATAGGGAGT[A/G]AACAAGATCATCAATCTGTGGCAGGTCAAGCACAG
577	2	2001	4.98	89865231	F1Dsnp	PHR	T	C	2	1,206,648	+	CAGAAAGCGGAGACCAAGCCGTCCTCAGAGACCAT[C/T]ACCGATTCGGCGAGATCAAATTCAAAACCCTAAAA
578	2	2001	4.98	89865232	F1Dsnp	PHR	T	C	2	1,221,056	+	AAAAACAAGAGGATGAAAGGCCAGTCATCTCATGC[C/T]ACATGGAAAAGTGAAACTGAAATGCAGCTTCGACA
579	2	2001	4.98	89809273	F1Dsnp	PHR	T	C	2	1,230,410	+	GGTGTCACTTCTGGATGGTTTTGTATTGAATCTAC[C/T]ATTCTTACTCTCGCAATCAGTGCAACGGCGTTTTC
580	2	2001	4.98	89809274	F1Dsnp	PHR	A	C	2	1,239,900	+	TACCTAGTAAAAAAAGCTGAAAGTAAATGGTGGAG[A/C]AGGTTGATAAAGCAAGAAGGAAAAGCTCCTGTGTT
581	2	2001	4.98	59_666633	GBS				2	1,254,762		GTTCCTCAAAGTGGCAGCCCTATGGTGCAAGTTTGCTGCAAGATAAGAGATTCTGGAAGTCACT
582	2	2001	4.98	89865235	F1Dsnp	PHR	A	G	2	1,254,900	+	CTTACCTCAAGCAGGAGAGGATGATCTACTCGGAG[A/G]GAGTGCTATGACTCTTGAGAAATTGAACTCCGCTA
583	2	2001	4.98	89809296	F1Dsnp	PHR	A	G	2	1,413,257	+	TATTTCCTGTAGTCCAAAAAGTGAGGTGCCTCAGA[A/G]TGGTAGTTTGCTACCATTTCACAGAAATGATTCGC
584	2	2001	4.98	89809327	F1Dsnp	PHR	T	C	2	1,640,491	+	GGTGCAATCCTTTTTGGGAAGCGATTGGAGGTCAA[C/T]TTCTCAAAGCATCCGAACATCACTCAGGGTGCCGA
585	2	2001	4.98	89809331	F1Dsnp	PHR	A	G	2	1,688,196	+	TCAGAACAAACAGGAGGATGAAAAATCCGTAATAC[A/G]AGTTGATGTTGATCAGGTGGAGTCTTACAGAAGCT
586	2	2001	4.98	89809364	F1Dsnp	PHR	T	G	2	1,866,485	+	AGAGATTCAATAATTGCCTTTAGTTCCTTTCTTTG[G/T]ATAGATATTTCTCCTGGTCCAGATGGAATGAGACC
587	2	2001	4.98	TP8289	GBS				2	1,889,127	1,889,067	TGCAGTCATCAAAGAAACCATTAACACCATCTTCTTCATTTTCAACAGAATAATTCTGGCAGTC
588	2	2001	4.98	89865321	F1Dsnp	PHR	A	G	2	1,899,427	+	TCAAGTGTCTCTCTCCAAGTGTGGATGATGTCTCC[A/G]TACACAACAGATGGTCTGTCTCTGTAGACTATGGC
589	2	2001	4.98	TP7301	GBS				2	1,971,063	1,971,000	TGCAGGTCCACTTCACCATTCCAAGGACCTTCGGGTGGGCGGCGCCCCTGCTTTCGCTGCACGA
590	2	2001	4.98	89865384	F1Dsnp	PHR	A	G	2	2,199,174	+	CAATTTTGTCTCGACAAGATAGCTGCAATGACGAC[A/G]CTTGCAGTCAGACAAGTGTAGTCTTCTAGGCCGAA
591	2	2001	4.98	89865401	F1Dsnp	PHR	T	C	2	2,260,726	+	CAGAGAGATTTTATTGACATTGGGCGTATTGCATC[C/T]ATAGAGAATAATCACAAACCTGTAGATGTTGCGAA
592	2	2001	4.98	89865443	F1Dsnp	PHR	T	C	2	5,313,832	+	ATCTCTTCCGTATGACTTTCAATTGCATTTCCTTA[C/T]TGAGCTTAAGATGCCTCGAAGCAACCTTGTTCAGC
593	2	2001	4.98	89809475	F1Dsnp	PHR	A	G	2	5,314,440	+	AGTTTGAAATGGATTCTCTTAAGTTTTTCAGTGTT[A/G]AGCATTGCTTAAAACTGAAAAGGATTCCAGAATTT
594	2	2001	4.98	89809476	F1Dsnp	PHR	T	C	2	5,315,433	+	CTGATTATGATAACTTCTCTTTCAATATCATAACT[C/T]CTGGAAGTAAACTTGCAGACTGGTTCACGTTCCAA
595	2	2001	4.98	89865444	F1Dsnp	PHR	A	G	2	5,320,730	+	CATACGTTTTCATACTATAACTGTGACAAAACATG[A/G]TTAACAGACACCACAAATGTTGTGTTTTCATTCAA
596	2	2001	4.98	89809477	F1Dsnp	PHR	A	G	2	5,429,267	+	AATTGAAAGTTATCGATTTCTCGTTGAATCTTCTG[A/G]GTGGTGAGGTTCCATTGTCTTTTGCAAACTTGGTG
597	2	2001	4.98	89809478	F1Dsnp	PHR	A	C	2	5,430,971	+	ATCTTCATCATGATTGCATTCCTCCAATCATTCAT[A/C]GAGATATTAAGGCGAACAACATCTTGGTAGGGCCA
598	2	2001	4.98	89809480	F1Dsnp	PHR	T	C	2	6,065,488	+	CAGGTCCTGGACCTTAGCAAAAGCTTCAAGCTCAC[C/T]GATCGCTCCCTGTATGCCTTAGCTCATGGGTGTCC
599	2	2001	4.98	89880106	snp	PHR	A	G	2	6,079,645	+	TGCCTAAACTTTGATATATGAATTTTTCGAGCATC[A/G]TGATCCATGTCACCATAACAAACCGACGGCTCAAT
600	2	2001	4.98	89865445	F1Dsnp	PHR	A	G	2	6,442,502	+	CTTGTAATTCAAGCCTGTCGTCGGCTTAGAGATAA[A/G]TGTGAAGGACTCAAAGTACATGGCTATGTCATTCA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
601	2	2001	4.98	89865446	F1Dsnp	PHR	T	G	2	6,447,951	+	ATTATTAGGTTTTTGAAGAACTTTCGGGACCAATC[G/T]CAGAATTCGGAGAGCGAGTATCTTACTGAAGGGAA
602	2	2001	4.98	89809481	F1Dsnp	PHR	A	G	2	6,449,999	+	CCCATTGTTTTAATTGCAGGTGGAACAATTGAAAG[A/G]GCTGGCGAAACAGCCTGATATATATGATCGCCTAA
603	2	2001	4.98	89809482	F1Dsnp	PHR	T	C	2	6,492,373	+	GTACTCGGAAAGAACACGCTGCTGGTAAGAACCAC[C/T]CTCCTAATAAATAAATCACAACCAATAAGCTGAAG
604	2	2001	4.98	TP8196	GBS				2	6,577,085	6,577,149	TGCAGTCAAGGATGGAGGCAAGCATTGGTTCCTCTAGCTGAACCATTAAGTTGCACCTATGGAA
605	2	2001	4.98	TP5189	GBS				2	6,638,601	6,638,636	TGCAGCTCTGCCTTCATGTCTTTGGCAGCAAGATTTCCCCTCAAGTCGACGAGAAAACACCAAG
606	2	2001	4.98	89809484	F1Dsnp	PHR	A	G	2	6,650,546	+	GAGCCGAAGAGCCAAATGCCAATCATTTTCTGAGC[A/G]CGAGGTCCTCCATTCACAGGAAACTTCAATGCCTC
607	2	2001	4.98	TP6395	GBS				2	6,869,999	6,870,048	TGCAGGCACCGCCACTTGCCGAAAGCAATATACAAGACAACTGCTCTCCGAGATCGGAAGAGCG
608	2	2001	4.98	89865448	F1Dsnp	PHR	A	G	2	7,045,763	+	GATGTCATCCCACAACGACTGAGCTGGCGCCCACC[A/G]TCTTATTTTGGACGTGATGACCTTGAGACACTAAT
609	2	2001	4.98	89865449	F1Dsnp	PHR	A	G	2	7,052,362	+	CGGCGACCATCTAAACAGAGACCTTCAGGGCTGAC[A/G]AACTCCATCTGTTGGAATATCATAACAACATCTTA
610	2	2001	4.98	89809485	F1Dsnp	PHR	T	C	2	7,191,098	+	GTAACAAACTAAGAAACACTTACCTATAAACCATA[C/T]ACCAGCCGCTGGAATGAATACAGATGTTAGAATAA
611	2	2001	4.98	89865450	F1Dsnp	PHR	A	G	2	7,284,687	+	CATGCGAGACAACAACTCAAAGGCTTCATCAACCC[A/G]GTCAGCCTCGCAAAGGCCATGAATCAAATAATTAT
612	2	2001	4.98	296_63903	GBS				NGH			TTTGTTGGAGACTTGCTACCATGAAAATGCCTGACGGTTCAAACATCGGAATGTGTGTATCACT
613	2	2012	7.42	TP4000	GBS				0	7,949,021	7,949,064	TGCAGCCCAAGTAGATTAGACCCACTAGCCCATACCCCATATCCTTCACTCTTCCCTTCAGTTA
614	2	2012	7.42	22_312130	GBS				1	10,389,454		TCTTCGTCGGAGCTGCCGTCGTGGGATTAGGYCAGAGAGCAAGAATGGATTTTCTCTTTTTAGG
615	2	2012	7.42	89809449	F1Dsnp	PHR	A	C	2	3,162,194	+	CCCTGAAAAATTTCAACTTCCCGAGGCTCAAAATC[A/C]CCTTCACCTTTAGTATCTAAACAAATTGGATCCAA
616	2	2012	7.42	89809450	F1Dsnp	PHR	A	C	2	3,172,078	+	AATGACTGCCCACTTGTTACATTGAATTCGAAAGC[A/C]AAGGGCCGCTACAGGGGCTTTCCTAGCAGCCTGAA
617	2	2012	7.42	89865421	F1Dsnp	PHR	A	C	2	3,210,206	+	GTGGTAATCCATGATTTTACAAACAGGAGGATTAC[A/C]AGAGTGTTGAACCTGTAAAATATACAACAAAATTG
618	2	2012	7.42	89809451	F1Dsnp	PHR	T	C	2	3,353,043	+	ACCGCTGCCATAATCCACAAGGCCTGTTGTGGGTA[C/T]TGCCGAAGAACTGATGTGATGATGCTTTTAACCAC
619	2	2012	7.42	89783360	snp	PHR	A	C	2	3,353,940	+	AGAAGTTTAGCCTTCTCCATGTGAACATTATGTGC[A/C]TTGGTAGCTTGGGCTTCCAGAATGGCCTGATTTGC
620	2	2012	7.42	89865422	F1Dsnp	PHR	A	G	2	3,406,991	+	TGTACGGGGAGTGGCAGGATACCCACATGGAGGTG[A/G]GGTACACTGACATCGATTACATGGTGTTCTCAGAC
621	2	2012	7.42	89809497	F1Dsnp	PHR	A	G	2	9,492,602	+	GGCTCCGGCAGGCTGTTGTGAACGTTGATAATGAG[A/G]TTGTCATTGGTGACGGAGTAGATTTCCGGCCCGGG
622	2	2012	7.42	89865460	F1Dsnp	PHR	T	C	2	9,866,365	+	CTTGTTCAGAGGGAATTCAGGAATGTTTGGAACAT[C/T]GCTGAATCGTCCGATGCAGAGGATCACAAAGTCTA
623	2	2012	7.42	89865461	F1Dsnp	PHR	A	G	2	9,940,259	+	CGGACTTTAAACTGCGATTTTCAATCCAGGTTTCA[A/G]CACCACATTCACTGCTATCCCTAACCAAGGCATAT
624	2	2012	7.42	TP2589	GBS				2	10,012,515	10,012,452	TGCAGATTTAGAAGTGAAATATTACAGACTTGCAGCAAATACCAACAAACCAACTGGAGAATTG
625	2	2012	7.42	TP5431	GBS				2	10,160,143	10,160,206	TGCAGCTGGGTGAACCATTGCTGGTCCAACTGGATGATGTTGTTGTATAAAATCTCTGGAATAA
626	2	2012	7.42	TP5646	GBS				2	10,197,190	10,197,147	TGCAGCTTCTTTCCTGCTCATCCTCCCTTGCTCTCACTGCAAGCATCTGCATCGTAAAAACTAA
627	2	2012	7.42	89865212	F1Dsnp	PHR	A	G	2	10,269,331	+	GTCCTGATTACCAATGTAGGTTCGGATGGGGAAGT[A/G]GTTGCTGTGAAGGTGAAGGGTTCGAAAACAGGGTG
628	2	2012	7.42	89809249	F1Dsnp	PHR	T	G	2	10,271,804	+	GCACTCCATTGCAAGATTAGGGAGGTTAAAACTTA[G/T]TAATGCTGTCAATAGAACGTTAAAGCCCTCAATGT
629	2	2012	7.42	89809250	F1Dsnp	PHR	A	C	2	10,390,652	+	CTCTTTGTGAAGAAGAGGAAAAGAACCAGTCTTGA[A/C]GAGTCCCTTGTGCTTGGGACACTAAAAAGATTGCC
630	2	2012	7.42	89865213	F1Dsnp	PHR	T	C	2	10,427,525	+	TACTGATTTATTGTTTATACAGAAAACCTTTACCA[C/T]CAAGCAGAGTAAAGAAAGAAATTGTTGAACCTGAG
631	2	2012	7.42	89819402	snp	PHR	T	C	2	10,504,200	+	TTTGCAGAGTCCATGACCATGTTCATGAAAATGGC[C/T]GAGGAGGAGATTATAAGACTTCAAGCTCAAGAAAG
632	2	2012	7.42	89809252	F1Dsnp	PHR	A	G	2	10,524,644	+	AGGAAGATAGAGCCTACAAAGCTCACTGTTTAGTC[A/G]TCCCGTTTCCAACCCAAGGTCACGTTAATCCCATG
633	2	2012	7.42	89865214	F1Dsnp	PHR	T	C	2	10,526,233	+	AGAAAGGGATAGTGAGAAGGGAAGAAATAGAATGT[C/T]GTGTGAGAGAAATATTGGAGGGAGAGAGAGGGAAA
634	2	2012	7.42	89809253	F1Dsnp	PHR	A	G	2	10,546,414	+	TGCCACTTGGGTCTTTCCCACCTTGATCAAGCTCA[A/G]GAATACATCAATGAGGCTGAAAAGGTTTGCCTTAT
635	2	2012	7.42	TP8148	GBS				2	10,557,830	10,557,893	TGCAGTATTAGCAAGAGTCACATTTATTTTTGCATGATACGAAACTGAAAAGAACTTTTGATTT
636	2	2012	7.42	TP7251	GBS				2	10,698,058	10,698,121	TGCAGGTATATTGGTCACCTTCCTTAAAGGGCCAATGTTCTTCATCAGATGCTTGACATCAAGT
637	2	2012	7.42	42_41656	GBS				2	10,823,904		CAACCATTTTCTCCAGGTTATCAACTTTCATCATCAAGCACACATGATTATACTTGATTTGTTT
638	2	2012	7.42	89809254	F1Dsnp	PHR	T	G	2	10,825,805	+	CAAGGTAGACGGGCTCGAGTTGCTGCAACATCTAC[G/T]ATTAATGGACATCTTACAACCATAGATGACACCCT
639	2	2012	7.42	89809255	F1Dsnp	PHR	A	G	2	10,841,616	+	AGAAGGTGCAACCATCCTCAACTGTGAAATGTGAA[A/G]ATTCAAAAAGTAGTGTCTCTATATTGTCTCAAGAG
640	2	2012	7.42	TP4577	GBS				2	10,982,679	10,982,616	TGCAGCGGAGCCTCATGTCGTTTTTGAGGGGGAAGGGGCACAATGCGGCGATCTGCAAGACCAA
641	2	2012	7.42	TP1663	GBS				2	11,014,972	11,015,035	TGCAGAGCTTCACCAACGTCTGCATTGTGTTATTTTTGATACAGTCCGTGGACCGTGTCGTTCT
642	2	2012	7.42	89809257	F1Dsnp	PHR	A	C	2	11,056,741	+	TACCCGAGACGTTTCATCGCGAAGATCAAAGTGTC[A/C]ACCATTTGATCGAACAAGTTGTGATACGTCAGACC
643	2	2012	7.42	89809259	F1Dsnp	PHR	T	C	2	11,244,399	+	GATCCAGAGAAGGGAAAATTTACGTACTAGTGAGA[C/T]GAAGTCCAGAAATTGGAAGCCATGGCTTTTGTTGG
644	2	2012	7.42	TP8579	GBS				2	11,273,046	11,272,983	TGCAGTCTTGTTTTACTAGATTCCTTCATCCCAAGGATTCATAACATAACAAAATTCTTCTGCT
645	2	2012	7.42	89809260	F1Dsnp	PHR	A	G	2	11,329,496	+	CTTTCTCTTCCTCAACTGCTTTTTGAATCAAAATT[A/G]CACTAGCTGCTTCCAACACATTACCAGTACTTCCT
646	2	2012	7.42	89809261	F1Dsnp	PHR	A	G	2	11,374,895	+	ACCTTAGCATGCAATTTCTCCATAGGCATCCATTC[A/G]CCAGGACCACAAAGATCAGATAGCACTGTAGCAAC
647	2	2012	7.42	89865217	F1Dsnp	PHR	T	C	2	11,374,919	+	GGCATCCATTCGCCAGGACCACAAAGATCAGATAG[C/T]ACTGTAGCAACAGATGACACCACATCCTTTTCTTC
648	2	2012	7.42	89865218	F1Dsnp	PHR	T	C	2	11,383,087	+	TGGATTTCCGGCGCCGGGAATGGGATCTCCGGTAC[C/T]GGGTTCTTGATCCACCGTAGTCTACTGTTGACCAC
649	2	2012	7.42	89809262	F1Dsnp	PHR	A	G	2	11,384,938	+	GGAATTCCTACACCTGAAATATATGAAACACCGAA[A/G]TTTACATCTAATCCTCTTCGAAAAAGAGAAGGTTC
650	2	2012	7.42	89865219	F1Dsnp	PHR	A	G	2	11,387,003	+	GGAGGTACTAATCCGAAAATGAGGAACGATAATAT[A/G]GCAACTGAGGCATGAAGAATGAAATTCTCTCTTTT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
651	2	2012	7.42	89865220	F1Dsnp	PHR	A	G	2	11,468,979	+	ATGGCTGTTCCTCGAGTAAACAAGAAATTGCTTCA[A/G]GAGCTTGAATCTATGGGATTTCCCACAGCTCGGGC
652	2	2012	7.42	89865221	F1Dsnp	PHR	T	G	2	11,508,271	+	TCTGTCTTCTTTGAAAGTGTGCTGAATTTTGTTCT[G/T]CTTTGCTTCAATAATAATAAGGTCCATGCCTACGA
653	2	2012	7.42	89809264	F1Dsnp	PHR	A	C	2	11,548,483	+	AGAATCCCAAGGGACAGATATCTGAAACAATCAAC[A/C]AAAAGGACCATAATCTACCTTTAGTCACTAATCTA
654	2	2012	7.42	89865222	F1Dsnp	PHR	A	G	2	11,552,904	+	ATACTCTAAACCTTTTTGTTTTTGCTACTTTAGGC[A/G]CTTGTTGTTCTTGTACATGATATGGGTCCAAATTG
655	2	2012	7.42	89865223	F1Dsnp	PHR	A	C	2	11,557,537	+	TAGTACTTCTCAGGTGGGTTCGAGCATGGCAATTC[A/C]TCAGTCCTGTATTGATTCATCTAATATAGTACCGG
656	2	2012	7.42	256_151247	GBS				2	11,557,568		TACTATATTAGATGAATCAATACAGGACTGATGAATTGCCATGCTCGAACCCACCTGAGAAGTA
657	2	2012	7.42	89865224	F1Dsnp	PHR	A	G	2	11,562,005	+	CGTGATCTAGTGCTGAGCCGGATTCGGAAAGACCG[A/G]AAGAGAAAGTTGATTGAAGATCAGATGAACGACAC
658	2	2012	7.42	89809265	F1Dsnp	PHR	T	G	2	11,585,983	+	TTGGAAATTGCAAAGCGTAAGAACACAATTGCAGT[G/T]CTGGAAACTGGAGCTGGAAAGACTATGATTGCTGT
659	2	2012	7.42	89809266	F1Dsnp	PHR	A	G	2	11,596,645	+	GCGCGCAGATGCTGCAAACAACCTTCATGTTTATC[A/G]AGAAGGTGTTGATTGGTATAGCCGGGCAGAAAATT
660	2	2012	7.42	89809267	F1Dsnp	PHR	T	C	2	11,600,125	+	TGGCACCACAGGTTTAGTCTCCATTTCACCACTAT[C/T]ACTATCATCCTCGTTCGACATGTCCTTTTCCAAAC
661	2	2012	7.42	89809268	F1Dsnp	PHR	T	C	2	11,601,745	+	TATAGGGAAATGAAGGTGCTCGATGGTGCTTCCAG[C/T]GTCCCTTGTATCCCCGAAACCACCGTTGTTGGGTA
662	2	2012	7.42	89865225	F1Dsnp	PHR	A	G	2	11,606,634	+	CTCCTAAGAGTATTTGTTAACCTCATGGAAGCATT[A/G]GCAGTCCTTTTCTTAAGAGATCTACTGCGAGTCCT
663	2	2012	7.42	89865226	F1Dsnp	PHR	A	C	2	11,894,411	+	GTCTGCCATTGAAGGCTGCTCCTTGGTATATCAAC[A/C]TCAGCTTCCTCTTGAGCAAGTCAATCTGTTCCTCG
664	2	2012	7.42	89809269	F1Dsnp	PHR	A	G	2	11,963,269	+	AACTGGTTGTCCAGCTCCAACTTGTAGACCTTGAA[A/G]CTCATCGTCTCCTTCATCCTAGCTTGATTCGTCGA
665	2	2012	7.42	89865229	F1Dsnp	PHR	A	G	2	12,016,024	+	ATGCTTAATGAACATTATTTTATACTTCAGTGTCC[A/G]ACAACAATAGTTCCTTTCTTTGGAGACCAACCCTT
666	2	2012	7.42	89865233	F1Dsnp	PHR	T	C	2	12,251,947	+	ATGTTTCTGCAGACAGACAGAGCTGCTATGCTTGA[C/T]GAAATAATGGATTATGTGAAGTTCCTGAGGCTCCA
667	2	2012	7.42	89865234	F1Dsnp	PHR	T	C	2	12,442,683	+	CAACTCCAACGAGCTCTATCCTGTATGGTTTTCTC[C/T]TTCTGCCTTCTACATGTTCTGGTTCTTCATCTTCG
668	2	2012	7.42	89809275	F1Dsnp	PHR	T	C	2	12,508,105	+	CATACATTCTCCATTCCAACCCAAGGTGGTGATGC[C/T]GAGCAGTTAAAGGAGAAGCTGGTGGCTGCTCTTTC
669	2	2012	7.42	TP6642	GBS				2	12,511,172	12,511,109	TGCAGGCGTCAATTGAGTCCATGTTCATAAGAACAACCACCACTGCGGCCACCACGACCATTCT
670	2	2012	7.42	TP1328	GBS				2	12,655,961	12,655,899	TGCAGACTTGAGGCAGAGCTTGGAAGTTGCTTTCATCTTCTACGAACAGGCAGTTGCAGGATAA
671	2	2012	7.42	89809276	F1Dsnp	PHR	T	C	2	12,671,917	+	AGTCATGGTGGCCTCCAAGTTCTTCATCAAGATGT[C/T]TGGGTTGATGTGCCCCCAGTGCCGGGAGCTTTGGT
672	2	2012	7.42	89865236	F1Dsnp	PHR	A	G	2	12,702,216	+	AGGGGTGGTACTCCCGCATGAGTGTCTTGTACATA[A/G]CTGGGAAGAAAGTCCTTGTATGCAAATGATTTAAA
673	2	2012	7.42	89809278	F1Dsnp	PHR	A	C	2	12,703,187	+	GCTCAAAGAACTCATTAGCCACCTTCAATACCTTA[A/C]GCAGCACATCGTCTCCAACCCCATGATTGATCAAC
674	2	2012	7.42	20_595807	GBS				2	12,705,516		TCTTTTTTCCTGCCTTAGATTGACTACATGCGTGTGAGTAAGTAAACTAGCTGCAATCTCACTA
675	2	2012	7.42	TP4913	GBS				2	12,750,201	12,750,159	TGCAGCTAGTACCTTGTCTTGCCAAGGCTCTTTGCCAGGATTTCCGAGATCGGAAGAGCGGTTC
676	2	2012	7.42	89809279	F1Dsnp	PHR	T	C	2	12,783,159	+	TTAGCAGCAACGCTAAGATTCGATTTTAAAAGGCT[C/T]GAGCACAACTTCGGTTTTTCCCTGCTTTTTGAAGT
677	2	2012	7.42	89865237	F1Dsnp	PHR	A	G	2	12,953,192	+	TCCCTTTCTTTTTCTTTCTTACCAAGCTCAGTCTT[A/G]CTTTTCTTGATTTTTGAATTTATACGAGACATTTC
678	2	2012	7.42	TP6743	GBS				2	13,091,071	13,091,134	TGCAGGCTGTCAGAAGCCTCAACATTATCCTCCTTATCCCCCCGTTCCTCGCCATCATCACCAT
679	2	2012	7.42	89865238	F1Dsnp	PHR	T	G	2	13,121,379	+	AACACTAAGGAGAAATGATTGTTGGTATGAACCTG[G/T]GAGGCAACATCAACACCAATTTCATCCAGCACCTG
680	2	2012	7.42	89865239	F1Dsnp	PHR	A	G	2	13,153,317	+	GAGCAAGAAATTCAGATTGGATTTCCTACAGATGT[A/G]AAGCATGTGGCTCATATAGGCTGGGATGGTCCAGC
681	2	2012	7.42	89865240	F1Dsnp	PHR	T	C	2	13,172,570	+	CTTGATTGCTGTGAGCCTTTGGCCAAGATCAAAGC[C/T]GAAGGCATTACATTTGGGAAAGTTGCGTGCTTGGC
682	2	2012	7.42	89865241	F1Dsnp	PHR	A	G	2	13,219,961	+	AACAAAAGAGAAAAGTTGATCAAGACACCCAAGGA[A/G]AGACCTCTTGAGAAGGGAATTATAGAAACCATGAA
683	2	2012	7.42	89865242	F1Dsnp	PHR	A	G	2	13,223,942	+	TATAATTTCTTCACTTGTTCAATTGAACTATTTCT[A/G]TCAGCTCCTTTGGGAGACAAACCATCAACAACCTT
684	2	2012	7.42	89865243	F1Dsnp	PHR	T	C	2	13,286,491	+	ACCTTATCATGTTTGGCAAAATATCTTCTCCATGA[C/T]GATGTTCTACGTTCAATTCCTCTTGTACATGAGAA
685	2	2012	7.42	89865244	F1Dsnp	PHR	T	C	2	13,292,577	+	GCAGTAGAAGCTGTGCAGTTTGTGATTTCATTTTG[C/T]TCTTTGCTGGAAACTCAGAGATTAGTGTTGCGGCC
686	2	2012	7.42	454_98920	GBS				2	13,304,596		CTGCAAGTGCGTCTCTTTCTTATTTGACCTAWTTTGATTAATCTGATTCTCCAAGTTCTTATCT
687	2	2012	7.42	TP4650	GBS				2	13,304,676	13,304,739	TGCAGCGGCTGTGTGCCTAATCGGAACAATTTCGGAGCAAAGTGTCCTCTGTGTAATATTCAAG
688	2	2012	7.42	TP7162	GBS				2	13,304,679	13,304,616	TGCAGGTAAATCCAAACAGAAGATAAGAACTTGGAGAATCAGATTAATCAAAATAGGTCAAATA
689	2	2012	7.42	89809284	F1Dsnp	PHR	A	G	2	13,306,456	+	AGGGAACTCAAAAGACAAAAGAAACTGGACTATGG[A/G]CCAGTCTCAGGGTCTAATTCTGAGCTGAAACTTGG
690	2	2012	7.42	89809285	F1Dsnp	PHR	A	C	2	13,307,719	+	ATAGATTTCCCAATGAGAAGTTGAATCGTAACAAG[A/C]ACAAGTATGACATCATTATCTCAGCAGTGTTTACT
691	2	2012	7.42	89809286	F1Dsnp	PHR	A	G	2	13,310,742	+	CATGGTAATGGTGTGCAAAACAAGACCAATGCCCA[A/G]TCTCTGCAGCAGTGTGATCCCTCTTGGGTTTTTGG
692	2	2012	7.42	TP2975	GBS				2	13,310,747	13,310,787	TGCAGCAATGTGATCCCTCTTGGGTTTTTGGTGTATTTCCGAGATCGGAAGAGCGGTTCAGCAG
693	2	2012	7.42	89865245	F1Dsnp	PHR	T	G	2	13,329,026	+	TTGAAATGGGGACCTATGGAATCATCAAGAGTGGT[G/T]CCTTGCTTTATGAAAAGTGTGTGGGATTGAGTTAT
694	2	2012	7.42	89809287	F1Dsnp	PHR	T	C	2	13,333,663	+	AACTCATGGAAGTTCTTTTGTAGTACTCTATCAAC[C/T]GCATCTTCAGTGTCAAAAGTTATGAAACCAAATCC
695	2	2012	7.42	89865246	F1Dsnp	PHR	T	C	2	13,339,441	+	TTATATTGAAGTTTATGAGTTTTGTTCTGTAGGGA[C/T]AAGCCAGTGGAACAACTGAGCTGCATTGCTAGAAA
696	2	2012	7.42	TP5522	GBS				2	13,343,817	13,343,880	TGCAGCTTACTCAGTCTGCCTAGAATCTGAGGAATTGTTCCTCCCAAGTGGTTCCTGCTTAGAT
697	2	2012	7.42	89865247	F1Dsnp	PHR	T	C	2	13,391,561	+	AGAGCCTCCTGATTGGTCTAAATTTTCAGGCTTTC[C/T]AGTGTTGACATTTCTTGATATGTCTCTCAACAGTT
698	2	2012	7.42	89809288	F1Dsnp	PHR	A	G	2	13,398,531	+	TGAGCCACAGGGGAAAAGCATCATAGGCTGGAGTC[A/G]AGATACGGAAATGAAAGAAGAAGGCCAGAATCACA
699	2	2012	7.42	89865248	F1Dsnp	PHR	A	G	2	13,403,596	+	GAACAGGGGTATTTACAGGAAAATCAAGGAACCCT[A/G]GCAGAGAATCTGTACCCCATGAATGACTGTTTTCT
700	2	2012	7.42	89809289	F1Dsnp	PHR	T	G	2	13,414,856	+	CTCATGCTTATGCTCGTACACAAGTTGGACTGCAA[G/T]CTCCTTTATCAAGATCGGAACATACATGTAGTCGG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
701	2	2012	7.42	89809290	F1Dsnp	PHR	A	C	2	13,417,796	+	ATTTTCTCCAAGACATCAGATGCATCCTTCTGCCA[A/C]ACTCTACTACGTTCTCCAGGGTCCTTCGACTCTTC
702	2	2012	7.42	TP5449	GBS				2	13,418,201	13,418,264	TGCAGCTGTAGAAAACTCCATGTAGCTTTTGATAGGATGGGCTTGTCTAAAAGCATGCCAACTG
703	2	2012	7.42	89809291	F1Dsnp	PHR	A	C	2	13,428,257	+	TTAATAAACCTAGCAACATTTCCATATTTTGTTGC[A/C]TCCAAACAAAGAGCGTCTTCATCTTTCAAATTGGA
704	2	2012	7.42	89809292	F1Dsnp	PHR	T	C	2	13,501,141	+	TGGACTGCTCGTTCATAGTAGCTTAAGGCTCTATC[C/T]TCATCATGGTGCAACTCCCATATAACCTTGGCGTA
705	2	2012	7.42	89865249	F1Dsnp	PHR	A	G	2	13,509,641	+	AGAGCCGCTTGATTACACATTGGTGTGGAGCCCTG[A/G]TGATGGGACTGAGGAAAGTTATGGTTCATGTGGCT
706	2	2012	7.42	89865250	F1Dsnp	PHR	A	G	2	13,538,349	+	TTTCCGATTCTCTTCCTTGATATAAACCATACCCT[A/G]TAACTCAAGCTCTGGTTGATGCCTGTGAAAACCAA
707	2	2012	7.42	22_801991	GBS				2	13,714,408		TCTCAGTACCGGAATCTGGGGATAGTGCTGCTATCTTAAATGCCCTGCATGATGGGAATGAAGC
708	2	2012	7.42	89809293	F1Dsnp	PHR	T	G	2	13,773,499	+	TCTTTCGAGGCTGAAAGAACTAGTGTCTTTGATCG[G/T]CTCATCCAGATGATTGGTTCAGAAATTGAGGTACC
709	2	2012	7.42	TP5930	GBS				2	13,908,462	13,908,504	TGCAGGAATAACACACACAAGCCGTGTATTGCTTTGATATAATCTCTGTTATTTCAGAAGTTTA
710	2	2012	7.42	89809294	F1Dsnp	PHR	T	C	2	13,966,380	+	ATGTTTGATTTTTTCCACAGGGACGCAATGTTGTT[C/T]TGGAGCAAAGCTATGGAGCCCCTAAGGTGACAAAG
711	2	2012	7.42	89865255	F1Dsnp	PHR	T	G	2	14,376,319	+	TTAACCTTAAATCATAATACCTTTTTAATTATTGC[G/T]ATCAGTCCATGAATAAATCTAGGAGGAGTGCAGTT
712	2	2012	7.42	103_311771	GBS				2	14,377,287		CGAAAAATGTAATGAGAAGTCATGTAATGACRGTGGGGATGTTAGGATTCTGAACCGGCGGCCG
713	2	2012	7.42	89809297	F1Dsnp	PHR	T	G	2	14,543,949	+	CAGTCTGGATTTCCAGTCCAAGTCAACTTCATCTT[G/T]GGGCACAACTGTTAAGTCCTGGGTTGGAGGAAGAG
714	2	2012	7.42	89809298	F1Dsnp	PHR	A	G	2	14,580,106	+	TAAGTGACAGATTAAAATCCCGCCTTGGACCTCGT[A/G]TAAGTGATCAGCACTCTCCAGACAGAGGTAGGGCT
715	2	2012	7.42	89865257	F1Dsnp	PHR	A	G	2	14,593,072	+	ATAGAGCACCTGCAGAGTCGACTTGTATGCTTGAA[A/G]CTCTAACTTGTGAATGTCCACATCAAGCATATGAT
716	2	2012	7.42	22_312165	GBS				4	16,402,942		AGAGCAAGAATGGATTTTCTCTTTTTAGGTCCGAGTCATACTTTCGTTTTTACTGCAGTTGTTT
717	2	2010	9.86	52_792148	GBS				0	1,350,878	1,350,941	AACTCTCTACAAGGTCTTGTTGTAAGGGATGYGCAATTGGTCAAAGGAAGTCTACCGGATCTAG
718	2	2010	9.86	89865254	F1Dsnp	PHR	A	G	2	14,339,699	+	TATTTACTGTCGAAGCCCCTCTTCATGCCTCAAAT[A/G]TCCAAGTTGTTGATCCAGTAACAGGGTATGGAAGT
719	2	2010	9.86	89865258	F1Dsnp	PHR	T	G	2	14,733,531	+	CGAATCTAATCAATTTACCTTGTTCTTTTGGTTTC[G/T]GTAGGAATGAAGTTGATTGCAAACTTTGTCTGTTA
720	2	2010	9.86	89809299	F1Dsnp	PHR	T	G	2	14,830,364	+	ACTGAAGGTGGTATCCCTCCTCTTGTGGAGTTGCT[G/T]AACTTCTTTGATACAAAGGTACAGAGGGCAGCTGC
721	2	2010	9.86	89865259	F1Dsnp	PHR	A	G	2	14,833,989	+	TTGTCTCTCCTAAAGGACATCTGTGTGGAAAACGT[A/G]TCTCTCATGTTTGAGTTATCAGAGGCCTATAATGC
722	2	2010	9.86	89865260	F1Dsnp	PHR	A	C	2	14,836,437	+	TTTGATTAACCGTTTGCTGACAAGACGAATGTGTC[A/C]AGCAGCTCCAAGACCTGGAGTTACAAGAGAACTGA
723	2	2010	9.86	89865261	F1Dsnp	PHR	A	G	2	14,843,460	+	GGAGGCTGAGGAGCTTTTCAAACCACTAAGGGAGC[A/G]TGGAAACTCCTATACTAAGATATGTTTGAGCAATA
724	2	2010	9.86	89809300	F1Dsnp	PHR	T	C	2	14,856,228	+	TGTGAAACTCTTGTGACACAAGACTACCGATATGC[C/T]AAGCAGGATTTGACCTCAATAAATGATATAGTTGG
725	2	2010	9.86	89865262	F1Dsnp	PHR	A	C	2	14,912,239	+	TAGGAGATTCAAAACAAGGGAGGAAACTCAATGAC[A/C]AAGTGCTTGGAAGATGATTGGAAGAAGACGAGGTA
726	2	2010	9.86	89809301	F1Dsnp	PHR	A	C	2	14,951,025	+	AGAATGCCTTGAAGATTACTTCACATTAGATACTG[A/C]AAAAGACAACCAGCCTTGCCGACGGAGTTCCGGTT
727	2	2010	9.86	TP4900	GBS				2	14,983,000	14,983,063	TGCAGCTAGCTGCATCAGTAATGTCAGTGATACGAGTCAAGTAACATGTGACGGGGAGGTGGAA
728	2	2010	9.86	TP9409	GBS				2	15,005,308	15,005,365	TGCAGTTGAAGCATGATAAACAAAGAAATTGATCGCTTTGCTTACTGTGAGTACAGAAGCCGAG
729	2	2010	9.86	89865263	F1Dsnp	PHR	A	G	2	15,024,471	+	ACCAATTTCTCAGCACTAACCACCTTATTCTTCGC[A/G]ATCATCAACAATTTACACAACTTAGCCACAATCAA
730	2	2010	9.86	TP6679	GBS				2	15,064,779	15,064,839	TGCAGGCTCACTTGAGTCAGCTGCAACATTTGGCTGCGGTGGTGCCACATCTGTTACGCCGAGA
731	2	2010	9.86	89809302	F1Dsnp	PHR	A	G	2	15,064,834	+	CTGCAACATTTGGCTGCGGTGGTGCCACATCTGTT[A/G]CGCCGGTTTTGATAATGGGAGCTCGGCACAAGGGG
732	2	2010	9.86	89809303	F1Dsnp	PHR	T	C	2	15,075,531	+	GGTTTATTCATACGAACCCTGGCTCGTTTCACCAA[C/T]GGCAGGTGCTCATCTCCATCTTCCTTGGAAAAATT
733	2	2010	9.86	458_47772	GBS				2	15,110,627		CGGCTTGATTGTTGTTCCAACTTCTAACTTAAGAAACCAATTAAACTCATCCGGCAAAGAAGTT
734	2	2010	9.86	89865264	F1Dsnp	PHR	T	G	2	15,138,528	+	GCTATCATCATGTTCATCATCAGAGCAAGAACATT[G/T]TTTGCTTTGATTTTTGGAGCAAAAGGGTTCATTCT
735	2	2010	9.86	89809304	F1Dsnp	PHR	A	G	2	15,164,451	+	GAGGCGCTTGATGGGATTCTTGGATTTGGACAAGC[A/G]AATTCGTCTATGATTTCTCAGCTGGCTGCTGCTGG
736	2	2010	9.86	TP9464	GBS				2	15,184,457	15,184,516	TGCAGTTGCAAAATGACATCATGTTTGGAAGCTTGGTGCACCAACTGAATCCAAGTAAGGATTC
737	2	2010	9.86	89865266	F1Dsnp	PHR	A	G	2	15,191,361	+	TTTGAGGAGTCAGGGCGATCTCTTGTACGAGGGAC[A/G]TTAGATTATCTCCAAGGCCTCAAGGTCTGTGTGGT
738	2	2010	9.86	89865267	F1Dsnp	PHR	T	C	2	15,264,209	+	TGCACCTTGGTTATCTTGCTTTTGCGCTGGTTTTC[C/T]TTCGGGTTAGACTTGAAATACTAAAGAAAAGGAAC
739	2	2010	9.86	89809305	F1Dsnp	PHR	A	G	2	15,268,918	+	ATCCTTTACTGGACACTGGTGAAGATTTATAGATC[A/G]CCACACATGCTTCTAGAGTACACGAAACCCGACTA
740	2	2010	9.86	89865268	F1Dsnp	PHR	T	C	2	15,304,097	+	CTCCCCAAGTCGAGTTTCAAAAGGAAAAGGTCCGT[C/T]GAAGCCGAGTGTGAGCTTTCCTAATAATATTGGGA
741	2	2010	9.86	89809306	F1Dsnp	PHR	T	G	2	15,333,519	+	GTTTTGCTTCCAACTGCAGCCTATTTTGAGTTTCT[G/T]CCATTTGATATGAATGAGGCTGAGGTTTCTACAGG
742	2	2010	9.86	89865269	F1Dsnp	PHR	T	G	2	15,333,537	+	GCCTATTTTGAGTTTCTTCCATTTGATATGAATGA[G/T]GCTGAGGTTTCTACAGGTAGAGAAACTGTTGATAT
743	2	2010	9.86	89809307	F1Dsnp	PHR	A	C	2	15,347,156	+	ACAAACATGAGAACTTGGTCATTGTCACAGTTGTT[A/C]CGGAGATAAAGAGCACGGCGGCTATCAAAATAAGG
744	2	2010	9.86	89809308	F1Dsnp	PHR	T	G	2	15,349,158	+	CTGTTTTATATGAATCACAATTAGAAGGAGGAACA[G/T]CAAACCATTGGTTGGTGTACGGATTGCAGATGAAG
745	2	2010	9.86	89865270	F1Dsnp	PHR	T	G	2	15,370,298	+	GACTGCCGGCAAGTATCTCCTTTGAAACAAATCTA[G/T]CAATTTGGCTTTAGGGAGACTGTCAAGAGTTGCTA
746	2	2010	9.86	89809310	F1Dsnp	PHR	A	C	2	15,441,078	+	CTGAGCTTCTTTCACTCATAGCAGAGCGTGCAGGC[A/C]TATTCGAGCTTCTGAGTTTCTTTCGTGTTTGCAAC
747	2	2010	9.86	89865272	F1Dsnp	PHR	A	G	2	15,468,138	+	TGGAGAAAATGAATATGATCCAACTAGGCAATTTG[A/G]TTCGATTCCAATAGAGGAACAGCTTGATGCTCTTG
748	2	2010	9.86	89809312	F1Dsnp	PHR	T	C	2	15,535,585	+	CATGATCATCAAACAGCCTCTTTCCCTGTATATTA[C/T]GCCTTTTCCGTGGACGACCCCTGCGCCTAACAGAG
749	2	2010	9.86	89809313	F1Dsnp	PHR	T	C	2	15,539,103	+	TTTATAGTTTATAAAAGTAACAAACCTTCATGGCA[C/T]TCATGTATTCCCAGACATCATCAATTACATAAACG
750	2	2010	9.86	89809314	F1Dsnp	PHR	T	C	2	15,553,410	+	GGACCATCTACTTTATGCAGTGCAAATGTGTTTGG[C/T]GTCTCAGCAGAGTCAATGCAGTTGTCTTTTGATTC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
751	2	2010	9.86	89809315	F1Dsnp	PHR	A	G	2	15,565,868	+	ATAGCGAAATTTCTAGGGGCAATATTGGGAGGAAG[A/G]TCGGGTGCAATTCGGTGTAAAGCATTTCCTTGATT
752	2	2010	9.86	89865273	F1Dsnp	PHR	T	G	2	15,566,629	+	TTTAAGCCATTACAACATGAACAGACCTCCATTTT[G/T]TGTTTTCCATTAACGGCTTCCAGGGCAGCAAGTGC
753	2	2010	9.86	89809317	F1Dsnp	PHR	A	G	2	15,597,226	+	CTCCAAGCTGCTTCAAGATGGGGTATTCATCACAG[A/G]GTGGAAGGTAAGCCAATTTGACTGGATAACGTAGG
754	2	2010	9.86	89865274	F1Dsnp	PHR	T	C	2	15,686,725	+	GGATTGCAGAAAGGGCAGGTTAGGGTTGAGCACTA[C/T]GCTTCCAAGAGGACTAAGTTTATTATGGCTCATGA
755	2	2010	9.86	89809318	F1Dsnp	PHR	A	G	2	15,766,650	+	GAGTTCTATTGGTTCCTGTTATCTTTGGTGAAGTT[A/G]GGGCACCTAAAATAGAGAAGAAAGGTTTTGGCACT
756	2	2010	9.86	89809319	F1Dsnp	PHR	A	G	2	15,881,956	+	TAGTCTTTCACATGAATGCCAAGAACTTTTTCGTA[A/G]TAGGAAGCTGCAAGAGTCACAAGGCCAACTTGATG
757	2	2010	9.86	89809320	F1Dsnp	PHR	A	G	2	15,885,307	+	CCGCGTCGCAAACAGAAGGCGGAATGGAGATCCCA[A/G]GTGTGGTCGCAGCTGCAATAAGCGCAACAGAGCTC
758	2	2010	9.86	89865276	F1Dsnp	PHR	A	C	2	16,016,072	+	AGTTGCAGCAATGTCATCGGAATCCTTCCCGGAAT[A/C]TTCACAAAGCCGCTCGAGCAACTCCTTCTTGGAGC
759	2	2010	9.86	89809321	F1Dsnp	PHR	T	C	2	16,019,954	+	AGGTTGTTGATGTAGATCGTCTGATTCGCCGGAAC[C/T]TCGCTGCCGCTGTTGTTCTCTCCCATGGCTTCTCT
760	2	2010	9.86	52_230526	GBS				2	16,038,439		TGCAGGCTCAATTATACTGATACACTCCCTCCATACTGTAGAGCACAAAGCAACAATTACGACA
761	2	2010	9.86	89865277	F1Dsnp	PHR	T	C	2	16,051,890	+	GAATGCCTGAATTACGATGGCAACAAAGGTAGCCT[C/T]ACTGTCTCGAAAATTCTGTCAACCTCCGACGATGC
762	2	2010	9.86	89809322	F1Dsnp	PHR	T	C	2	16,052,630	+	GTGAATGGGAGAATGGAATACTTTTCGATGATGAA[C/T]TGGACGAAACATCATTGTTTGTGGACTTGAGATGC
763	2	2010	9.86	89865278	F1Dsnp	PHR	A	G	2	16,054,461	+	GTGCAAGTCCCACTCAAATAGATCGAGAAATGCCC[A/G]GTTTCTGTGTTCAACTCGTAGCCTGTAACTCCTAT
764	2	2010	9.86	89865279	F1Dsnp	PHR	T	C	2	16,119,609	+	GGAACCGGAGACGACTGCGTTTCCATCGGCAAGGG[C/T]GCCCGCCAAATCACCGTCAACAACGTTACTTGCGG
765	2	2010	9.86	89865280	F1Dsnp	PHR	A	G	2	16,123,100	+	GTACCCAAGTGATGGTAAAGAGATACACCGGTACC[A/G]GAGAGTGGCGTACTATGCTTGAAAGAGAGAAGAAA
766	2	2010	9.86	89865281	F1Dsnp	PHR	T	C	2	16,159,860	+	TGCTGCTCTGAACAAGACTCAGGAGGAGTTGAAGA[C/T]ATGGTTTCGTTGAAGCTCCAGAAGCGGCTCGCCGC
767	2	2010	9.86	52_30308	GBS				2	16,185,805		TGAACCTTGGACACAAGAACCGGGTTGTTGGTGCAACTGCTCTAAACGATCGAAGTAGTCGCTC
768	2	2010	9.86	89877514	snp	PHR	A	G	2	16,186,240	+	GCTCCATCAGTAACAAGGAGATCCCGGACTTGCTC[A/G]TTGTAAATTTCAATCATCTGAACAGAAACATCATA
769	2	2010	9.86	89865282	F1Dsnp	PHR	T	C	2	16,202,375	+	TCAGTTACTCTAAATATGACAGCTAGTCATACTCA[C/T]AGGCAATGAAATAACCTCTTGCATAAAGTTTTTTT
770	2	2010	9.86	52_13398	GBS				2	16,204,753		CTTCTTTTTCTTAGGGTGCTTCTTATTTACAAAAGACAGATGATCATTGATGATATGCATATGC
771	2	2010	9.86	TP1532	GBS				2	16,205,168	16,205,110	TGCAGAGATGGATTCGTTTTCGCTGCCAAGGAAGTATCATTGCTTGATCAAGAAAGTCCGAGAT
772	2	2010	9.86	89809323	F1Dsnp	PHR	T	C	2	16,237,850	+	TGCTCTGAGTGACCTCCTTCCACATAGACTTGTCG[C/T]ATCTCGCATAGAACCTCAGGGCTCCAACAGCAGTG
773	2	2010	9.86	89865283	F1Dsnp	PHR	T	C	2	16,238,125	+	AAAGAATCAGCCTTTTTGTTCTCCTCTTGGCAATG[C/T]TCTTTCAACTTGAGCAGCAAATCGCTTCTTCTGCG
774	2	2010	9.86	89806654	ins	PHR	-	AGCT	2	16,238,379	+	GGAATCACAGAACCCTTGCCATTGGCAAAGCTAGA[-/AGCT]AGCTTGAACACCATGGCCAAGACTGGGCCTCAGTC
775	2	2010	9.86	89809324	F1Dsnp	PHR	T	C	2	16,309,940	+	TACGGATTTGGGTACGATTCAACCAATGACGACTA[C/T]AAGCTAGTGAGAGTGGTAGTGTTTACAAAAAATGA
776	2	2010	9.86	89809325	F1Dsnp	PHR	A	G	2	16,310,497	+	TACTCGAAGAAGTTGACATTTTTGGTAAGCCCTCC[A/G]GGTTTTCGACTGCTATTTCTCTGGGAAACCTTCAT
777	2	2010	9.86	TP899	GBS				2	16,353,873	16,353,936	TGCAGAATTATAAGCAAGAAGTGAGGAAAAACAGAAATCTAATATCAAGAGGTAGATCTAACAA
778	2	2010	9.86	228_260132	GBS				2	16,353,992		CCAAGTAATAATTAAGAAGAAGCAAGTTTACRTCAGTTGTAGACATTCGAGTATCATTGTTGTT
779	2	2010	9.86	TP9685	GBS				2	16,402,840	16,402,781	TGCAGTTTCAACATCACTAAGTAGCGGTGGCTCAGACGGCTGGGACAACCATGGGGTCATCGGA
780	2	2010	9.86	89809330	F1Dsnp	PHR	A	G	2	16,587,490	+	TAGAGAAAGAGATAACCAAGTCATTAACCATGATG[A/G]AAGAAGGTTCAAGCCCAATGGAGGTAGATCACAAT
781	2	2010	9.86	53_361904	GBS				2	16,894,549		CTAGGATCTCCAAATCGGCTTCAAATGAGGGGTAGGGAGGACAAATTTGTCCTTCGTTTTACTC
782	2	2010	9.86	89809332	F1Dsnp	PHR	T	C	2	16,952,670	+	TAGCGAAAGTGTGTGCGCTTGTGTCTGAAACACAT[C/T]TACACCCAGTGAGCACATGGATGTATCAGAGGACT
783	2	2010	9.86	89809343	F1Dsnp	PHR	A	G	2	17,292,573	+	GGCAAAAAGAAGGCTTGTGAAGACCATGGTGTTCC[A/G]TTCCATTCTGAAATTCGTGGCCTCCGGTTTCTGTT
784	2	2010	9.86	TP1690	GBS				2	17,335,234	17,335,171	TGCAGAGGAACAGAAAATAGAGGCGAAGAAGTGCAGAACGGAAACAAACACCATAGCCTTCACC
785	2	2010	9.86	89865291	F1Dsnp	PHR	A	G	2	17,366,859	+	GGTCTACAAGCACAAAAGCAACAAAATTTACAACA[A/G]CCACAACAAGAAGCTTCATTCTTTGTCTCTGCTCA
786	2	2014	12.30	53_422162	GBS				2	16,961,072		AGCCTTGGTTGTATTGGATGAGAGTGTTGTGTGTGTATGTTCAAAACATAATAGGTGACATT
787	2	2014	12.30	89865286	F1Dsnp	PHR	T	C	2	16,968,953	+	CTCATACATATCACTCTTCAATTTGGAGACTTTGG[C/T]ATCCATCTTGCCCTTTTGCTCATGCAACCAATCCG
788	2	2014	12.30	89809333	F1Dsnp	PHR	A	G	2	16,991,770	+	AGGTGGAGGGTATATGTTACATTTGAGGTCTCAAG[A/G]GTGTTGGTGAGGACGCGGACCACCTCATCCTGCTG
789	2	2014	12.30	53_475759	GBS				2	17,014,991		GCGTTGTTCTTTCCATTCGTCAGATCATACTRTCCGATACGAAGCAAATTGAGTCAGTCGGTTT
790	2	2014	12.30	TP9456	GBS				2	17,015,092	17,015,031	TGCAGTTGATCAAATTAAATCGAGTGTATATTGTACATATATGCAAACCGACTGACTCAATTTG
791	2	2014	12.30	89820574	snp	PHR	A	G	2	17,016,165	+	TCAACCTCCTAAGATCAGAGCCGTCAACTTTCACC[A/G]TAAAAATCTCACCGTACGGCTGATAATGATGCGGG
792	2	2014	12.30	89806670	ins	PHR	-	ACT	2	17,083,106	+	AAATTTCTTTCTTTCAAAACTCAAAAGACAAAAGA[-/ACT]ACCTCAAATATAACTAGCATTATATATTAACCAGA
793	2	2014	12.30	89809334	F1Dsnp	PHR	A	G	2	17,095,269	+	CATTACACAGTGGAACTTAAAGATTACGCAGTTGA[A/G]TTGACTGAAGAAGGAATAGCTCTTGCTGAGATGGC
794	2	2014	12.30	89809335	F1Dsnp	PHR	T	C	2	17,098,618	+	TGGGCTGTGAGACTTATTTCAAAAATTACTGATGA[C/T]GAGGATGTACCAATTGAAGGTGATGCCATTGTGAG
795	2	2014	12.30	53_585865	GBS				2	17,125,381		TGAGATGAAGGTAAGGTGTAGGAAGTGCCTCAGGTGAGGCAAAGATTGTAAAAAATAAAAGTCT
796	2	2014	12.30	89865288	F1Dsnp	PHR	A	G	2	17,177,933	+	AAAATTTATCAGAATCTCCTTAGAATGCTTCTGAT[A/G]TGAATAGAGCACCAGGTTTTCCACAAAGTTCTGTA
797	2	2014	12.30	89809339	F1Dsnp	PHR	A	G	2	17,221,682	+	TCTGCTGCCATCTCCTTGGGGACTCCATCCCAAGT[A/G]GCTGAGCCTCCTCTTAGTGATTTCTTTGGAACTAA
798	2	2014	12.30	89782070	snp	PHR	T	C	2	17,234,058	+	TCATATGACTCTGGTCTACCATTTTGTGGTGCATA[C/T]GTGATTTCTTCATCATTTATGACATACAGATCACT
799	2	2014	12.30	89809340	F1Dsnp	PHR	T	C	2	17,234,236	+	GAAGAACCTCTGAACCAGGTCTTTTGTTAGGAAGT[C/T]CATTTGTCCTATCCGAATAAGGATATTCACCTTCC
800	2	2014	12.30	89809341	F1Dsnp	PHR	T	G	2	17,234,731	+	TTTCTGGAGTATCTGAACTGAGCTCTTCTGGATTA[G/T]TAGGAACCTCCAGACAAGGCCTTTTACTGGAAACC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
801	2	2014	12.30	89809342	F1Dsnp	PHR	T	C	2	17,238,256	+	CTTGCCTAAACTGGGAATGACTTTCAGTAGACCGC[C/T]GACTATCTACATCCATCGTCTGTTTGCAAAACGTA
802	2	2014	12.30	89865289	F1Dsnp	PHR	A	G	2	17,256,816	+	TTTCCTGGAGGTGGAACACAGTTCATTCATGGGGC[A/G]GATGAGTATTTGGATCAGATTTCTAAGGTTAGCCA
803	2	2014	12.30	89865290	F1Dsnp	PHR	T	C	2	17,257,422	+	GGGCAGCGCAGCCTGTTTATAAACATGAAGTAGCC[C/T]TACAAGAACAATGGAAAGGTAGCTCATCATGTAGC
804	2	2009	17.30	TP4059	GBS				0	9,422,760	9,422,818	TGCAGCCCGCACACAAAACCAATGAAACCATTTTTGGTCATTCTCATCATTACAAAACCTCTTG
805	2	2009	17.30	TP7157	GBS				0	9,714,318	9,714,381	TGCAGGTAAAATGCTGTTGAACCACGTTTTTGAACTCAGCGCCAAGCAAAACATTTCCCAAATT
806	2	2009	17.30	89809438	F1Dsnp	PHR	A	C	2	2,337,342	+	ATACCACAATGGCCAACTGCGATCCAATATAACAA[A/C]ATGATCATCTGGCTCTTCCAAGTCCCAAATCTCCT
807	2	2009	17.30	89809440	F1Dsnp	PHR	A	G	2	2,368,516	+	ATGAAGCCAGGAGTGTCGTCTTTGAATCCATATGC[A/G]GCAGCATACATTCCCCTCTCCAAAAGGGAGGCAGA
808	2	2009	17.30	TP1168	GBS				2	2,373,197	2,373,260	TGCAGACCTTGTTTTTGTGATCGATGAGAAGCCTCATGATGTATACATAAGAGATAGCAATGAC
809	2	2009	17.30	89865415	F1Dsnp	PHR	T	G	2	2,418,539	+	TCTCCAGAAACCATATCGTCCCTCTTGACTTTGCT[G/T]CAGTCCAGACCGTGCCTGAGTCTCATGTATGGTCC
810	2	2009	17.30	89865292	F1Dsnp	PHR	A	G	2	17,418,642	+	AATGTTATGAGTTTCTATATTTGGTTTCGACTGCT[A/G]CTGAAGATGGAATGATGACATTTTACTCATCTGGG
811	2	2009	17.30	TP4739	GBS				2	17,441,536	17,441,599	TGCAGCGTCTGCCCCTGCCTCAACTTGGCGCCAACCTCCCCCTTCATCGTGGCCTCCGCCACGT
812	2	2009	17.30	89865307	F1Dsnp	PHR	T	C	2	18,452,770	+	TCTTTGTCAGGTTTTTTGATACCTATAAGGGACTT[C/T]ACCCATTTGCCTGAAGCACCCATATTTGTAAGAAT
813	2	2009	17.30	96_501866	GBS				2	18,477,188		CCCATGTTATCATCTCCAGTGTCTCTTCCAGCGTTCCATATCCTCCTAAAACCAAACGCAATAA
814	2	2009	17.30	89865308	F1Dsnp	PHR	T	C	2	18,486,382	+	ACTTTTCCTCTGATCTAGTCCCGGCAATTTCTTCC[C/T]CAGTGATGCCATCTCCTTTTCCACACCCACCAAGT
815	2	2009	17.30	89809362	F1Dsnp	Other	T	C	2	18,487,324	+	AGCATGCCTCAATTGGTTTCTTTTGGTAACCATTA[C/T]CTGTGAAACGAAGCTTATGTAGAAGTAGTTCCAGA
816	2	2009	17.30	96_482827	GBS				2	18,510,995		ACTTGGTGGGTGTGGAAAAGGAGCTCAGTGAYCCCTTTATGAAATTGCCGGGACTGCGTCGGAT
817	2	2009	17.30	89865309	F1Dsnp	PHR	T	G	2	18,511,366	+	ATTAGCAGTTGGTGTTTTATCTGCTTTTTCTAGCA[G/T]TACAACTCCACATTTTTCTATACTGCATTCAAGAT
818	2	2009	17.30	89809363	F1Dsnp	PHR	T	C	2	18,518,394	+	TGCCTCTGGTTTCGTTTGATCTCTTTCAGAAGCTG[C/T]TTTTCCTTGGCCAAATTCTTGCTTCCATGAACCAT
819	2	2009	17.30	316_152328	GBS				5	7,371,622		ATTAGTCTAGTTATAAACTTGCCAAATCATTGGAAGGCCGTGTCATGTGAGAGTTTATCTGCTA
820	2	2009	17.30	316_152333	GBS				6	7,583,831		TCTAGTTATAAACTTGCCAAATCATTGGAAGGCCGTGTCATGTGAGAGTTTATCTGCTATGTTT
821	2	2009	17.30	89866382	F1Dsnp	PHR	A	G	6	13,354,398	+	ATTAATAGGCAAAACAGCCGCCCTACTAATACAGT[A/G]CACCTTTCTGACTTGCACCTCCACCTTCAACAATT
822	2	2009	17.30	89866383	F1Dsnp	PHR	T	G	6	13,380,971	+	TTTGATGCATTTGCAGCCTGCATCTGGAACTCCAT[G/T]GCCAGGGAAAGATGTTGTTGTTTGCAAGTATCCTT
823	2	2009	17.30	89866384	F1Dsnp	PHR	T	C	6	13,435,275	+	CAAAACGTTTCGGATAACAGTAAACCTGAAGGAAG[C/T]GCAGAGAAATTGGTAGCAGAGGCACTACACACCAC
824	2	2009	17.30	89810425	F1Dsnp	PHR	T	C	6	13,479,729	+	AACTTTGTCCTCCAAATCTTTAAAATTGCTTTGTA[C/T]TGATTCTTGCAGTGTTAAAAACAAAGCATCATTCT
825	2	2009	17.30	89866385	F1Dsnp	PHR	T	C	6	13,562,790	+	GCGGCGGTTTTGCCCGGAGATTCGGTCGCCGGACT[C/T]GTAGTTGCAAATGGCGTCTCCAACTTCTTGAACTT
826	2	2009	17.30	TP1080	GBS				6	13,562,848	13,562,785	TGCAGACCAACAGAGTGTTGTACAAGTTCAAGAAGTTGGAGACGCCATTTGCAACTACAAGTCC
827	2	2009	17.30	89866386	F1Dsnp	PHR	A	G	6	13,564,268	+	TTACTTGGACCGAAGCTTTACCAGGTTTGATCCTT[A/G]CTGGATTTACAGAGTTGGCGGTTCTTCAAGTGGTA
828	2	2009	17.30	89866388	F1Dsnp	PHR	T	G	6	13,729,403	+	TTGCTTTGTGTATAATAGAAGTCTTCGACAATCAC[G/T]GAGAATTCAACCTCTGGACATCTACCAACTGGTAA
829	2	2009	17.30	89866390	F1Dsnp	PHR	T	G	6	13,771,181	+	GGTTTCCTAGGTGACGAAGGCGGCGCACAGAAACA[G/T]GAAGGAGGCCAAGATGGCAATAGCCATATCTAGAC
830	2	2009	17.30	96_348573	GBS				6	13,771,600		AAGAGTTTCTCTTCAGAGCCCAAAATAATGGGTTGGGCTGTTCATGTTTAACCCAATCCAGTTC
831	2	2009	17.30	TP6783	GBS				6	13,786,588	13,786,527	TGCAGGCTTTTACCTCTTCAATTTACTGAAATCCAACTCAGAAATTGGGCCGTATTTACTCATT
832	2	2009	17.30	316_152341	GBS				7	9,490,907		TAAACTTGCCAAATCATTGGAAGGCCGTGTCATGTGAGAGTTTATCTGCTATGTTTCTGCAGAC
833	2	2011	19.74	89865298	F1Dsnp	PHR	T	C	2	18,053,695	+	GTTAGCTACGAGATCGATGCCAATGGAATTTTAAC[C/T]GTGACCGCAGAGGAAAAACGACTCCGACTTAAGAA
834	2	2011	19.74	89809354	F1Dsnp	PHR	A	G	2	18,083,897	+	CTTTCTGAACCAATCTTCATTCGCATTGCATTCTG[A/G]TCTGGACGAAAGAGGAGGAGATTTCCATTTTCTTT
835	2	2011	19.74	TP1023	GBS				2	18,150,628	18,150,565	TGCAGACAGGTTGCCAATTTCCACTATATTGGTATTAAATGACAACAAACAAGTATAGCTATAA
836	2	2011	19.74	89865299	F1Dsnp	PHR	T	C	2	18,156,463	+	ATTTGAGTTCAGCTGAATTGTCATGAATTCTGATT[C/T]GTTTTATGAGCCCTGAATCCCCAAAGAAATCAGGA
837	2	2011	19.74	89809356	F1Dsnp	PHR	T	C	2	18,240,337	+	ATATGGACAGTCTGGAGCATATTCTGGTGCAACAC[C/T]TCAATATAATGCATCTCAGCCTTCTTATCCTGGCT
838	2	2011	19.74	TP364	GBS				2	18,241,771	18,241,811	TGCAGAACACAGGCAGTGTTTCATTCTCTTCCATAATCCTTTCGTTCTCTATAACAATGCTCTT
839	2	2011	19.74	89865300	F1Dsnp	PHR	A	G	2	18,247,855	+	ACTTTTAAGATAGATGTGAAGATATGAACCTTGAG[A/G]GTCATATAGTCACGACTAAGTATATGTCTTCCATT
840	2	2011	19.74	89809357	F1Dsnp	PHR	A	G	2	18,262,818	+	ATCTGCGTACATCTCCTCAATCATAGGTTTCCATA[A/G]CCGTACCCTAGCATTTATGAACCAATTCGAAACCT
841	2	2011	19.74	89865301	F1Dsnp	PHR	A	G	2	18,264,189	+	GGAGTTTTCACTCCAGGTTCCGAGGGAGCTGCTGC[A/G]TACTTGTTGAGCTCCCACTGTTGAGTATTTATGCT
842	2	2011	19.74	89865302	F1Dsnp	PHR	A	G	2	18,280,561	+	ACAGCACCGTCCGGAGGGAACCACCTTAAAAGTAC[A/G]CCAAGGTGCACTAAACCAGGGATTAGCTTAAATAG
843	2	2011	19.74	89865303	F1Dsnp	PHR	A	G	2	18,302,807	+	TTCATGCTCAATGTCGTTTGCGCTTGATGGCCTTG[A/G]GGGAGAGATGGTGTTTGGTGAGGCTTCAACGGCAC
844	2	2011	19.74	89809358	F1Dsnp	PHR	T	G	2	18,304,459	+	TTATGACAGCTTCAAAGACTTCAATGCAGTATCCA[G/T]TGACATTACTTGTGTTAGTGCCACGATCATATGTT
845	2	2011	19.74	89865304	F1Dsnp	PHR	A	C	2	18,304,518	+	CGATCATATGTTACATTTACAAATTCTTTGAAACC[A/C]CTCTTCACTGGGACTAAAACTTTTAGTTTCATTCC
846	2	2011	19.74	89865305	F1Dsnp	PHR	A	G	2	18,329,058	+	TTCCGTTTTTGCGCAGATGCAGCTTTCCCAGATGC[A/G]CCTGATGAACTTTCACATGATTTACTTTTAAGAGG
847	2	2011	19.74	89865306	F1Dsnp	PHR	T	C	2	18,330,943	+	GGATCGGAAGCGCTAATCGCAAGCGCCAACTGGAC[C/T]TGAAACTCCTCCTCCAAGAAATTGAAATCCACGCC
848	2	2011	19.74	89809359	F1Dsnp	PHR	A	C	2	18,367,470	+	TGCAGAGGATCGACTCGATCATTAGGTACAAGGAC[A/C]TGATCAGCAGAGGCAGCGACAAGTGATTATCATTC
849	2	2011	19.74	96_587786	GBS				2	18,381,667		AGGCTTTGAATGCGAGCAAGGGAAGAGTGTCRTTTGGGGTTGGGTTGGAGAGAGAAAGAGATAA
850	2	2011	19.74	89809360	F1Dsnp	PHR	A	G	2	18,389,115	+	AACCTCTTACACCCTAACAACATGAATGACTGAGC[A/G]AAAAGATTAATCCTAGCAAAACACATGACAGGGTA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
851	2	2011	19.74	89809361	F1Dsnp	PHR	T	C	2	18,400,751	+	ACGACTTTGTTCAGCTGTCCCAACTCTGATCTATG[C/T]CTTGATACCTGTTGTGAAAAGAAAATGAAAAACAC
852	2	2004	22.18	6_858910	GBS				2	17,486,472		ACGCCACCGCTTCTGCTGCTGACAACGGCGCKTCCGAGACCGCCGAGACTGGTAGCCCCGCGGC
853	2	2004	22.18	TP2230	GBS				2	17,486,537	17,486,476	TGCAGATCTACTCCAAGGAGATCAGCAAGCGCATGCTCGATGTCGTCAAAGCTAAGAACGCCAC
854	2	2004	22.18	89809344	F1Dsnp	PHR	A	G	2	17,500,543	+	TAATTCAGCTTTGGTAAGTCTTGCTCATTCATTAG[A/G]CGATGTTCTCCAACCTTTGCGTCTATCTCAGTTCG
855	2	2004	22.18	89809345	F1Dsnp	PHR	A	G	2	17,502,108	+	GGTGTAATATTTCTCTTCTGATTCTTGCAGTGACA[A/G]TAGGTTATCAATCATCAACTTACTCCTAACCTTAT
856	2	2004	22.18	89809346	F1Dsnp	PHR	T	C	2	17,542,840	+	TGCTCTACTGATGGTACAATACATGTCTGCAAGGT[C/T]GGAGAGAACCAACCAATCAAAACTTTCTTAGGCCA
857	2	2004	22.18	89809347	F1Dsnp	PHR	T	C	2	17,609,873	+	AACAATACCGGAATCCCACTGGAAAGAGTTATTAC[C/T]TTGTCGTCGGTTCGTGCTCCTAAACTAGCCGGTGA
858	2	2004	22.18	89809348	F1Dsnp	PHR	A	G	2	17,670,540	+	TTTTATTTTGCTTCATGGGTGCAGATGACATATTT[A/G]GAAGAGTGTTCCCTTCTGGATCGGGATTACTCTAA
859	2	2004	22.18	6_704083	GBS				2	17,676,231		AAAGCTTGATAATCCAACGGGTAAGACCCCARAAAGTCGCACGWTTCAACGGCCGGATCAAGGT
860	2	2004	22.18	89865293	F1Dsnp	PHR	A	G	2	17,775,510	+	ATTTGTGGCCTGATGCAGAAATATGTATCAACAAA[A/G]CCAAGCTGATTGAGTTTTATTCTCCCCAAAGTTGG
861	2	2004	22.18	6_583665	GBS				2	17,775,842		TCAACCAAGCCTCATGGTTTGTTGGTTCTAAYCGCAGAGCATTCATTAAAAAGCTTCTTGCAAT
862	2	2004	22.18	89809349	F1Dsnp	PHR	A	G	2	17,787,347	+	TCTTTACGAGTCTCATGATAATGTTCTTGGCATTG[A/G]AATGAAGAAAGAATAGTTCCACTTGGCCAGGAAAA
863	2	2004	22.18	89865294	F1Dsnp	PHR	A	G	2	17,824,804	+	TACAATTCATTTGAGGGAGTACTTTACTGCAGGCC[A/G]CACTTTGACCAACTCTTCAAAAGAACCGGGAGTCT
864	2	2004	22.18	89809350	F1Dsnp	PHR	A	G	2	17,835,947	+	GTTTTCGCTGTGTTGGTGGAGTTGTAAGGATTCAG[A/G]GTCTTGATCATGGTTGCGAAATTCTCTAGTCTCTG
865	2	2004	22.18	89865295	F1Dsnp	PHR	A	G	2	17,853,727	+	ATAAATTCAAAATTCTTCCTACCAAAGAGTTTCTT[A/G]GTTTGGCTGTCTGTCCACTTGCGTTTTAATTTCCC
866	2	2004	22.18	89782212	snp	PHR	A	C	2	17,951,703	+	CCGTCAGCAGCATGTTCTTCCAAAATCTTGCGAAA[A/C]TCATCCCGGTTTTTCCTCTCAATCCGCCTCAATTG
867	2	2004	22.18	89809351	F1Dsnp	PHR	T	C	2	17,953,408	+	CGCCTCTCTTCATTCTCCAGCTTTTTCCTTTGGCC[C/T]AAGTACTATAAATAAACCAATTGTTTAGTTTTAGG
868	2	2004	22.18	89809352	F1Dsnp	PHR	A	C	2	17,988,274	+	TCTGCAGACATCACCAGCATGGGAGATGGCAAGCT[A/C]GAATTGGGAGGGTTGCAGGAAACAAGGACCTTTAT
869	2	2004	22.18	89865297	F1Dsnp	PHR	A	G	2	18,007,304	+	TTACCCCATAGCGATGGAAACTCAGGGAATGAGTA[A/G]CACTTCCCACCTTGTTCAATATCCATCTGATTCGA
870	2	2004	22.18	89865346	F1Dsnp	PHR	A	G	2	19,940,765	+	ACATTAGTCCTAATTGTTTCAGTCTTGTGTGACTC[A/G]CACCAATCAACATTAGGCCGTCCAGTAAGTCCAGC
871	2	2004	22.18	89809389	F1Dsnp	PHR	A	G	2	19,941,392	+	TTATGAAGAATCACATCAAATGCTTCAGCAACATC[A/G]TCACAATACAAATAGCTTCGAACATTTGATCCATT
872	2	2004	22.18	89865348	F1Dsnp	PHR	A	C	2	19,956,910	+	CTTCCCAAATCTACTCTCAATTTGCCTTCTTCTAC[A/C]AGAACAGTTAGATCACTTGATGAAGTAGAGGCCTT
873	2	2004	22.18	89865349	F1Dsnp	PHR	A	C	2	19,988,004	+	GGCTTGGCTGTGATCATTTGCAAAAACATTATTCC[A/C]AGAGAGTACACATCAGACTTCACGCCGAGCATGCC
874	2	2004	22.18	89865350	F1Dsnp	PHR	T	C	2	19,990,071	+	TTCATTACAGTGCCTGGAATATCTGATTGTTTGAA[C/T]CTGCACAAGTTTTTGAAAAGTAGTTAAACATATGT
875	2	2004	22.18	89809390	F1Dsnp	PHR	A	G	2	20,005,649	+	GTCTTCACAATATCTGCCAGGCATGCGATAACCTG[A/G]TCCCCTTGACGTCTAACTAAATCAGCTCGGAGGTC
876	2	2004	22.18	89865351	F1Dsnp	PHR	A	G	2	20,092,263	+	TCATGGATTCTGGGGTTGCTGAAGATCTTACCGGC[A/G]TTACCTTTTTGAGGAATGGAACCGGGATCAGTTAC
877	2	2004	22.18	11_369028	GBS				2	20,110,189		ACTGGATATATATAAAAGCGAGTCCTGACTCGGTCTTATATGCATGTACCTAAGCTGCCCTAGG
878	2	2004	22.18	89865352	F1Dsnp	PHR	A	G	2	20,124,962	+	ATCTTCGCGAATTCCAAGAAGGAAGACGCGATTCA[A/G]AACCAGTACGAGTTTTTCGTGCAGAGAATGGGAGG
879	2	2004	22.18	89865353	F1Dsnp	PHR	A	G	2	20,146,609	+	TTCAGGCATGAGCAGCGGTAAGGCTGATCCTGCTC[A/G]TGGTTTGCAAATTGTTGGTATGAGTGCCACTATGC
880	2	2004	22.18	89865354	F1Dsnp	PHR	T	C	2	20,152,087	+	TTATAGACACCTCATTTTTATTGTTGCCACCAGTT[C/T]ATATACAAGATGGCATTGACATGTGCATTGTGGCC
881	2	2004	22.18	89809391	F1Dsnp	PHR	T	C	2	20,155,270	+	TATCCATGGACTAATGTCTTTCTTTTACAGGGATC[C/T]GCTGCTGATATAATTAAGATTGCAATGATAAATAT
882	2	2004	22.18	89809392	F1Dsnp	PHR	A	C	2	20,204,176	+	TGCTTCAGACTATAAACACTTCTATTGCCAGTATA[A/C]TGAGCCATCTTATGTCAAAAAATTGAAGCTTGAGA
883	2	2004	22.18	89809393	F1Dsnp	PHR	A	G	2	20,216,689	+	AATGCTGTTGTTAATGCTTTTTCTGAAGCTGGGAA[A/G]ATGGAGGAAGCAATGGATGCGGTTAGGAAGATGAA
884	2	2004	22.18	89865355	F1Dsnp	PHR	A	G	2	20,217,823	+	TCTACTCTCTTGCTTGTTGCAGATGCTTGGCGTTC[A/G]ATTGGATTAACAAAAGAGGCAAACAGGATACTGGG
885	2	2004	22.18	89809394	F1Dsnp	PHR	A	G	2	20,219,775	+	ACAATAAAAGTTGAATTTCACTGTACCTGAAATAT[A/G]TGATCAGCCAAGTATACCCCAATATTAATGAGAAG
886	2	2004	22.18	89865356	F1Dsnp	PHR	T	C	2	20,248,919	+	GAGTTTCTGAAGAAATCGATAAGCGAAAGCGAGGA[C/T]GGGATGATCAGCTTGGCGTTGATATGCTCGTTCAG
887	2	2004	22.18	89865357	F1Dsnp	PHR	T	C	2	20,278,482	+	ATTGCCGAAGGCCCTAACATGAATGTGGCTTTTGT[C/T]ACAAAAGATAAGGAACTTCTGATGCCTCCATTTGA
888	2	2004	22.18	89862952	ins	PHR	-	ATAT	2	20,325,111	+	ACTTAGTTAAGGAAAAGAAGAGATGTGTCATATGC[-/ATAT]ATACTGCATGTCATACAGTTTATGAAGTTATAATT
889	2	2004	22.18	89809395	F1Dsnp	PHR	T	C	2	20,334,411	+	ATTTCAATCCCGGAATTGTAACTCGATGTGCTTAT[C/T]AGCAATGAGTTTCCTGTAGTAGTAGCAGGACATGC
890	2	2004	22.18	89865359	F1Dsnp	PHR	T	C	2	20,337,736	+	AATGACTAAACTGGAAGTTACCTCCACTTCTCTCG[C/T]AGTTCTTTCTTCTCGGATAAAATCCAGGTTACAAA
891	2	2004	22.18	89809396	F1Dsnp	PHR	A	G	2	20,338,933	+	TCAACCATAAACAAAGTAGAGAGTAAGCTTACAGC[A/G]TGGACAGGTCCCTGTGCACCATGATGGGTCATCCG
892	2	2004	22.18	89809397	F1Dsnp	PHR	A	G	2	20,341,174	+	CAACAAATCCTAGTACATAGATTGCATCACTTCCA[A/G]CAGGTTGAATAATATGTTGGACCTCTAGACTGAAA
893	2	2004	22.18	89809398	F1Dsnp	PHR	T	C	2	20,375,095	+	CCGGTGGACATGGAAAGTGCTTCTATTGCCTTGAT[C/T]TGTCTTCAACAGAATGTGCCTTTTATAACCATTAG
894	2	2004	22.18	89809399	F1Dsnp	PHR	A	G	2	20,379,782	+	ACACGTTCAATGCTCTTGCTTCCCATAATTCAGCC[A/G]CAGTTGTTGTTGAGTTTATCAAACAGTTAGCAGCT
895	2	2004	22.18	89809400	F1Dsnp	PHR	A	G	2	20,386,076	+	AATTTTGTTTATAGGTTTTCTACGCAACATATTTT[A/G]CCAAATGGAGATTTCATCGTGGTTGGAGGCCGTCA
896	2	2004	22.18	89809401	F1Dsnp	PHR	T	C	2	20,432,124	+	CCAGTGAGTTCAAAACTCTTCTTCCACAGTTGAGA[C/T]GGCACCGGAACAACAGAGAACCCCAACCCGACCAA
897	2	2004	22.18	89865360	F1Dsnp	PHR	A	G	2	20,467,466	+	TCCGGGGATGCTTCCTACAGGCGTCGAAGTCCATA[A/G]AGAAGGCAATGGTGAAATGGAAGATGAAGATGACA
898	2	2004	22.18	TP8329	GBS				2	20,547,776	20,547,839	TGCAGTCCAGCGGTCTAGTTTTGCTTTACGGAGGAGAGGGTAAAACAGACGCCAAATAATCACA
899	2	2004	22.18	89865361	F1Dsnp	PHR	T	C	2	20,566,209	+	AATGCATGTGATGATAAAACTTGAGCGTAGACGAG[C/T]CGATGTAGTTCTGCTATACTAATTCCCCCCAAGTT
900	2	2004	22.18	89865362	F1Dsnp	PHR	A	G	2	20,570,549	+	TGCGGTTCTCGAGGGAGAAGGCGAGCGGCGATGCA[A/G]AGACGACCATGGAGAGATTGGCAAGGTACAAGAGG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
901	2	2004	22.18	89865363	F1Dsnp	PHR	T	C	2	20,713,702	+	CCATTTATTTCAATCTCGCATGTTTCCTTGGATTC[C/T]GAGAAAGATACAGCAGATGGATGTACCAACTCCTT
902	2	2004	22.18	89809402	F1Dsnp	PHR	T	C	2	20,713,737	+	CGAGAAAGATACAGCAGATGGATGTACCAACTCCT[C/T]ACCCTGTTGTGAAGGCTTTACCCCATTCCACACGC
903	2	2004	22.18	89865364	F1Dsnp	PHR	T	C	2	20,742,425	+	GCTATTCCGAGTAATGCAGCTGACAATGTCTACTG[C/T]ACACTGCTGGCTCAAAGTGCCGTTCATGGAGCAAT
904	2	2004	22.18	89865365	F1Dsnp	PHR	A	G	2	20,742,488	+	GGAGCAATGGCAGGGTTCACGGGCTTTGTAGTTGG[A/G]CCTGTCAATGGAAGACATTCTTACATTCCTTTTAA
905	2	2004	22.18	89782694	snp	PHR	T	C	2	20,746,502	+	GCTAGTACTATTAATGTGAAGTTTTTGAGCTCAAC[C/T]GCAGTTGGTGTCACGCTATATTTCTTGTCCGGGTT
906	2	2004	22.18	TP2233	GBS				2	20,820,192	20,820,149	TGCAGATCTATGTAAGCTGCTTCGGTTGTAGTAGTTTTGTGTGTGTAAATATGTGTCTAATATT
907	2	2004	22.18	89809403	F1Dsnp	PHR	A	G	2	20,858,531	+	ATCCTAACATGCCCTGGGATGAAGCTCAACTTTGG[A/G]TTGGGTATATAGCAGATAATGGGTAAGCACAGTTT
908	2	2004	22.18	89865367	F1Dsnp	PHR	T	C	2	20,889,015	+	CATCTCTTAGAGAGTGGAATAACAGTATGGATATA[C/T]AGGTGAGAACCATGAGAAGATCCTTGAATTGATTG
909	2	2004	22.18	89782728	snp	PHR	A	G	2	20,891,895	+	GGAGACATTGATCCTTACAACATCTACGCGCCAAA[A/G]TGCGACATGTCATCTGGAACCAAAGTCTCAGAAAC
910	2	2004	22.18	89865368	F1Dsnp	PHR	A	G	2	21,049,162	+	GAAAAGGAACTGATGAAATACCTAACTCATCCCCC[A/G]GTTCACCCTCAGGTTTATCGTCATGTTCATTGTTA
911	2	2004	22.18	89809405	F1Dsnp	PHR	T	C	2	21,106,499	+	ATAGAAAAGGAATTGTCAAAGGTTTCCAGATCATC[C/T]CGAGGACCAGGGGTGTCTCAAAATATTATGGTATT
912	2	2004	22.18	89821689	snp	PHR	A	G	2	21,155,003	+	ACATACCTAACAAGGAAACCAGTGAAGGGGACTTC[A/G]AAGATCCGTTTGATCTCATGTCTGTACCTGCACGG
913	2	2004	22.18	89809406	F1Dsnp	PHR	T	C	2	21,176,724	+	GGAGCCAATACCAGCCTTGCCAAATTACTCTGGAC[C/T]CGTTCTCCTGCATATTATAGTTGCATGTTAAGACA
914	2	2004	22.18	TP1745	GBS				2	21,186,307	21,186,266	TGCAGAGGCAGCTGCCCCTGACCAAACCCATCTTGACCTCCGAGATCGGAAGAGCGGTTCAGCA
915	2	2004	22.18	TP7169	GBS				2	21,285,686	21,285,749	TGCAGGTAACTATGTACTTGGCGCAAGTCATTTCGGATACGCAAAAGGCACAGCAAGAGGGGTG
916	2	2004	22.18	89809407	F1Dsnp	PHR	T	C	2	21,287,281	+	GTATAACCACATCGTATCAAGCCCTGTAGTAGCAA[C/T]CAACTACTAGTAGATAGTATCAGCATTTCCATTGA
917	2	2004	22.18	TP3991	GBS				6	30,167,313	30,167,359	TGCAGCCCAAAATCAATGTCACGTGGCGACCCAGGTCTCACCTATAACCCGAGATCGGAAGAGC
918	2	278	24.65	89809387	F1Dsnp	PHR	T	G	2	19,918,674	+	CGATTCGACTCGGATTCAGCTCAATGTCTCAACCG[G/T]CATCGGAAGCCAATCCGGACACCTCGAAACCGGAG
919	2	278	24.65	89809388	F1Dsnp	PHR	A	G	2	19,927,151	+	CTGAAATAATGTTCTGTTTTGTAGGATGAAGCGCA[A/G]AAATCTAGTGATGCTGGTCTCTTCCCTGATGTCAT
920	2	276	27.09	89809385	F1Dsnp	PHR	A	G	2	19,872,764	+	GACATAACAGAAATTCTCAATCTTGAAGCTAATTT[A/G]GATGCCTTGAATCGTCATGAGGTTGGAGAGGTAGA
921	2	276	27.09	89809386	F1Dsnp	PHR	A	C	2	19,872,831	+	TAGATAAGATTGAGAGTATTGAGGAGGACAACTGT[A/C]AAGACCTTCCGGACCCTAAATTAGCTGAAGAAGAT
922	2	276	27.09	89865345	F1Dsnp	PHR	T	C	2	19,883,907	+	AAAGATTCTCCCTCTCCTGTGTTACTGAGTCCAAA[C/T]TCCCACTTAAGTTTGATATTTGACCCTGTAGAGTG
923	2	2007	29.52	89865334	F1Dsnp	PHR	T	C	2	19,537,365	+	ATACAGCTAATTTGCAACTACTACACCTTGAGACA[C/T]GATGGATCCAGAGCATACATGAGATATTGGAATTT
924	2	2007	29.52	89865335	F1Dsnp	PHR	A	G	2	19,552,975	+	GGTTGTATGGCAGCAGCGTATGTAGGATTTGTGTA[A/G]CCAAGACCAATAAGAAACAAAAGCTGGTTGCCAAA
925	2	2007	29.52	89809379	F1Dsnp	PHR	T	G	2	19,571,184	+	GTGGCCCTCCATGACATTCTTTTCAATTACAGGCA[G/T]GACTATTTCTCTGAGGCAGAACCAGCTGTTGCAGA
926	2	2007	29.52	11_733781	GBS				2	19,575,589		GTATCTGACAATGACATGTACGCTTCTCTCATCAACGATTGTTCCGACTCCGGCGCGGCTCTCC
927	2	2007	29.52	89809380	F1Dsnp	PHR	T	G	2	19,615,745	+	CATATGGTCCAGAACTTTGCAAAACTCTGTCAGCT[G/T]CTAGGTTTCAAGGCATAGCTGGACATTTCAGTGTT
928	2	2007	29.52	89865336	F1Dsnp	PHR	A	G	2	19,640,131	+	GGATAATAAATGTCAACGGTCGTGGAGCAAGAACA[A/G]TTGGATTTTGGACACCACAACATGGACTTGTTAGC
929	2	2007	29.52	89865337	F1Dsnp	PHR	A	C	2	19,641,250	+	AGATGTTGAAGCAAGTAGGTTTTGAAGATTCCAAG[A/C]TTCGGGATTTCGGGACAATGGAAGCAATTCACGAT
930	2	2007	29.52	89809382	F1Dsnp	PHR	T	C	2	19,658,299	+	AACCACACTGTTTTTGTTTCAGATGAATGAGGTTC[C/T]CCTTCTTTATCTCCATTCATTGAGGCCTCGCTCTT
931	2	2007	29.52	89865338	F1Dsnp	PHR	T	C	2	19,660,305	+	GGCTTCTGTCTCGACTCTCTTACTCTCCACAACAA[C/T]ATCAAGCTTCTTTAGAGGAACATCTGGCGCCCATA
932	2	2007	29.52	TP1882	GBS				2	19,664,119	19,664,182	TGCAGAGTGATTTGATGTATAACACTCGTCACTAAGGGGTTGGAGACGATGGAGTGAAACATCA
933	2	2007	29.52	89809383	F1Dsnp	PHR	A	C	2	19,683,535	+	ACCAAACCCAACCCACCCAGCTTACAATGGAAGTT[A/C]GCACTTGTCTCTCTTCGTCTTCCTCCGCCAAATTT
934	2	2007	29.52	89865339	F1Dsnp	PHR	T	C	2	19,683,674	+	GGGGAAGAGCAGAGCACTTGTTGCTGTGAGCTCAG[C/T]TTCATCCATTGCCAGCACCACCACTAGTGTCAGTA
935	2	2007	29.52	89865340	F1Dsnp	PHR	T	C	2	19,723,506	+	TTCCTCCAAGACTTCCACCCCATTTCTTCGCAAAT[C/T]TCATCACTGTGGTTGATGCTGAAAGTAGAAATGCA
936	2	2007	29.52	89865341	F1Dsnp	PHR	A	G	2	19,744,449	+	TTTCCCCCTGAATGAATGTTGTTTGCAGACCAAGG[A/G]TAAAAATCCCTGCAGCTGTTATGATGCCAATTGCA
937	2	2007	29.52	89809384	F1Dsnp	PHR	A	C	2	19,748,367	+	TGTGTTTTGGTTTGAGGATTTGAAGTAATGGGTGG[A/C]GTGGAAGTGATAAAGAGCAAAGGCTGTTCTAGACT
938	2	2007	29.52	89865342	F1Dsnp	PHR	T	C	2	19,762,134	+	CTGAGGTTTACAAACAGCTTTGTGGTCCACGTGTT[C/T]TAGTAATGGAGTGGATAGATGGTATCCGGTGCACT
939	2	2007	29.52	TP5474	GBS				2	19,776,028	19,776,091	TGCAGCTGTGATGGCCATATGGTTAGGTGACGGGCATGGTTTCTGGCGATAATAGCGCATAAAT
940	2	2007	29.52	89865343	F1Dsnp	Other	T	C	2	19,788,172	+	GATCCCATCTCCGAGTATCAGACCATTCCTCTCAA[C/T]AAAATTGAGGACTTTGGTGTGCACTGTAAACAGGT
941	2	2007	29.52	89865344	F1Dsnp	PHR	T	C	2	19,850,216	+	CCTGTTGTCCAAACATTGTCTAACATTACAAGGAT[C/T]TTCTTGCTGCCTTGAGATAGTCTTTGACGTAGCAT
942	2	2006	31.96	89809368	F1Dsnp	PHR	A	G	2	19,186,159	+	AGATGGTAGTGGTAATATCACATTTGAAGAACTAA[A/G]AACTGGATTGTCAAGACTGGGATCTAAGCTTACAG
943	2	2006	31.96	89809369	F1Dsnp	PHR	A	C	2	19,211,702	+	GGAAGCCTCATCAAAATGGGGTGAGGACAAGATTT[A/C]TGTGGTCGTTGAAAGCAAAAGGGACAGAATCAAAG
944	2	2006	31.96	TP5908	GBS				2	19,238,702	19,238,765	TGCAGGAAGCGCTATCGATCGCAGATAACGTGGAGAGACGAAAGAAAGAGCACTGAGATATTGG
945	2	2006	31.96	89809370	F1Dsnp	PHR	T	C	2	19,243,212	+	GCTTTTTCTACAACAGATGGCTACTCCTTGGATGT[C/T]TTTGTCGTTGATGGTTGGGAATGTGAGGTATCACC
946	2	2006	31.96	89865326	F1Dsnp	PHR	T	C	2	19,243,218	+	TCTACAACAGATGGCTACTCCTTGGATGTCTTTGT[C/T]GTTGATGGTTGGGAATGTGAGGTATCACCTTACCT
947	2	2006	31.96	89865327	F1Dsnp	PHR	T	C	2	19,263,058	+	TTATATCAGCAGTTTTACAGTTGATGGTGTCTCCA[C/T]TGTTGTCAGTACTGGAGATCTCGGCAGTCTTTCCA
948	2	2006	31.96	89865328	F1Dsnp	PHR	A	G	2	19,281,795	+	AAATGTTTCACTATCATCAGCAACAAGTATCCCCC[A/G]GTCAACATAATAAAACTCAGAATCACTAAATCCAT
949	2	2006	31.96	89809371	F1Dsnp	PHR	T	C	2	19,286,874	+	AAGATGCTCCAAAATATAAGTTGGTCCGAGTTGAT[C/T]TGAAGGAACCAACTGTTTGGACTGACGTGATTAAA
950	2	2006	31.96	89809372	F1Dsnp	PHR	T	C	2	19,287,050	+	AAATCAGGTAGCTTGGTGCATCAGTTGCCCATTGA[C/T]ATTGGCACAGTTACTGGGATTTCTGCAAGACGAGA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
951	2	2006	31.96	TP7057	GBS				2	19,298,151	19,298,111	TGCAGGGTAATATATCAAACAAAGGTGAAAGAAAGAAGCCGAGATCGGAAGAGCGGTTCAGCAG
952	2	2006	31.96	89865329	F1Dsnp	PHR	T	C	2	19,302,010	+	TCATCAACTCTAAGAATCATCTCCGCAGCCTCTGT[C/T]GCAGAGAGCAAGACGGCTTGCTTAACTTTAAACGC
953	2	2006	31.96	89865330	F1Dsnp	PHR	T	C	2	19,305,076	+	CCAACAAGGACTTTAGCAGCTGCATTGTCAATATG[C/T]AGGGACTTTAAGATGGTAGCCCCATCATTGGTAAC
954	2	2006	31.96	798_19605	GBS				2	19,311,012		TCTTTTTGCTTATTACCAAAAGAACGAAGAARAAATAGAAAACGTCAATTTTTTCCGGTGGGGG
955	2	2006	31.96	798_19520	GBS				2	19,311,089		ACGGACATTAGGTTTGTGGTTAATCGAGAATGTCTGACGCCTCTGCTGGATTCATTCACATGCA
956	2	2006	31.96	89865331	F1Dsnp	PHR	A	C	2	19,320,696	+	GTTTGTGAGGTATTTCCTTTGTCATCTTGACATGG[A/C]ATTTGTCCACTTGAAAGAGAATCTCTGGCTTGGAA
957	2	2006	31.96	89809373	F1Dsnp	PHR	T	G	2	19,382,517	+	GACAGGCCTGATGTTGCTGGGAGAGTTAAGATCCT[G/T]CAGGTTAGTTAATTCTATCAGTTCTGTGAATTCAG
958	2	2006	31.96	89809374	F1Dsnp	PHR	T	C	2	19,403,252	+	GGACTGTTCAAGAAAAGATCCGAATTCGGATACTC[C/T]CTCAGAATCTTCTCCACTATCGACGGCCCGGTAAG
959	2	2006	31.96	89809375	F1Dsnp	PHR	T	C	2	19,417,085	+	TTTGAATAGAAGTTGGGGAATAGTGCTTTAAGGGG[C/T]GCCAATGTTTCTTCCCCTCCATACACTTCCCCGGA
960	2	2006	31.96	TP9366	GBS				2	19,421,100	19,421,147	TGCAGTTCTCACCGTCCGCTTTAAGCTTTAGGATTTCCGAAAGTATTGGATTCTTGTGGAGATA
961	2	2006	31.96	89809376	F1Dsnp	PHR	T	C	2	19,484,981	+	AATCTCATTCATATAAAGATTCTGAGATTAGTAGG[C/T]GTTATAGAAGGGAGATGAGCCGAGACAGTTCTGCT
962	2	2006	31.96	89865332	F1Dsnp	PHR	A	G	2	19,510,345	+	GCAAAACTCATTTTCCTGTTATTTGTTGTGGCAGC[A/G]CGAGCTTATTTGCTGGGATATAACTGTGCGGATGA
963	2	2006	31.96	89865333	F1Dsnp	PHR	A	G	2	19,513,500	+	TGCATACAGAATGCAGAGATTTATATGTTTGATGA[A/G]CCTTCAAGTTATCTTGATGTGAAACAAAGGCTCAA
964	2	2006	31.96	89809377	F1Dsnp	PHR	A	G	2	19,517,065	+	CTAGCTTCTGTGCTTCCGGTCTTCAAGACTTCTAT[A/G]ATAGCTGGTATGGCGTCTTCTCTGGTTATGAGCTT
965	2	264	34.40	89865320	F1Dsnp	PHR	T	G	2	18,954,757	+	AACGAGAAATGCTCCTAACCTCAGCTCCTTAACAA[G/T]AAGCATCAGCTGCGTAGGATCTTGACTATCCCAAT
966	2	264	34.40	89809367	F1Dsnp	PHR	T	C	2	18,957,628	+	AACTCCAGTGCCTTGAGAAATGAAGCACGCCACTT[C/T]AGCATTGGCTACCAATTTATAGACTACCTCTTTCA
967	2	264	34.40	89865322	F1Dsnp	PHR	T	C	2	19,006,773	+	CTCTGTTCACTGATTTGCAAATACATAATGCAGAT[C/T]AAGTTAGACAAAGAGAAGAGAATCCTCTCTATTCG
968	2	264	34.40	89865323	F1Dsnp	PHR	A	G	2	19,007,864	+	CACCCCCTCTGAGGAAGAAACTGAAGAGGACGCTG[A/G]GAAAAATGAAGATGAAGATGCTGAGAAGAAACCAA
969	2	264	34.40	89865324	F1Dsnp	PHR	A	G	2	19,008,861	+	AATATACAAGATTCTGGAATGAATTTGGCAAGTCT[A/G]TTAAACTTGGTATTATTGAAGATGCGGCCAACAGA
970	2	264	34.40	89869691	codon	PHR	A	G	2	19,009,322	+	ATTTAATTGTTGCAGGTTATCTTTTTCACCGATCC[A/G]GTTGATGAGTATTTGATGCAATACTTGATGGACTA
971	2	264	34.40	89865325	F1Dsnp	PHR	T	C	2	19,056,385	+	AAACGTGACAGACTGGCCGGGAACTTTCCGGTGAG[C/T]CCGATTCCGTTGAGGCCCAGATACTCCAAGCTCAG
972	2	264	34.40	89821117	snp	PHR	A	G	2	19,130,958	+	TCAACTCCCTGCAAGAACAAAGCTCTCACTTATGG[A/G]TCTTCACCAAGTGCCCAAGTTATCTAGTGAGCATG
973	2	2005	42.22	89865310	F1Dsnp	PHR	T	C	2	18,681,368	+	GACATGAAGCCCCATGGTACAAACTTTGAGGAGTA[C/T]GGGAAGTTGTGTCGAGAAAGGACAAACAAGTCCAT
974	2	2005	42.22	TP7569	GBS				2	18,696,749	18,696,686	TGCAGGTTCTGTCCCTCTCTTCAGCGCCATCAACGCCCTCATCCTCGTCCCTATCTATGAAAAA
975	2	2005	42.22	16_1198141	GBS				2	18,699,917		TAACTCGTATGAGTTCTCTTGGGTCCACCTGTATGCAATGTTTTGGGGACCAGAGTGTACAACT
976	2	2005	42.22	89821010	snp	PHR	A	G	2	18,736,224	+	AGGACCCACGAGTTTCTGCAACTGAAAATGCCTCC[A/G]AAAATCAAAGCAAGGTTGATGACAAACTGGATGAT
977	2	2005	42.22	89865311	F1Dsnp	PHR	A	G	2	18,738,242	+	GAGAAAAGGAGCCAAGTGTAGCAGAGAATCCAGTC[A/G]TCCCTCATGGATCACAAGTTCAGGTGGGTGGTTCT
978	2	2005	42.22	89865312	F1Dsnp	PHR	T	C	2	18,738,859	+	AGGAATGGGAAGAGACGCAATTCATTTGGTTCAAC[C/T]AAACCTGATCAGGCTGATCAAGAGCCAAGAGATAG
979	2	2005	42.22	89865313	F1Dsnp	PHR	A	C	2	18,738,949	+	CCCCGTTTCATGCAAGTCACAGAGTCAGCTAGAGC[A/C]AAGCTTCAACCAACTACCTCCCCCAGATCGAGTCC
980	2	2005	42.22	89865314	F1Dsnp	PHR	T	C	2	18,762,591	+	CAACAAGCCAGCTGTTTCTCTGACTTTGTCTTCAT[C/T]AGAAAACCATTCTTCCTGCAGTTTATTGACATTCC
981	2	2005	42.22	TP5895	GBS				2	18,762,611	18,762,566	TGCAGGAAGAATGGTTTTCTAATGAAGACAAAGTCCGAGAAACAGCCGAGATCGGAAGAGCGGT
982	2	2005	42.22	89865315	F1Dsnp	PHR	A	G	2	18,767,527	+	GAGTTCATGTGCCCCATCTCAGGAACCCGGATAAA[A/G]GGTCTTTTAATCATATTGGCCCACTCAGTTTCTGC
983	2	2005	42.22	89865316	F1Dsnp	PHR	A	G	2	18,767,959	+	TTGGAACCAGGCCATCTCAGTGGATCGAGATCACT[A/G]ATATTAACTATTGTACCCATATATCTGCACAATTT
984	2	2005	42.22	TP2671	GBS				2	18,784,310	18,784,367	TGCAGCAAAACCAAACCTCTCAACCAAAACGCAGAGCTCACCGTCGTTTCACGCCAGAAACAAT
985	2	2005	42.22	89878178	snp	PHR	T	C	2	18,893,642	+	TTGCCACAGAAGGTGGATGCGCAAATGTCACATAT[C/T]TCTTCTTTTGGAATTCAAGTCCAACATCATTCATA
986	2	2005	42.22	11_1400972	GBS				2	18,902,795		ATCACAAGCCCAACTTCCTTATCTTCATTCTTCTGTGCAGCATCACAATCTCATTCCTTTCTCT
987	2	2005	42.22	89865319	F1Dsnp	PHR	A	G	2	18,904,085	+	TTAATTTGAAAAATACCGACCGACTGTCCAGGCTT[A/G]ACTCAGATGGATCACGGAAGTTGACAGCATTGCCA
988	2	307	44.66	89809434	F1Dsnp	PHR	T	C	2	22,693,947	+	AGTATACAGTGTGATTTTCCAGGATTCCTTTGTTC[C/T]TTTGGCATTAAGCTGGGGACCTTTCTTCTAGTATC
989	2	307	44.66	89865405	F1Dsnp	PHR	A	G	2	22,694,418	+	AAAAGTGAGCTCAGGCCATCATAGTATGACTTATC[A/G]ATCTCATCTTTGAACATGAGTTCCTCCTCATTTGT
990	2	307	44.66	89865406	F1Dsnp	PHR	A	G	2	22,701,593	+	CTGTACGAATCAAAAATCGCAATGTTTCAATCATC[A/G]TCCTCACTGCTGAGTAATGCAAATGAAAAAGGGTA
991	2	2017	47.13	16_1064920	GBS				2	22,618,051		ATGCTATTGTCCGATTCTGCAGAGTGTCCCARATCCGCAACTCACCGTCTGCTGAACTGAAACA
992	2	2017	47.13	89865402	F1Dsnp	PHR	A	G	2	22,618,082	+	GCTGATGCTGTTGTCCGATTCTGGAGAGTGTCCCA[A/G]ATCCGCAACTCACCGTCTGCTGAACTGAAAATAAA
993	2	2017	47.13	16_1064956	GBS				2	22,618,087		GCAACTCACCGTCTGCTGAACTGAAACAACAACAAATTTGATCAAACAGATGAATTCAATTGAC
994	2	2017	47.13	89865403	F1Dsnp	PHR	A	G	2	22,623,704	+	GCGTAACAAAGTCAAAGTCTCCACATCAAATGGGA[A/G]TATCTTTTGTGGAGATGCAGTCTTGGTTACAGTGC
995	2	2017	47.13	89809431	F1Dsnp	PHR	A	G	2	22,624,551	+	CTGGCCAAAGAGTTGTTGACTCTTCCTGCTGAAAC[A/G]TTGAAGTCCTTTGCTGGCACCAAAGAGGGGCTAAC
996	2	2017	47.13	89809432	F1Dsnp	PHR	A	G	2	22,653,148	+	GAGAAGTTGACCGGAATGTCACCGGTGAATGCATT[A/G]TACGAGAGATCAAGGTACCGGAGGCTCGCCGGAAT
997	2	2017	47.13	89809433	F1Dsnp	PHR	T	C	2	22,665,864	+	TCTCTTGAAGGTGAAGGTATGGTTTTAAGTGCTTG[C/T]GAGTATTATAGAGAGGCTGCTATACTTTGTCCGAC
998	2	2017	47.13	89865404	F1Dsnp	PHR	A	G	2	22,666,587	+	GACGTACCAGTGTCGTATTCAGGTACTGGTGCTCC[A/G]CAGAGGTCCATACGGAAGCCTAATCTGGAAGAAAT
999	2	2017	47.13	16_1129858	GBS				2	22,671,308		TATGAATGAATCAGAGAAGGTTTGCTTGGAATTTGTGAACAGCTGATAGGAGCACAACTGCAGA
1,000	2	2017	47.13	16_1130744	GBS				2	22,672,241		ATTAGTTGTGCTTATATTTGGTTTAAGATTGAGCAGTTTTTGATTCTATATATTTGTTTTGGTT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,001	2	2016	49.59	TP8767	GBS				2	22,537,194	22,537,131	TGCAGTGCAATTCAGGAAAAATTGAAGGTACTTGTGCTTGTTTCTCGGTCACATTTTCATACTC
1,002	2	2016	49.59	89809430	F1Dsnp	PHR	T	C	2	22,543,403	+	TGTAAACTACGTGAAGGTCTGGGTGTTGCAACCAA[C/T]AATGTTGCCGAGTACCGAGCTGTTATTTTAGGGTT
1,003	2	2016	49.59	89812770	codon	PHR	T	G	2	22,569,219	+	ATTTGGATCAAGGAAAAAGGTTTACATACTCGATG[G/T]GGGGAAGTGCCTCCATTGCCTCCATGCTTAACAGA
1,004	2	2016	49.59	1155_3031	GBS				2	22,569,410		GTTCTTTTACCACCCCACAGGTAACCTGCCCAAAAAAAACAAAATTACTTACATAACAAGCAAC
1,005	2	2016	49.59	TP1928	GBS				2	22,579,004	22,579,067	TGCAGAGTTGCAGAATTATACATCAGAAAAGCTCAGAGCTTCTTCTTCTTCTACACATTACACC
1,006	2	2002	54.60	89865386	F1Dsnp	PHR	T	C	2	22,105,372	+	TATAATGCAGTTCGAGGAGAATGGTGAATCAGTTG[C/T]GTACGCATTACAACAAATGTGTGCTCATTTACGGG
1,007	2	2002	54.60	89809420	F1Dsnp	PHR	T	C	2	22,121,637	+	TGCACGAAGCTTTTGTTGGGATAGAATTGGGATGC[C/T]ATTTATTTTAAGTGACAGCAACTTGTTCTCATCAA
1,008	2	2002	54.60	16_579376	GBS				2	22,136,570		TCCAACAACTAGGGGTTCCACACAAATGGGCSGCCGTTGTCTGGCTGTGCGGGCCCATCTCAGG
1,009	2	2002	54.60	89809421	F1Dsnp	PHR	T	C	2	22,137,150	+	ATGGTTATGGTGTCTGTACGTGAGAAAACGATGCC[C/T]AGTCGTGATGACGAGAAAGGCGAGGGAGGAGTGAG
1,010	2	2002	54.60	89809422	F1Dsnp	PHR	T	C	2	22,143,414	+	ACACTTTCTCACCTTTCCTTCAAGGACCCATTGTT[C/T]GACCTTCTTAATTCCCATGGTGGCAAGCAGCCTTT
1,011	2	2002	54.60	89865387	F1Dsnp	PHR	T	C	2	22,143,540	+	ATAGAAGACAGGCAACTGAAGGCACTTCTCAAACT[C/T]CTTTTCTCGCTATCATATGGTTGGTTGTTAGGGTC
1,012	2	2002	54.60	89865388	F1Dsnp	Other	A	C	2	22,150,792	+	AGGAAGTTTGCAATTCCTCATGCATTATAGGTGTG[A/C]TTATAGTTGCTTCACTCCCTGGTTCACTTGGACTT
1,013	2	2002	54.60	89865389	F1Dsnp	PHR	T	C	2	22,172,394	+	GACTACCACCTAGCTTAACCCCTGTTAGTGTTACC[C/T]TATTTATCGTTGGGACTGGAGGGTAAAGCCGCATC
1,014	2	2002	54.60	89865390	F1Dsnp	PHR	A	G	2	22,172,569	+	ACATTCTCAGACTTCAACCTCAAAAATGAACTTGC[A/G]ATCTTGAGGTTGTTCAAATTCTGTGCGATTGGAAG
1,015	2	2002	54.60	89865391	F1Dsnp	PHR	A	C	2	22,172,747	+	GCAGAATGTCTTGCATTCATCTATGACTTCCTCCT[A/C]ATCTAATTTCTCATCCTCACCATCCTGACCTTTAT
1,016	2	2002	54.60	89821940	snp	PHR	T	C	2	22,173,438	+	TTGGGTTGCAATCCTCCGGTGAAGAGCCCATTTCT[C/T]GCCGACCAACCCAGCAAGTCCCTGACCAAACAGGG
1,017	2	2002	54.60	89809425	F1Dsnp	PHR	T	C	2	22,220,065	+	AAAGCATTACAATAAAAAGCTTGATGACTTGCAAA[C/T]TGCTCTTGTGAAGCATATGGAACAGTACGTGAATT
1,018	2	2002	54.60	89865392	F1Dsnp	PHR	T	C	2	22,273,404	+	TACATGCTCTCCGGCAAACATTCGGTTGATCTTAT[C/T]TTTGAGACCAGCAGCCTGCAATTTAGCAAAGACAA
1,019	2	2002	54.60	89865393	F1Dsnp	PHR	A	G	2	22,284,497	+	CTGCTGGCTCTACCCTTTTCTGCTCCATTGTGGCC[A/G]CCGACTTTATCATGGGTTCTATGTGTCACTTGCTC
1,020	2	2002	54.60	TP5914	GBS				2	22,285,770	22,285,725	TGCAGGAAGCTTCAGAATATATGACAAGCTCCCAAAGGAAAAGCCGAGATCGGAAGAGCGGTTC
1,021	2	2002	54.60	89865394	F1Dsnp	PHR	T	C	2	22,299,493	+	CACTTTGATCCCACGTAATTATCACGTCGCTTGGT[C/T]TTGTGGTGCTACCTCTTAATGTTATGAATGGCTTG
1,022	2	2002	54.60	89865395	F1Dsnp	PHR	A	G	2	22,310,237	+	AATGATAATGTTAATACATCCTTATCAAGGAGAGA[A/G]GCCCCAAAAGCAGAATCAGTACATCCGATATCCAG
1,023	2	2002	54.60	89865396	F1Dsnp	PHR	T	C	2	22,311,416	+	TCATCCTCATCTTCCTTCTTCTCCTTCTCCTTCTC[C/T]GAATCCTTACTTTTCTCTGGAACCTTCTTCTTAAC
1,024	2	2002	54.60	89809426	F1Dsnp	PHR	T	C	2	22,338,101	+	TCAAAATCTGGTTCAGCTGGGAGCAACAAATCAGC[C/T]TACACTAACTCCATGGACATTGAAGACCAAAGGTA
1,025	2	2002	54.60	89865397	F1Dsnp	PHR	T	G	2	22,360,176	+	GGGGTGAGGGAAGGTGTGGTTAAGGAGGAGGGAGT[G/T]GAAGTTGGAGTGGTGGTTCTTGTTAAAAGTGGCAG
1,026	2	2002	54.60	89809427	F1Dsnp	PHR	T	C	2	22,386,047	+	GTTGCCTTGTGGGAGAAGAAAATTGGAAAAGTTCT[C/T]ACGAAGGTCTATGTTCCAGAGGACAAACTCCTCAA
1,027	2	2002	54.60	16_866356	GBS				2	22,418,456		TGCTCGAAAGCTATTTCCATAATGTAACAAATACTTTGAAGTTAAAGTTGCCATGTTCTCAAGC
1,028	2	2002	54.60	89809428	F1Dsnp	PHR	T	C	2	22,431,275	+	AGAAGCCAAGGACACCAGTCTATAAATTCTGAGGA[C/T]GATTTTTTTACCAACTCTGTTGTGAAAGGCTACTA
1,029	2	2002	54.60	89879171	snp	PHR	A	G	2	22,432,313	+	ACATCCAAGATGCACAGAACATTCTTCATAAGCCA[A/G]TTCTCTTTGCTGAGTTTGGAAGGTCTTTGAAAGAG
1,030	2	2002	54.60	89865399	F1Dsnp	PHR	A	G	2	22,500,158	+	GGCGTGTTTGGGCGGATTAGTGTTGGTTGTGTTGC[A/G]TATAAACAATCTGGTAGCTCTTCTGGAGGTGTTAA
1,031	2	215	57.03	89865385	F1Dsnp	PHR	T	C	2	22,052,314	+	CAGAGTTACTAATCGTGAGGATGCCCAGGAGGTGT[C/T]CGACAATTTGCTTCAAAGGCGTTGGGTTGTGCGTT
1,032	2	2003	59.50	89878887	snp	PHR	T	C	2	21,507,636	+	AGACCAACTATTTCCCCCTCAACACCATCAATTCT[C/T]GTCTCATAAAAATCTTCCATAGAAGATCTTTTTCC
1,033	2	2003	59.50	89809408	F1Dsnp	PHR	T	C	2	21,537,184	+	CAACCCATGAGCTTCCATATGATCACTCCATACTT[C/T]TGGAGAACCTCATGGATCCAGCCCATGTTCCAATC
1,034	2	2003	59.50	89865370	F1Dsnp	PHR	A	G	2	21,551,553	+	GCACGCCACTAACCCTTGAATTGCGGAGAGGCCTG[A/G]TTCTTGAACCATAAGGTACAGACACTCTGACACGA
1,035	2	2003	59.50	89809409	F1Dsnp	PHR	T	C	2	21,557,289	+	CAATCCAATTTTGCTGCCACTTCTACATTTATAGC[C/T]CGGTAATACTCGGTCATTGCTCAATCCATTTAGTC
1,036	2	2003	59.50	89809410	F1Dsnp	PHR	T	C	2	21,582,167	+	CTTGTGAACTTGATGGTATTTTCTCCGCTGTCTAC[C/T]CGGCTGGTGGTGATCGCACTCCTTATAGCCCAGCT
1,037	2	2003	59.50	89865371	F1Dsnp	PHR	A	C	2	21,597,669	+	CCGTAATCCATAAAAGTTCGGGTAGACTTGTTCTG[A/C]GAAGTTTGCATGAGAATGATGGTGTGCTTGTTAGC
1,038	2	2003	59.50	89865372	F1Dsnp	PHR	T	C	2	21,599,629	+	TCCACTTGATAATGTCACCTAAGAAACCTCCCGCA[C/T]TTGATTTCAGAAACTGATAAACCGGAGCTGTGCTG
1,039	2	2003	59.50	89865373	F1Dsnp	PHR	A	C	2	21,609,365	+	CTAATCTTTTGCACAAAACCAGGCAGGACCGGCTC[A/C]TGTTCTCCTTAAGGCGGAGGTTCCATGGTCAGTTA
1,040	2	2003	59.50	89809411	F1Dsnp	PHR	A	G	2	21,622,224	+	CTGCAGCCGCCAACCATCATGTTCTTGTAGACTGC[A/G]TAAGCATCATCTGTATTTCCAGAAGTGCTATACAG
1,041	2	2003	59.50	89809412	F1Dsnp	PHR	T	C	2	21,624,772	+	TGAGCAGACCCATAACAGCTTGAACATCCCTTCTC[C/T]TTCCCAATGCGACCATAAGAGCTGAGTATGTCTTG
1,042	2	2003	59.50	89865374	F1Dsnp	PHR	T	G	2	21,634,509	+	TTGGTCGTCGCTCATTAACAGATAAGCATCCCATC[G/T]AGACGCCCACTTTACATCACTCTCCTAAAGAATAC
1,043	2	2003	59.50	TP3681	GBS				2	21,636,833	21,636,893	TGCAGCATGTTCGCTCCTTGTAAACTTCAAGTTATGTATATACCGTATAACAACCGCAGTATGC
1,044	2	2003	59.50	89865375	F1Dsnp	PHR	T	C	2	21,643,434	+	AAACTAGTACCTAAATCCAATGAGGATAAAGTCGT[C/T]GAAGTTTGCATGGATGATTTCCCTGGTGGTGCGAA
1,045	2	2003	59.50	89809413	F1Dsnp	PHR	T	C	2	21,644,412	+	CATGGATCCTTGGTGGGTGTTGGTAGACTGATTGA[C/T]GGGTATCTTGCCGAAATTGCACATGACCCTAATCT
1,046	2	2003	59.50	89782856	snp	PHR	T	C	2	21,644,480	+	TCTTAACCTTGGTAGTTTCATAGACTTGTCACAAT[C/T]GCTTCCCGAGTTAGCGAGGCCAATTCATGATGGAT
1,047	2	2003	59.50	89865377	F1Dsnp	PHR	T	C	2	21,722,509	+	ACCGATTTCACGGCTATATCTTGACCCACTACCCT[C/T]TTATGAAGTACCTGTTCTAGCATGACTAGCTTGTC
1,048	2	2003	59.50	89865378	F1Dsnp	PHR	T	G	2	21,736,671	+	AACCTCTGAGACGGACTCGTCGAGAAGGTGCTTGA[G/T]GGAGCTGTGATCTGAGAGATTGACCTTCTTCGGCT
1,049	2	2003	59.50	89865379	F1Dsnp	PHR	A	G	2	21,743,728	+	GTTTGGCAATCGTTCTACTTGCCCTGCTTTTTGCT[A/G]TTGCTGAGCTCCGTGGTTTCTTTTTCGGCTCATTA
1,050	2	2003	59.50	89809414	F1Dsnp	PHR	A	C	2	21,810,221	+	TTTTGGAATCCAATCTTTCAGTGTCAGCCTTGGCC[A/C]AAAAAAGGTCACTAACTTTCATTTCACCAAGGCAC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,051	2	2003	59.50	89809415	F1Dsnp	PHR	T	G	2	21,824,505	+	TGGAGTTCATTGGTTCTGAGGGAGGAGACTGGTGT[G/T]GCGAAATGGAGGCCAACGCTGTAGATCTTATTGAT
1,052	2	2003	59.50	89809416	F1Dsnp	PHR	A	G	2	21,843,059	+	ATGGAGTGTTTGAGTATAGACATTACAAGTGGAAA[A/G]CCCCTTGCGAAAAGACCAAGACCAACCACACACAC
1,053	2	2003	59.50	89809417	F1Dsnp	PHR	A	C	2	21,870,030	+	CAATCAACCTCAATTGCACCCTCCATTATATCAAG[A/C]ACTAGAATCTTGAAGATCTCATCCTTTGAAAGTGT
1,054	2	2003	59.50	89865380	F1Dsnp	PHR	A	G	2	21,878,122	+	GAATGTTAAGTAGCAGACCTTGTGATAGATGGCAT[A/G]GTAGCCACAATCCCAGCACAGATGTATATTATAGG
1,055	2	2003	59.50	89865381	F1Dsnp	PHR	T	C	2	21,878,173	+	GCACAGATGTATATTATAGGAATCAGTGTCTTAGG[C/T]TTGTTTTTGCGGAGCCACATCAAAGATCCCAATGC
1,056	2	2003	59.50	89809418	F1Dsnp	PHR	A	G	2	21,902,593	+	TATGCTTTCAGTCCTTGATGGATCTCACGTTGCAG[A/G]CTTTGATGCTGATACCGTCGTGAAGGCAACATGTG
1,057	2	2003	59.50	TP3087	GBS				2	21,906,269	21,906,332	TGCAGCACCATTATCAGCACAGCACGAGTTCACTGAGGACTGCACAGTGAATGGCTATCATGTC
1,058	2	2003	59.50	89865382	F1Dsnp	PHR	T	G	2	21,906,419	+	CAAATGTGGCCCGACCCATTAGAGTTCAAACCGGA[G/T]AGATTTCTCACCACCCACAAGAACATTGATGTTAG
1,059	2	2003	59.50	89865383	F1Dsnp	PHR	T	C	2	21,918,385	+	TATAAAAAAGCATACAAAGTAAGATCTCCCACTTT[C/T]CAAACTCTATTTGACGAGTATGCACAGTCTGATCG
1,060	2	2003	59.50	89809419	F1Dsnp	PHR	A	G	2	21,984,645	+	GGGAAAGGGGAGCTAACAATGGCCACCACTAGATT[A/G]TTGCGCACGTTTAAGCCTATGACTATTCATTCCTC
1,061	2	2003	59.50	TP7703	GBS				NGH			TGCAGTAAACGTGCCAGCGTGAGGTGAAGAACTTGCAGCGCAAACGACACACCTGGACAGGACC
1,062	3	3007	0.00	89879639	snp	PHR	T	C	2	3,038,028	+	GTGGTTGGTCGGCATCGCCATGGCTTGCAGTACGG[C/T]GGCGAGATACCAGAAGCAGTCTTCACTGCATCTTT
1,063	3	3007	0.00	TP3267	GBS				3	1,289,780	1,289,843	TGCAGCAGATCAACTAGATTGTTAAGATATGGGAATCATATGTCCTCACTTGCATCTTTTTGGT
1,064	3	3007	0.00	89865479	F1Dsnp	PHR	T	G	3	1,291,295	+	GACCTTAAACTCGGGGTCTATATGAAGATTCCGCC[G/T]CGGTGCATGTACACAGCTCAGGTCTTTTTCATTCT
1,065	3	3007	0.00	TP345	GBS				3	1,291,910	1,291,973	TGCAGAACAACAACATTCTTGTTCATTGGTGGGGGAGTGAACTTGATCATTGCCCATTGGCATC
1,066	3	3007	0.00	89809521	F1Dsnp	PHR	A	G	3	1,313,622	+	GGTAAATCAATGTCACAAACTGCAGGGTTGAAACT[A/G]TCGGAGATCGACATGAAGCTGGCTGAGATTAACCA
1,067	3	3007	0.00	89865482	F1Dsnp	PHR	T	C	3	1,314,165	+	TACTTGAAGGATGCGTCCACATCCAATGGTGCTGG[C/T]ACATCTTTGTCCCATCAGGCTAATGCTGTTGCTGC
1,068	3	3007	0.00	TP7408	GBS				3	1,314,227	1,314,161	TGCAGGTGATCACCATTTGCCAGTGCAGCAACAGCATTAGCCTGATGGGACAAAGATGTACCAG
1,069	3	3007	0.00	89865483	F1Dsnp	PHR	T	C	3	1,320,461	+	GAGGTTGACTGATAGAGTTGTTGAGGTTCGAATGT[C/T]GGTCCTTGAACATGTTAAGAGCTGTATGCTGTCAA
1,070	3	3007	0.00	89865484	F1Dsnp	PHR	T	C	3	1,323,895	+	GCACATTTAAGGCTCGCTTCTGCAAAAGCCGTTCT[C/T]CGTCTTTCAAAGCACTGGAATCATAAGATACCTGT
1,071	3	3007	0.00	89865485	F1Dsnp	PHR	T	C	3	1,333,468	+	AAGAGGAATCATGATGATCAGCACTCTTTCATGCT[C/T]AAGCATGGATCACTCTTGGTGATGAGAGGTTATAC
1,072	3	3007	0.00	89865486	F1Dsnp	PHR	A	G	3	1,342,536	+	TTCAAGCCAGTCATATCTAAAACTTTCACACACGT[A/G]GTAATAGGCTTACCATACTTCTTCGACGCAGAAGG
1,073	3	3007	0.00	89865487	F1Dsnp	PHR	A	G	3	1,350,222	+	TACAAAAAGATTCCAAAAGTCCACCAGTCAACAGC[A/G]CTTCCATGACCTTCACCCTTGATAATCTCAGGCGC
1,074	3	3007	0.00	89865488	F1Dsnp	PHR	T	C	3	1,355,770	+	ACTGCATCACGATTGGTTGCAATGAAAAGGCATCC[C/T]GGATTTTCACGTATACAAAGGGTTCCATACCTGCC
1,075	3	3007	0.00	89865490	F1Dsnp	PHR	T	C	3	1,408,871	+	ACAGCTAGTGATGAGCTATCTGGGAAGGTCTCTCC[C/T]GCAGATATCGAGTATTTTGAAGAGGTATCTGGAAA
1,076	3	3007	0.00	89865491	F1Dsnp	PHR	T	C	3	1,409,370	+	GTCATACACATCAAGGGAAGAGGGGCTGGTAGTTT[C/T]GGAGCATACTCAAGTTCAAAGCCCAAATCTTGCTT
1,077	3	3007	0.00	89809526	F1Dsnp	PHR	A	G	3	1,415,158	+	CAAGGTAAGTGGGTTCACTCCCATATGATCAAATC[A/G]GGTGTTAACCTTGTTGCTTTTGTTGGGAATACTCT
1,078	3	3007	0.00	89865492	F1Dsnp	PHR	A	C	3	1,426,720	+	TCATAATCTTGGGTCTTCTTATTGCAAATAGAGCA[A/C]GTGAAGCCATCAAACTCTTCGATTCAATGCCTTGC
1,079	3	3007	0.00	89865493	F1Dsnp	PHR	A	G	3	1,435,660	+	ATGCAGAGCGAAGATATATGGCCATGCTTGAGAGA[A/G]CTTGTAAGATGCTTGCTGATCAATTTATTGGAGGT
1,080	3	3007	0.00	89809530	F1Dsnp	PHR	A	G	3	1,440,295	+	TCGACTCCAGATTCTGGTTGTCATGTTATTTCTCC[A/G]GCTGAGAGCCCAGACGCAGAGAGGTCGTTGAAGAA
1,081	3	3007	0.00	89865495	F1Dsnp	PHR	A	G	3	1,446,047	+	TTTGATGGAAGAAGAATTAAAGCGGCTTCATTTGC[A/G]TCTGCCCTACATCCACTGCATTATAGTTGAGAGTA
1,082	3	3007	0.00	89809532	F1Dsnp	PHR	T	C	3	1,466,976	+	CCTTGGAACCTTTATAGCTTCTGTTGTTACTGGTG[C/T]TCTAGTGTATGTCTTCTGTTTTATCATTCATAATA
1,083	3	496	2.47	89809519	F1Dsnp	PHR	T	G	3	1,279,499	+	TTGTGCTCAAGGTTGATATGCATTGTGAAGCTTGC[G/T]CCAGGAAAGTTGCTAGAGCCTTGAAGGGTTTTGAA
1,084	3	TP6259	7.47	TP6259	GBS				3	1,277,332	1,277,394	TGCAGGATCCAAAGCTGATCCTGTGCATGTTTAGGCTAGCTGATCGGGTCATGATTCATCTTTG
1,085	3	495	9.91	89809514	F1Dsnp	PHR	T	C	3	1,217,738	+	AGTCGAGTAGCAATTAGTACCTCAGCAAGATCCAC[C/T]GCAAGGCATTGGAGCTGGCCAGTGAGAGAAGTGAC
1,086	3	495	9.91	89865478	F1Dsnp	PHR	T	C	3	1,217,906	+	AACAAAATCGTGCTCTTCAACGATTTGATTTCCTC[C/T]CTTTGCTTCAAACACAAGTCCTTCAATTTTTCCAC
1,087	3	495	9.91	89809516	F1Dsnp	PHR	T	C	3	1,238,828	+	ACAAAGTCTTCATCCGCCTCTTTTGTCACCTTGCA[C/T]GCCTCAAGAAGTTCTAGAGTATCATTTTCCCTTTT
1,088	3	498	12.35	89865476	F1Dsnp	PHR	A	C	3	1,195,845	+	GGCATGGACACATCATGGGGTGCGCTGATGAACAA[A/C]GTAACCAAAACTCCTAATCAGGCTCATTTACCAGC
1,089	3	498	12.35	89865477	F1Dsnp	PHR	T	G	3	1,201,655	+	AGCTTGCTCTATCTGGGCCAAACTACGAGCCCGAA[G/T]CAGCAAGGTTGCCTTTCCATCCTAATGCTGATGAT
1,090	3	3014	14.81	89809507	F1Dsnp	PHR	T	C	3	1,063,588	+	AATGCACGAGTTCAATGACCTGAAAATGAATGTTT[C/T]TTGCAAGAACTTAGGTACAAGAAAATGCATTGATG
1,091	3	3014	14.81	TP3969	GBS				3	1,070,768	1,070,831	TGCAGCCATGTTTACTGTACTGATTGCGTGGTGAAATACGTGGACTCTAAGCTCCAAGAGAATA
1,092	3	3014	14.81	89809509	F1Dsnp	PHR	A	G	3	1,094,293	+	CTACTTCTCTTAGTTGGCTCAAGGCACCCTTGACC[A/G]TGTCATACTTGCTCTGAAGATTCATCGAGTTGGCA
1,093	3	3014	14.81	1_2326216	GBS				3	1,137,887		CATACACGATGTTCTCCGCCGCATGACTTTTCCAAGGCATCATTCGAAGCCACGCAAGCTCCCG
1,094	3	3013	17.25	89865787	F1Dsnp	PHR	T	C	3	973,644	+	CTTTACATGTATATCCTCTATTCCCCAGATTGGCA[C/T]TATCGCAGTACAATGCCGACCTTCCTCTTCCTATA
1,095	3	3013	17.25	89865788	F1Dsnp	PHR	A	G	3	973,824	+	ATATACACACAGGACGTGTATGCCAAGAGGCTTGC[A/G]AAGCTCTATGTGGCCACTCTTCTTATAGGGAGTTT
1,096	3	3013	17.25	89865462	F1Dsnp	PHR	A	G	3	1,004,296	+	TGGACAAAAGCAGTTGTCATTGAATGGTGTCACTC[A/G]TAAATTCCTTGAAGATGGAGATGAAGTCATCATCA
1,097	3	3013	17.25	TP4030	GBS				3	1,005,505	1,005,443	TGCAGCCCCACGATCCGACGGCTCACCTTCCGCCTGGCCTCCCTTACCGCGGGGTCCACCCCGA
1,098	3	3013	17.25	89809501	F1Dsnp	PHR	T	C	3	1,027,121	+	CCCATTTTCTTATAACACTATCTTTAGCGGAGACA[C/T]GACTGTATGCTTCTTTCTTTGAGATACTATCAAAA
1,099	3	3013	17.25	89809502	F1Dsnp	PHR	T	C	3	1,027,157	+	GACTGTATGCTTCTTTCTTTGAGATACTATCAAAA[C/T]CAGCATGAGCATCTGTCCTCCTTAAGATTTTGTTG
1,100	3	3006	19.77	1_2128493	GBS				3	897,986		CACAATCTAGCTCAAAAATTGAGGAATCAGACAAATAAAGCACCCAGCTTCGGACAGTGTTGAA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,101	3	3006	19.77	1_2135225	GBS				3	900,701		TGTCAGTCGATGCAGAAGCAAGTTCAGTGTTGGACAAGAATTTCACATAGGAAACAGCTTTCCC
1,102	3	3006	19.77	89865779	F1Dsnp	PHR	A	C	3	906,748	+	CTGGAGTACTTACCAAAGTAAGGAACCCTCGCAAT[A/C]GTTTCCAGTACAAAGAACCTCGCATAATCACGGTC
1,103	3	3006	19.77	89865780	F1Dsnp	PHR	A	G	3	906,796	+	AAGAACCTCGCATAATCACGGTCATGGTAAAGAGT[A/G]TCAAGTATCTTAATCACTGTATCCTGAAACGATCA
1,104	3	3006	19.77	89809824	F1Dsnp	PHR	A	G	3	937,194	+	CATAAGCTTGATATCAGTGATGAATTCAAGCGTGT[A/G]ATTGCATCTCTACGTGGGCATGATGACAAGATTCG
1,105	3	505	37.74	89865751	F1Dsnp	PHR	T	G	3	771,647	+	TTACTCAATGCAACCCTGGTTGTTCCCAAATTTTT[G/T]TATAGTAGTATATGGAGAGATGTAAGGTACTATTT
1,106	3	505	37.74	89809801	F1Dsnp	PHR	A	G	3	778,438	+	AGAATATCCGGCTTTAGTACATCAGCAGGCTTCCT[A/G]GCTCTGTCTATGATATTTGGTCCTCTTGAAGAGAA
1,107	3	3008	40.28	89865708	F1Dsnp	PHR	T	C	3	569,293	+	AAGATTCCGGTTCCTTTCCCTAATCCTGCTGGAGA[C/T]CACACTGTACTAGCTGGTGACTGGTTCAAAACTAA
1,108	3	3008	40.28	89809750	F1Dsnp	PHR	A	G	3	569,707	+	ACATATAGATTTAGGATATCAAATGTAGGGCTTAC[A/G]ACATCCCTTAACTTCAGAATTCAAGGGCATAAGAT
1,109	3	3008	40.28	TP9367	GBS				3	576,971	576,919	TGCAGTTCTCATAGCTTGATCAGCTTGATCACCAAATGACGAGTAGCTTGGAGAATATACAACT
1,110	3	3008	40.28	89809755	F1Dsnp	PHR	T	C	3	578,306	+	TTGCCATAGCACTCATAATAAACTGGAAGATTTAG[C/T]AACAGGAGCCCATATTGATGCCGCAATGTCTCCAT
1,111	3	3008	40.28	89865722	F1Dsnp	PHR	A	G	3	616,409	+	CCATTTGACGTTGTCTAACTTGCAGGGTTATTCCT[A/G]GTCGTCTTGCATATGACACAGAGACTATGCCGGTA
1,112	3	3008	40.28	89865723	F1Dsnp	PHR	A	C	3	616,612	+	AGACAACATTCTTTCTCTAAAGAAACAATTCGAAG[A/C]GTTTCGTATCATGTATGATCAAGTACTTGCAGAAA
1,113	3	3008	40.28	89809771	F1Dsnp	PHR	A	G	3	632,940	+	TCACCACTCACCGAAAAATAACACTTGTTGGAAGG[A/G]ACCCACAGATTAGAGCTGCCAGTGTCAAAAATCAC
1,114	3	3008	40.28	89865726	F1Dsnp	PHR	A	G	3	645,634	+	CGGCAACATTCCGATTAACTACCCTTTCGGCATTG[A/G]TGAAGGCTGTGGCAGCCCTTATTACAGTCACCTTC
1,115	3	3008	40.28	TP8890	GBS				3	647,925	647,988	TGCAGTGGAAGCATGTGTGATATCAACGAGGCCATCAGCTCCACGAGCCAAAAAGCAATGATCA
1,116	3	3008	40.28	TP8239	GBS				3	647,928	647,865	TGCAGTCACCGTCACTAACAACTATTTTTCCCAGCACGACAAGGTAAGCAAGAAATAGCTAGCA
1,117	3	3008	40.28	1_1898745	GBS				3	647,978		AGCAATGATCAACCCAAACATGCGAAGAAGCAAAGATACTAATGGAATCACCGTCGCTCCCTAG
1,118	3	3008	40.28	89809774	F1Dsnp	PHR	T	C	3	650,992	+	TGATTCTCCCAGATGTTGCAATAGGCTATTAGTTG[C/T]TCCAGATACTCTACATCCTTGTCAAGGTTCTTGGT
1,119	3	3008	40.28	TP2757	GBS				3	658,532	658,595	TGCAGCAAATCTCAGTGTACTTGCACTTGTAACCGCACATCCCGCAGTTCAATCTATCAGTCTT
1,120	3	3008	40.28	89809776	F1Dsnp	PHR	T	G	3	662,856	+	ATGGATAGCAAAAGGCCAAGACCTTGATCTCTTTC[G/T]TCAAACAAATGGTGTTGGCCAACCCATGGTTTTCG
1,121	3	3008	40.28	89809777	F1Dsnp	PHR	T	G	3	667,626	+	AAGACTGCTAATGGTTTGAGAATCAAAACATATGC[G/T]AGGGATTCAAAACCCTTGAAGGCTTCAAATATTGT
1,122	3	3008	40.28	89865730	F1Dsnp	PHR	T	G	3	670,627	+	GCTGGAAACTACGTGCAATTGGCGCATACCTTTGC[G/T]TCGATGAACAGATGGGACGACGTTGGTGAAGCATG
1,123	3	3008	40.28	89865736	F1Dsnp	PHR	A	G	3	701,404	+	TCATAGGATGCCAGCCTTTACTTTCTGTTTTATTT[A/G]GAGAGTTGTTCCACAATGTATAAGTTAATGTCCTT
1,124	3	3008	40.28	89865738	F1Dsnp	PHR	A	G	3	708,705	+	ACTGGAATAGGTTCCCCCCAATAACGTTGCCTAGC[A/G]AAAAGCCAATCCCTCAACTTATAGTTCACCTGATA
1,125	3	3008	40.28	89865740	F1Dsnp	PHR	A	G	3	709,699	+	TATTACGTTGCTCCAAAGATGGTGTCCGGTCTGGT[A/G]GTGTAGATTGTAATCTTTATGTCTCTCTCTTGTCC
1,126	3	3008	40.28	89865745	F1Dsnp	PHR	T	C	3	719,268	+	TTGTCCTTCCCATCCTCATCTGATTGGTCCTGCAG[C/T]AACTCTTCCTTTTCATGCTCTAGTAACTCCGAGAA
1,127	3	3008	40.28	89865748	F1Dsnp	PHR	A	G	3	753,534	+	GGGGTTTTAGAACTGAAAGCAATTTATCAGACTTT[A/G]TCCACTCATGGTTTGCTGAAGTCAGTAAATTGAGC
1,128	3	3008	40.28	89865750	F1Dsnp	PHR	A	G	3	763,597	+	ATATTGGTCGTTGATAGGATACATGGAAAGAACGG[A/G]TCAGGATCAATTAAAAGAATAAAATCACCTATCAC
1,129	3	3008	40.28	1_2031411	GBS				3	766,650		GCTTCAGTGAGCTCTTCTTGGTCCACAACTTYAGTGCTGCGGAGGCGTCCGATAATGGCCTCGA
1,130	3	3008	40.28	TP1893	GBS				NGH			TGCAGAGTGGCCAAAGTATTTTTCGACGCTGAAAATACAAAGGATCATGTAATTAATTAAATTT
1,131	3	507	42.84	89809718	F1Dsnp	PHR	T	G	3	476,437	+	AACAATGGTGTTGATTTGAATGTGGCTTGTGAGGA[G/T]GAGGCGTGTGCTACCGAAGATTCTGAGCAAGGGGA
1,132	3	507	42.84	89865688	F1Dsnp	PHR	T	C	3	476,791	+	GATGATGAAGAAGAGTACAGGAAATTTCTCACCGC[C/T]GTTTTACAGGGTCGAGAAGGTGATGACCAGTTGAC
1,133	3	507	42.84	89865689	F1Dsnp	PHR	T	C	3	477,005	+	CTAAGACTAGGCAGAATAGAAAGTCCTCCGCTCGA[C/T]CTAGGAAGAACTTAGGACAGACAAAGAGGTCATTG
1,134	3	507	42.84	89809721	F1Dsnp	PHR	T	C	3	477,595	+	CTTAGTTTGATTGGGAGATACATGGATGATATTGA[C/T]ACCGGTATGTTAATGAATGTCTCTACTATCTCTTC
1,135	3	507	42.84	89809725	F1Dsnp	PHR	A	G	3	490,668	+	ATACGTGATGGACTTTGTCTTTTCTGAGAGTGAAG[A/G]AGGCGGACTTTTTGATAACAAAAATGAAATGGATT
1,136	3	507	42.84	89809726	F1Dsnp	PHR	A	C	3	492,809	+	ATCTGAGACTTATTCTAAGGAGATTGCTAGAAATC[A/C]TGCAGTAGCTCCGCACCTCTACAAGTTCCATGGCA
1,137	3	507	42.84	89809729	F1Dsnp	PHR	T	G	3	503,641	+	GTTAATATTTTTCCTTTCAATACCACAGCTACACT[G/T]GGGACAATCCTGTCTAGACACCGTGCGAAACCGCG
1,138	3	507	42.84	89865698	F1Dsnp	PHR	T	C	3	524,023	+	AGAAGCTCCTCCGTTTTTAACGGAAAATTGTCCGT[C/T]AGCCAAACGGAAGGTCTCAGGCTCTTCACGTACTC
1,139	3	TP3055	45.41	TP3055	GBS				3	370,092	370,029	TGCAGCACATATCCACCGAAAACACTACATTATGAGTCATGAAGAGCTCCAACAACCCATCTTA
1,140	3	1_1627828	47.97	1_1627828	GBS				3	364,775		AGCTGAGTATAGAAGAAGGCCTTCAAATTTGCGGATTAGAATACGGAAATTGAAGGTTAAGTTC
1,141	3	3009	53.61	89809715	F1Dsnp	PHR	T	C	3	47,063	+	ACTGAGAACTGTCCATGCATTGCATACTCTGGAGA[C/T]ATATAACCACTTTAAACCAACAGCATCCATAAAAA
1,142	3	3009	53.61	89809778	F1Dsnp	PHR	T	C	3	67,041	+	CCATTTCTGGCTATAGTAGACACACATTCTTGGCA[C/T]TTTTCAGGGGTCACATCGCCACGGCAACTAAATGA
1,143	3	3009	53.61	89809804	F1Dsnp	PHR	A	G	3	79,522	+	ACTTGTGCTTGATAGGTCTGGTGTGCACTGCACAA[A/G]GCTGTACAACTGCTGAAAATCTGTGAAATTTTCTT
1,144	3	3009	53.61	89865778	F1Dsnp	PHR	A	G	3	89,927	+	GTGTTCTGGTTGTCACAAAATATCCTTGCCATTCC[A/G]AAGTCTGATATTTTTGGAACCATTTCATGGTCCAA
1,145	3	3009	53.61	89908206	mSNP	NoCls	C	G	3	90,407	+	TCTTGATAGTCTTTTAATCGCAACTTCTTTCCCAT[C/G]TAGCCAACCCTGAGAGTATTTCCAAAATTGTTACA
1,146	3	3009	53.61	89809524	F1Dsnp	PHR	T	C	3	140,513	+	CGCTTACTATTCCAGGTCGAAATCTTGAACCTAAT[C/T]GTCGACGTTAAATCTAAGCGAAACACCACGTTCCC
1,147	3	3009	53.61	89809525	F1Dsnp	PHR	T	C	3	140,615	+	CGTTGGCTACTTACCGTCAAGCTGGCACCTGTAAA[C/T]GATCCATCTACGGTTGTTGTGTTCTTGGGACCTTG
1,148	3	3009	53.61	89865507	F1Dsnp	PHR	A	G	3	161,317	+	AGGGACGACCGTTCTTTTTCGACATCTTTTCCATC[A/G]TAAGCACATAGACCTCCACCAAACCATCATCAAAA
1,149	3	3009	53.61	TP7851	GBS				3	164,357	164,379	TGCAGTACCACGAACTAGTTATACTACTAAGCAGATACGTTATCGATTAATTATATGGAACTGA
1,150	3	3009	53.61	89809542	F1Dsnp	PHR	A	G	3	171,361	+	GAAATCAAGAAAGCTTACTATAAGCTCTCTTTGAA[A/G]CAGTGAGTCCTATTTTAATTTTTTGTTTGATTTAT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,151	3	3009	53.61	89865520	F1Dsnp	PHR	T	C	3	188,017	+	GAAGTCCTTGTAGGAAGACACAAATGGAGATTTTT[C/T]CCAGTCTGTCTTCTCAAGTCCACCTCTCGTCGCCC
1,152	3	3009	53.61	89809549	F1Dsnp	PHR	A	C	3	193,437	+	TTCGAACCAGACCTCAAGTCCCACTGCCAAATCAT[A/C]CAACTCTCACTCGGGTCTGGCCTCATCCGACCCGC
1,153	3	3009	53.61	1_1465489	GBS				3	197,885		CGCCTCCTCTCCTCCGATTTCCCTCCTCCTTRTCCCTCTTCGTCCTCCTCTAAATCTCTCTATA
1,154	3	3009	53.61	89865667	F1Dsnp	PHR	T	C	3	326,786	+	TCAAAGAAAAAGCGACTAACCATCATGAATGTCAG[C/T]GAGTTGCTGAGGAATATAATCTTAGCAAACGACTC
1,155	3	3009	53.61	89865670	F1Dsnp	PHR	T	G	3	331,960	+	AATGATCGTAGTGTGGTAATCCTGTTGGCATTCCT[G/T]TCATCTCAACTGATTGGGAAGAAAAACATGGTAAT
1,156	3	3009	53.61	89809697	F1Dsnp	PHR	A	C	3	338,913	+	CAACTTCGGCAAATGCTGGCATCCAATCCAACTCT[A/C]CCTCTGGCCCTATGTAGTGCACAATCACCTCTTTT
1,157	3	3009	53.61	TP5159	GBS				3	340,202	340,265	TGCAGCTCTAAACACGGACTTGATAATATTTGGAGCAATGCCTTCCACATTCATAAGGCATGTC
1,158	3	3009	53.61	89865672	F1Dsnp	PHR	T	C	3	348,597	+	GAAGGTGAAATGGTGGGTCGGGTGGTTTCTGGTGT[C/T]ATTGAAGGTTCATTTGATGCCGGCTATCTTCTTAA
1,159	3	3009	53.61	TP2807	GBS				3	3,314,787	3,314,850	TGCAGCAACATTTATTTTTTAGTGAACCAAATGGGCTTGGTTGGATATTCATTGGGACTGGGTG
1,160	3	3009	53.61	89866201	F1Dsnp	PHR	A	C	5	23,408	+	AGCCTCATTCAGTGTCCTAAAATCAATTTCGAGTT[A/C]AGAATTGTACTCCTGTAGACTCCTGTTGTACTCCA
1,161	3	3009	53.61	89866331	F1Dsnp	PHR	T	C	5	74,502	+	TATGGATGAAATGGGTACATTAAAGAAGAGCACAT[C/T]TGGGAATGTCAAAGGAATGATTGAACTTTTGGAGG
1,162	3	3009	53.61	89866344	F1Dsnp	PHR	A	G	5	89,352	+	GTAGCTGAGTTGATGGATTTATACCTTGCAGAAGT[A/G]GCTCCAGACTTTCATTTGAGACCTTCAAAGTTTGC
1,163	3	3010	56.15	89809609	F1Dsnp	PHR	T	G	3	2,544,827	+	TGATCAGCAGGTTGTGCTTGAGATTTAGAGGAGAA[G/T]GCACGATTGAGGATAGCAGCCAACCGGACTCCACC
1,164	3	3010	56.15	TP635	GBS				3	2,546,398	2,546,335	TGCAGAAGCTGTTGAAAATTTACTACCTCATGATGTCAATGGCGATTTGTCGGCTCTGTGTGTG
1,165	3	3010	56.15	TP34	GBS				3	2,548,274	2,548,310	TGCAGAAAACCAATAGATTATTGAGTTAGAGTTCAACATTATTGAGAAACTTATTCTTTTTCCA
1,166	3	3010	56.15	89809621	F1Dsnp	CRBT	T	G	3	2,762,463	+	AGGAAGAAGAAGAGGAGAAAGGAGGCTGAGAAGAA[G/T]CAAGGGGAGGCTTTGAGGCGTAAGCTTCTTGAGCT
1,167	3	3010	56.15	89865607	F1Dsnp	PHR	A	G	3	2,921,208	+	CGGGAATAACCCGCTACGGGTTGTTGTTTCCGGGC[A/G]TTTTTGCTGTCTCGAGTGGGAAGCTAGCATGGGCA
1,168	3	3010	56.15	89809652	F1Dsnp	PHR	T	C	3	2,921,864	+	GTAATAATCAATTTAGTAGCAAAAATGTCAAAGTT[C/T]ATTCCTGCTTTAAAGTGGTGGAGATTGGATGAAAG
1,169	3	3010	56.15	89865622	F1Dsnp	PHR	T	C	3	2,984,837	+	CCCTTATCCTGGTCCTGGTTTCTATCATTGTAGTG[C/T]GGTACTGCACCATGGTTTTGCTGATCGAAAGACTC
1,170	3	3010	56.15	89809664	F1Dsnp	PHR	A	C	3	3,030,214	+	GGGGGGAAACACATTGTATATTCGTGTTGCTCATG[A/C]CGATTTAGGTTCTCAAATTCTGTTTCTCTTTCTTG
1,171	3	3010	56.15	89865658	F1Dsnp	PHR	T	C	3	3,137,958	+	GAACTTGTGGAATGAAGGCAGGGGACTGGAGTTAC[C/T]GGACGAAGTATTAGGTGATTCATATGCATCGTCAG
1,172	3	3010	56.15	89809690	F1Dsnp	PHR	T	C	3	3,140,724	+	AGTTTCCTTCTGGCGGAGTAGATGTTTATATTCGC[C/T]TATCACACTCAGAACTAGGTAAGTGATAATACCTC
1,173	3	3010	56.15	89809691	F1Dsnp	PHR	A	G	3	3,140,942	+	TAAGTACTATTGGTTGTGTGAGTCTTTTGGCTGCC[A/G]TAGTCTTCGGTTTGCAAAGGTTCTATGCCAATCAA
1,174	3	3010	56.15	89809692	F1Dsnp	PHR	A	G	3	3,141,489	+	TAGGGGATGCTACCCGAAGGGAAGGAAATAGCAGT[A/G]AAAAGATTATCTAGTAGCTCAGGACAAGGAGTTGA
1,175	3	3010	56.15	TP2071	GBS				3	3,177,032	3,176,970	TGCAGATATACAGACCAAATAGGAATTGGTCCAAGCTCTTGTTGGGAAGGTACTCATAAATTAA
1,176	3	3010	56.15	89865666	F1Dsnp	PHR	A	C	3	3,244,178	+	ATATTCTTCTGGCAAGTATGAAACTTGGGTTCGAC[A/C]GGAAAAAAGGCATCAATCGGTTTATAACTTCTTGG
1,177	3	3010	56.15	89809693	F1Dsnp	PHR	T	C	3	3,246,656	+	TGGACATAGTTGATTCATCATTGGGTCAGTCATAT[C/T]CTACTCATGAAGCTATGAGATGCATCCAAATTGGG
1,178	3	3010	56.15	89865668	F1Dsnp	PHR	T	C	3	3,279,398	+	GCCAGCAATATTCTGCTAGACGCTTCCATGAATCC[C/T]AAAATTGCGGACTTTGGTATGGCTAGAATATTTAG
1,179	3	3019	58.66	1_565030	GBS				3	2,492,721		GCTGCATGATCCCATATCTTCTCTTTGTAACTCGCCTTTGCAAACTTCATAAAAATCTCTGCAT
1,180	3	3001	61.30	89809535	F1Dsnp	PHR	T	C	3	1,513,090	+	TATTTCAGTTCAAGAATCAAATGAAGCAAACTCCC[C/T]ACCAGATCGGCGCAGAGGTTTTAACTGGTGGCTTA
1,181	3	3001	61.30	89865504	F1Dsnp	PHR	T	C	3	1,553,324	+	TGTGTTGTCTCGTAGGTGTCCTCTTGACAATATTC[C/T]TGCGACGCGCCATTAATTCGTTCTTGCAGCGGATA
1,182	3	3001	61.30	89865505	F1Dsnp	PHR	A	G	3	1,555,710	+	CTTTAATCTGTTTCTTTATCACTTATTCCAGAAGC[A/G]GTGGTGAGGCTTTTGCTTCCAAATTGTCGTTTCTG
1,183	3	3001	61.30	89865508	F1Dsnp	PHR	T	G	3	1,644,104	+	GGAGGTGCTATTAACTGTGATGCATATCATATGAC[G/T]GATCCAAGAGCTGATGGACTTGGTGTATCCACATG
1,184	3	3001	61.30	89809539	F1Dsnp	PHR	A	G	3	1,675,858	+	AGAATCCCATGCTAATCAAACAAGTTCTTGAGTGC[A/G]TTTCGTTTGCCACATGGTTGCTGAGGCATCAACTC
1,185	3	3001	61.30	89865512	F1Dsnp	PHR	A	G	3	1,686,286	+	GCTATCGTGCATGCGACATATCCAGGTTTTTCTCT[A/G]TAGTCCACCCTCACACAAAGCAAAATAAAAGCTCC
1,186	3	3001	61.30	89865513	F1Dsnp	PHR	T	G	3	1,741,477	+	CTACTGTATGTCATTGAGGATCGGTGGGAGATTGA[G/T]CTATGGATATTGAAGGACTCTCGGAATCACCAGTG
1,187	3	3001	61.30	TP3649	GBS				3	1,747,623	1,747,568	TGCAGCATGCACTAAGCTAATAGAGATACCTCACTAGCTAATACTACTACCCCATGCCGAGATC
1,188	3	3001	61.30	89809545	F1Dsnp	PHR	T	C	3	1,822,238	+	AACATTTCAGCATCATCAGTTGTCAGTAAATGGCG[C/T]GGTATGTTAAAACTGAGATATTTTCTGAATGTTTT
1,189	3	3001	61.30	89809546	F1Dsnp	PHR	A	G	3	1,834,018	+	GGGACAAGATTAGCTAGCAGCACGGTTGTGTCATC[A/G]TCGGTGAAGACCTCATTCCCTACTGCAATGCTGGT
1,190	3	3001	61.30	89865519	F1Dsnp	PHR	T	G	3	1,846,821	+	GACGTGGAGGATAACGATTCATTCACATTCAATGA[G/T]ACATTTACAGCTCCTCTCTACCGTATTAAGGTACA
1,191	3	3001	61.30	89809566	F1Dsnp	CRBT	T	G	3	2,072,970	+	CTGCTGGTGTAGATGTTGATGTGGACTTGGTTTTT[G/T]TATTCAGTGCTATCACTACAAATGGCAATCGACCC
1,192	3	3001	61.30	89865537	F1Dsnp	PHR	T	C	3	2,094,581	+	TAGGTGGTGTCTTTACTATCAACAGTTGTGGAGCA[C/T]CTTGTTACAGGTGAAACTATGCAAATGACAACTGA
1,193	3	3001	61.30	89865538	F1Dsnp	PHR	A	G	3	2,096,192	+	CAATTGATAGATGATGTCCTTGATTTTACCGGCAC[A/G]TCAGCATCTCTTGGAAAGGGTTCTTTATCTGACAT
1,194	3	3001	61.30	89865543	F1Dsnp	PHR	A	G	3	2,121,302	+	TCCAGCATTGCATAGTACACAATCTGATCATGCTT[A/G]TACCGCCACTGCCTATCAGCCCAGTAAAAAAAATT
1,195	3	3001	61.30	1_331935	GBS				3	2,277,261		ATCTTGAAATATAGAAACCTTCAGGAAGATGRTCAATGAATTGGGGACGACTTGACTTTGGCAT
1,196	3	3001	61.30	89809585	F1Dsnp	PHR	T	G	3	2,283,314	+	CAAGAGTACCTTAGGAACAGCCAGAGCATCAAGAA[G/T]TCCAAGGAGGTCATTGATGAGGTCACTGGAGGAGG
1,197	3	3001	61.30	89809586	F1Dsnp	PHR	A	G	3	2,290,357	+	CTATGCATCCACAAGCTTCTCCATCCATGAAAATT[A/G]GTTCTGCTAGTAGTCCGGTATCTGAGGACCAAATT
1,198	3	3001	61.30	89809588	F1Dsnp	PHR	A	G	3	2,323,590	+	GGGGATTCGGGGATCACAAAAAGAGCAAATCCAAG[A/G]AAGACTGAAGGTATGATTCCCACACCAAGCATCAC
1,199	3	3001	61.30	89865560	F1Dsnp	PHR	T	C	3	2,323,707	+	ATGTATCCAAGAAGGATGCCTAGATTTATGAAGAT[C/T]TCAGGAAATGAAGTAAGAGAACCCCTAGCTACTGA
1,200	3	3001	61.30	89865681	F1Dsnp	PHR	T	C	3	4,004,530	+	TACAACATGTGGTTGGCAGCAGAAAATGGGATGTT[C/T]TTGCGTCTTACAACAGGAGAATGGATGACAACTAT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,201	3	3001	61.30	89809704	F1Dsnp	PHR	A	G	3	4,012,471	+	CCGAGGACGGTATTGCTCTTGGAGCATTGCATGCC[A/G]CCAAGAAGAACATTCTGGTGGCTTGTAGTGCAGGC
1,202	3	3001	61.30	89809705	F1Dsnp	PHR	A	G	3	4,066,670	+	TGATCAAGAAGACTTTTCTGTTGAGCTTTCAAAAT[A/G]GTATCCGCAAAGCGACTCTTCAGCATGGCAGCACG
1,203	3	3001	61.30	TP2376	GBS				3	4,098,096	4,098,159	TGCAGATGGCAAGCTATCGTACGTCCAAGAACGAAGATGGTTGAGTCCAGAAATGGCTGAAGCA
1,204	3	3001	61.30	89865682	F1Dsnp	PHR	T	C	3	4,098,117	+	GTAGCAGCTGCGGCTGCAGATGGCAAGCTATCATA[C/T]GTCCAAGAACGAAGATGGTTGAGTCCAGAAATGGC
1,205	3	3001	61.30	89865683	F1Dsnp	PHR	A	C	3	4,104,496	+	CGTCTGTTGATAATGGAAATGTGTACCCAGCTTAT[A/C]TTCGCTTGCAGAAGAAATGAGACATTTCTCTGATA
1,206	3	3001	61.30	89865684	F1Dsnp	PHR	A	G	3	4,120,365	+	CATTAACAAGGGACTTCCCCATTGCTTCACTATCT[A/G]CTAATCCTGTCAATTCAGCTATCTTTGCATTCCAT
1,207	3	3001	61.30	TP6914	GBS				3	4,156,274	4,156,335	TGCAGGGCAGTTTCTGAAGCTGATTGGCTTGCTATACACCAAGTACCACCTGAAGATGCAGGCG
1,208	3	3001	61.30	89809706	F1Dsnp	PHR	T	C	3	4,168,848	+	TGCTTGCACTTGAGCTTTGGAAGTTTCCGATCTGG[C/T]CCTGAACCTGATCTTGCAAGTTCTCATCCACTGAA
1,209	3	3001	61.30	89865685	F1Dsnp	PHR	T	C	3	4,174,288	+	GAAGATTGGCTCCGTAATGCCCAGTGGCTACATCC[C/T]GCTGTCAGTTTAGCTTTAAGAGATGAAAGTCGACT
1,210	3	3001	61.30	89809707	F1Dsnp	PHR	A	C	3	4,174,321	+	CCCGCTGTCAGTTTAGCTTTAAGAGATGAAAGTCG[A/C]CTGATTAGTGATAAAATGAAACACCTATTATATGA
1,211	3	3001	61.30	89809708	F1Dsnp	PHR	T	C	3	4,176,628	+	GGCCGCTTATTTACAATTCAGGATGTGATGCAGAG[C/T]ACTGTTCGTGCATGGTTGCAGGTCTGTACGCAAAC
1,212	3	3001	61.30	192_147644	GBS				3	4,199,110		TTTGACAGCAAACCTGCAAAGTCAACCAAACMCCCATCAAAATGTAGTCACTACGCAGATAGGA
1,213	3	3001	61.30	273_124863	GBS				NGH			AAGTGCCATTCGCTTCAAGTGCTTGTAACTCCGACTGCATTGCCTCTTGCCATTCAGGCTGAGC
1,214	3	149	63.82	89865679	F1Dsnp	PHR	A	G	3	3,762,176	+	ACCAACAATTGCTCGTTCTAGTGCGGAGTCCGAAT[A/G]TCGCTCTTTAGCCCATGCAAGTGCTGAAACAACTT
1,215	3	3018	66.46	113_323342	GBS				3	4,391,336		TCAAGTGTCGATTGGGCCTATGATAATGTCAACATTGGGAATGGTCAGATGGGGAGTTGGCAAA
1,216	3	3018	66.46	89809709	F1Dsnp	PHR	T	G	3	4,392,052	+	TTCTTGACAGAGAATCCCGGTTCAACTGACTCGCA[G/T]GAAGTACAGTTGGAAAGAAAGGATTCTGATGGTAG
1,217	3	3018	66.46	89865686	F1Dsnp	PHR	T	C	3	4,393,142	+	AGAGCTCTTCAAGATCATCTGGCCGAGTTAGCTTC[C/T]TCTCCACAATCATCTCAACCATGGAATCTCTGAAG
1,218	3	3018	66.46	89809710	F1Dsnp	PHR	T	G	3	4,396,922	+	TACTTGGGAAAAGAAAATTGGAGAAGGAAGTTGGG[G/T]TTTCCACCATGTCTTGAGGACTTCAGCAAAGTATC
1,219	3	3018	66.46	89809735	F1Dsnp	PHR	T	C	3	5,291,491	+	ACTTTTGATTATGCTCGGCATTTCTTGTCTTGTTG[C/T]AGCCGAATGTTAGGTTTGGAGTATCAGTCAAAAAG
1,220	3	3018	66.46	89809736	F1Dsnp	PHR	T	C	3	5,292,380	+	GAATTGGTCTGGGTTTCGGCTTCAGGGTTATAGCA[C/T]TGGATCCTAACTTCAGAAAACTGTCTATTGATGCC
1,221	3	3018	66.46	113_372124	GBS				3	5,295,664		CAAATGTCCTTCTGCAGTTGTTGTAATGCAAATATGCCTCTGTAATATTGTACGATCCAGGAAA
1,222	3	3018	66.46	89809737	F1Dsnp	PHR	T	G	3	5,302,921	+	TTGTAAGGACTAGGATAGGTAAGACCAAAAATACC[G/T]TGAGCTGCTTAGCTACATCTCGGGCGGAAGAACCA
1,223	3	3017	68.92	TP6536	GBS				3	4,444,896	4,444,958	TGCAGGCCCACCCTGTCAGTTGGACAACTATGTCAGGTAACACCACCAATCTTTCACTAACTGC
1,224	3	3017	68.92	89865699	F1Dsnp	PHR	A	G	3	5,240,544	+	GTATGATCTCTTAATTCCTTTAACCATCTTTCCAC[A/G]CTTTGAAATGTTGAATTCCGAGTAACATCATATAC
1,225	3	3015	71.41	82_248994	GBS				3	4,471,957		TTTGATCAAGTTCTGCTTTCACTTAATAAAASCAACAAAGCTTTTGTGGTTTAATAATCATGTA
1,226	3	3015	71.41	82_248966	GBS				3	4,471,985		TCCCGCCCCGGTTCAAGTGATGCAGACTTTTGATCAAGTTCTGCTTTCACTTAATAAAASCAAC
1,227	3	3015	71.41	89809711	F1Dsnp	PHR	A	G	3	4,538,078	+	CAGCGTTGTAGTAGTTGTTGCTGTTGCTGTTTTGA[A/G]TGGTAGGGGTAGTAGTAGTGTGACCTCTCTGCTGT
1,228	3	3015	71.41	89809712	F1Dsnp	PHR	A	G	3	4,561,272	+	AAAGCACGAGACTTTCAATCACTGTAGTCATCATC[A/G]TCTGAAGCTGAATCAGAGCCATCATCATTTATAAT
1,229	3	3015	71.41	89809713	F1Dsnp	PHR	T	G	3	4,563,498	+	ATTTTCCTTGAAGGATGCCTCAATCTTTTGCAACA[G/T]TAAGCGTAAATGGGATTCTCTAATGCCACGTGTAT
1,230	3	3015	71.41	89809714	F1Dsnp	PHR	A	G	3	4,565,367	+	GTCAGAGCAACAGAAATTGAAGCCTCTGGCGTCTT[A/G]CTTGTTGTCAGGTCTCGAAGGCCAGATTTCTTACA
1,231	3	3015	71.41	TP9813	GBS				3	4,623,652	4,623,715	TGCAGTTTTCAGGAGGTGAGAATAAGCTCAGTGGGCCCTTGCCTGAGAGTATAGTGAAACTACG
1,232	3	3015	71.41	89865687	F1Dsnp	PHR	T	C	3	4,662,421	+	CTGATATATTTGTGGAAGTCAAAATTGCTCCCTTC[C/T]GCAAAATGAGCCTAGAGGAGCAGCAACATAAAAAC
1,233	3	3015	71.41	82_58283	GBS				3	4,678,021		TCTTATCTTATTCACTTGGTAATGGGCTCTGCTAGATAGGGTTTATAAGCCGGACTTGCTATTG
1,234	3	3015	71.41	TP793	GBS				3	4,678,113	4,678,072	TGCAGAATCATACTACTATGTAGGGGTGGAATGGTAGATCACCTAATACGTACTGTTAGACAGG
1,235	3	3015	71.41	89809716	F1Dsnp	PHR	T	C	3	4,726,981	+	GAATTGAAAGTGGGAGTTGAAGTTGAGAAAGGAGA[C/T]GAAGATGGTTTGTTCACCAAGGAAGGTGTTTGCAA
1,236	3	3015	71.41	89809717	F1Dsnp	PHR	A	C	3	4,747,514	+	GAAGAAGAGTTTAAAGCTGTGCACAAACTTTTCGG[A/C]GTGAGCAACATGTCGAAGTTGCTTAAGCAACTAGA
1,237	3	3015	71.41	89809720	F1Dsnp	PHR	A	G	3	4,771,568	+	CCGGAGAAAGACTGGAGAGGAGTTCAATTTCACTT[A/G]TGTCGAATGCTTGTTGTACACATTTCACCATCTTG
1,238	3	3015	71.41	89809722	F1Dsnp	PHR	A	G	3	4,811,666	+	CCCTCAGTCAGAGCTTTCTCAATGTCAATTGTCCC[A/G]CACACTCTATCTTCTGTAGCACCCAGAGGTAAATC
1,239	3	3015	71.41	89809723	F1Dsnp	PHR	T	G	3	4,850,428	+	GTCATTAGCGCCAAAGAAGACGGTGACAGCTAACG[G/T]CACTTCACCGCCGCCGTCTTGACTCCCCGGAAAAA
1,240	3	3015	71.41	TP1253	GBS				3	4,861,407	4,861,344	TGCAGACTCCACAATCTCTCCACAGAAACTAGTACTCACAGCACCCCAATAAGTCCCAATGAAA
1,241	3	3015	71.41	89865690	F1Dsnp	PHR	T	G	3	4,879,918	+	TGGCCTTCTCTAAACCAACTCTCGAGAAGAAGCTC[G/T]TCCTAGCATACCTACTGCTTCCTGCAAACTTTGAT
1,242	3	3015	71.41	89809724	F1Dsnp	PHR	T	C	3	4,887,542	+	TTGCGATCTTAAGAAGCTCCAAACAGAGGCTTCTT[C/T]ATTTCCTGACCATTCCCGCCAGCCCTGCGGTCCAA
1,243	3	3015	71.41	89809728	F1Dsnp	PHR	T	C	3	4,990,162	+	AGGACAGCTGAGCTTTGGCCTTACCCTTACAACCC[C/T]GAATATGGACACAACCTTAATGTTCAGTACTACCA
1,244	3	3015	71.41	89809730	F1Dsnp	PHR	T	G	3	5,062,235	+	TACCACGGTGCATGAAGAGGAAGAAGAGAAAGGTA[G/T]GAAGACTGTTGTGATTGAATCCTACGTGGTGGATA
1,245	3	3015	71.41	89865692	F1Dsnp	PHR	T	C	3	5,067,380	+	ATGCAGCAGCAAGCAAAAGCAGAGCTGCCAAAGGA[C/T]GCTCCTTCAAGTTTGGATTGGAGGAAGAAGGGAAT
1,246	3	3015	71.41	TP3735	GBS				3	5,089,393	5,089,454	TGCAGCATTTCTGCATCTGGTTCATCAGGCAATGGGGGCTAGATGGAACCCTTTGGGGTTCCGC
1,247	3	3015	71.41	89865693	F1Dsnp	PHR	A	C	3	5,098,123	+	TTGGACGAAGCAGTATCGGGTTGTTTCCCTTCCAC[A/C]GTATCGCATCTTGTCCGAAGAAAGGTGTGTGGTCG
1,248	3	3015	71.41	TP1608	GBS				3	5,099,556	5,099,497	TGCAGAGCCGCCAGCCTCATCGTCAGCCTCTCTTCCTCGCTTATTGTCTTGCTCTGCAACCCGT
1,249	3	3015	71.41	89809732	F1Dsnp	PHR	T	C	3	5,147,714	+	AAGAGCCAATCGCAAAATGGATGCTAAACACTCCT[C/T]AACAGTATCATGATCTTCCTCTGTCCCAAGTAAAT
1,250	3	3015	71.41	89809733	F1Dsnp	PHR	T	C	3	5,163,954	+	TATCAATGGTGAAATTATTCTGGTGTAAGGTAAGC[C/T]GACGAAGGTTTGTTAAGGCACATAGCTCACTAGGA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,251	3	3015	71.41	89865694	F1Dsnp	PHR	A	G	3	5,165,137	+	ATAGCTGGTTATTGCTCAGGCTGATTACTTGGAGA[A/G]CTGTTAAGTTGAAGATGGCAGCAGGTATGGAACCT
1,252	3	3015	71.41	89865695	F1Dsnp	PHR	T	C	3	5,165,170	+	GAGCTGTTAAGTTGAAGATGGCAGCAGGTATGGAA[C/T]CTGAAAATTGATTACCATACAGGTCGAAGGTTTCG
1,253	3	3015	71.41	89865696	F1Dsnp	PHR	A	G	3	5,165,313	+	AATCGGTGCAAACGTCCCAATTCCAAAGGCATGGC[A/G]CCATGAAAACTGTTGTTTCTTAAGCTAAGCTCAAC
1,254	3	3015	71.41	89865697	F1Dsnp	PHR	A	G	3	5,178,262	+	ATATTCGGCAAGACTCTTCATTCATCATCGAAGCC[A/G]TTGAGCTTTCTGGACCTCGGTAACAACAAAGTCTC
1,255	3	3016	73.90	TP4328	GBS				3	5,362,894	5,362,957	TGCAGCCTTATGAGTTCCCTCTTTGGCCTTCTCCGCCATTGTTTCCGCCGCGCTCTTTGTCTTC
1,256	3	3016	73.90	82_390938	GBS				3	5,396,549		AGTCCTGAACATCAGAGTGCAAAAGACCTTTGGCATGGATCAGAGCCCACAACTGATTCTCTTT
1,257	3	3016	73.90	82_390982	GBS				3	5,396,593		GCCCACAACTGATTCTCTTTGCTTGCAACCTRATCCGACCGCAGTTTCAAGAGTCAAATTGAAA
1,258	3	3016	73.90	89865703	F1Dsnp	PHR	A	G	3	5,408,868	+	TTGTGTTTGGAACACGCGACCTTGTTGGCGGTTTC[A/G]GAGGAACCGGTGAGCATTTGGACGACTTGCTTGAA
1,259	3	3016	73.90	82_420699	GBS				3	5,414,579		ATACTATTTTTCCTTCTGTACAGAACGAATTTACAGACTAGTTTATTTACGCAATTAATTTCCG
1,260	3	3002	76.37	89809746	F1Dsnp	PHR	A	G	3	5,554,455	+	TTTGTGAAAGTAAGGGTGAGGTCTGTTCGAATTCC[A/G]CAGATTGGGGATAAATTTAGTAGTAGGCATGGACA
1,261	3	3002	76.37	89827633	snp	PHR	A	G	3	5,610,569	+	CGCATAATGAGTAGTAACAACAGCTAAGTTAACAC[A/G]ATCTTTGAGATACTGCAAGATGCTGGTAGAAAGAG
1,262	3	3002	76.37	89809747	F1Dsnp	PHR	T	C	3	5,658,669	+	AGTCAAGGTAGCAGAAGTTCAGATCACCACACTAA[C/T]TGAGATGCTTATGAGACTAGCAATCAAGCTGGACA
1,263	3	3002	76.37	89809748	F1Dsnp	PHR	T	G	3	5,659,041	+	CCTCCTCCAACTACAGCCAAATGGGAATTTTTCGA[G/T]TAATCTTTGTTCGATCATCGATCATCGCATCTTTC
1,264	3	3002	76.37	89809749	F1Dsnp	PHR	T	C	3	5,675,189	+	TCTCCCCCATGGCCAGGTGCATTGCATCATTTTCC[C/T]TTTGTGCAACTTTAATCTTCCTCTTTAGGGATCTA
1,265	3	3002	76.37	89809751	F1Dsnp	PHR	A	G	3	5,702,008	+	TTGTGCTCTCAGCAACCTTCACTTTTCTGGTTGAG[A/G]TTAAGTAATAATAATCTTTCTGGGGAGCTTGGACC
1,266	3	3002	76.37	89809752	F1Dsnp	PHR	T	G	3	5,705,515	+	TACGAGTGCTATGACTTGGTTAAGATGTGTTGCTA[G/T]GCAATTGATCGTAGCTGTGGTAATTTGGTTGATAT
1,267	3	3002	76.37	89865709	F1Dsnp	PHR	T	G	3	5,705,532	+	GGTTAAGATGTGTTGCTATGCAATTGATCGTAGCT[G/T]TGGTAATTTGGTTGATATCAGTATCGACCATTTTG
1,268	3	3002	76.37	TP8539	GBS				3	5,707,220	5,707,247	TGCAGTCTGCACCACTCAATCTACATGTTTCTGTTGGATCATAAATATCTTTGTCCTCGTATTC
1,269	3	3002	76.37	89809753	F1Dsnp	PHR	T	C	3	5,730,259	+	ACAGTGAAACCCTAAAATCATCCCGCCATGATGAG[C/T]GAATCCTCTGATCGACGCAAGAGAATCCGCCGCAA
1,270	3	3002	76.37	89865710	F1Dsnp	PHR	T	C	3	5,731,757	+	CTTGTCCTGATCTTGGCTCACTTGATCTGCGCCAT[C/T]GTTTCATTCTCAATCTGGAGGGAGATTGGAGAAGT
1,271	3	3002	76.37	89865711	F1Dsnp	PHR	T	C	3	5,747,743	+	AATCTCGTCGATATCAGTATTGAGTACATCGGCAC[C/T]GATCAACTCCTCAAGTACCTGGCTGAGAGGTATTG
1,272	3	3002	76.37	89865712	F1Dsnp	PHR	A	G	3	5,768,146	+	TGCAGCAGCTCCATCGTTGATCTCCCTTTGGTGGT[A/G]GAAACTTGCTCTCCTTTGTTTACTCCCTTTGTATC
1,273	3	3002	76.37	89809754	F1Dsnp	PHR	A	G	3	5,769,718	+	ACTATGACTACTTCTCTCCCTCAGTTCAATGGGTT[A/G]AGACCCAAGATCTCATCCAATGTACAGAGCTTGGT
1,274	3	3002	76.37	89865713	F1Dsnp	PHR	A	G	3	5,776,324	+	CCACGAGTTTGTACATAGAGGGCAAGTATGTGACC[A/G]TGATGTCCACATTCAGACTGCAGCTCACGTGTACC
1,275	3	3002	76.37	89865714	F1Dsnp	PHR	T	C	3	5,778,465	+	TTCAGATCCCTAGATGTAGAACTCACTAGCCTTAC[C/T]GAGCTTGAAGTGACCTGTGATGTCAATTCATCAGC
1,276	3	3002	76.37	89809756	F1Dsnp	PHR	T	C	3	5,790,508	+	ATTCTCAACAGCATCCCAGTTGTTGTGACAGTAAC[C/T]TCGTTTGGGGTATTCACTTTTCTTGGAGGTGAATT
1,277	3	3002	76.37	89865715	F1Dsnp	PHR	T	C	3	5,790,792	+	CTCTGCATCTGCTGACTCAGTCTACCTTGACAGGT[C/T]GTAAATGCAAACGTATCCTTGCAGCGTTTGGAGGA
1,278	3	3002	76.37	TP1158	GBS				3	5,961,703	5,961,650	TGCAGACCTGTATTGTTGCCGTCCTGGAAAGGAAATACATGTAGTAAGGCTACAATGATGTGAT
1,279	3	3002	76.37	TP2287	GBS				3	5,973,063	5,973,000	TGCAGATGACATCCTACGACTGAGTCAAATGAATGCAGATTTCTTTGGTGGAGTTGACGCTGTT
1,280	3	3002	76.37	89809758	F1Dsnp	PHR	T	C	3	5,981,937	+	GCAGTAGTTCTCGTTCTGTTGAATTGGTCTTAGAA[C/T]TGATTGCTGCTCTAGCTCAGTCAGCATTTCAAAAG
1,281	3	3002	76.37	89865717	F1Dsnp	PHR	T	C	3	6,003,062	+	TTCTTGGAAGCAGCCAGCTCTGGGGCGCGGTAGCC[C/T]AAGACACCAGCATCAAGAATCTGTTCAATGGTGCC
1,282	3	3002	76.37	89865718	F1Dsnp	PHR	T	C	3	6,004,711	+	AGGTGGAGCTCTTGCAGAGTAGGCATGCTTAGCAA[C/T]TCAGCAAGAACTGTGCCATCTAACTGGTTAGAACT
1,283	3	3002	76.37	89809760	F1Dsnp	PHR	A	C	3	6,018,261	+	ATAATGCAATATAATGAACACATTTCACTTCCTCA[A/C]CATCTCAACTCCTTCTGTAGTAGATTCATTAAACC
1,284	3	3002	76.37	89809761	F1Dsnp	PHR	T	C	3	6,020,277	+	CTCGATAGCATTAATAAACCCGAATTTCTCCTTAT[C/T]CGGGATGAACTCAATGACTAGTGCATCCCTATTGA
1,285	3	3002	76.37	74_237349	GBS				3	6,032,575		ATCCGGGCATTACTGAAGACCCTGAGAATTCKTTCTCATCAACACCCACGTGATGAACATGCAA
1,286	3	3002	76.37	89809762	F1Dsnp	PHR	T	C	3	6,040,454	+	ACTACCTACCCATCTGTAATTAAGAGGAGCAGCTA[C/T]AGCACCAACGTATGCAATTGCAAGTAACCACTCCA
1,287	3	3002	76.37	89865720	F1Dsnp	PHR	T	C	3	6,087,987	+	GGAATCGATTTATCTTTGAATCAACTCACAGGTAG[C/T]CTCCCTGCAAATATAGGCCTTGCCATTCCAAACTT
1,288	3	3002	76.37	89865721	F1Dsnp	PHR	A	G	3	6,136,169	+	ATGGCTCAACCATCTCAGGCATACAAAGAGGAAAG[A/G]GCGTTTCAAAGAGTTTTGTGGAGCAAGATCGGCGG
1,289	3	3002	76.37	89809763	F1Dsnp	PHR	A	G	3	6,155,283	+	CCAGGAAGCTTTGCATGTCTATACCGGCAATCAGG[A/G]CCATTTGGACAAAAACCTAACTTGTACCTGCAATG
1,290	3	3002	76.37	89809765	F1Dsnp	PHR	T	G	3	6,169,441	+	TTGATGTTCATGGAGAACTGGTAGAGGGAAATACT[G/T]TAAGGGGCCATGCAGAGATTGCGTGGTGTGGCGGC
1,291	3	3002	76.37	89809766	F1Dsnp	PHR	A	G	3	6,203,074	+	TTGGTTGCAATGGCACTCAATGATATTCCAGTCAG[A/G]AAAGTACATGTGCCACATAATGTAACCAACAACAG
1,292	3	3002	76.37	89809768	F1Dsnp	PHR	A	G	3	6,216,785	+	TGCTTAATTACCAGAGTGTAGAAATTCCTAAGATC[A/G]TCTCCACCTATATCAACTCGAGGTCGGTGGACAAC
1,293	3	3002	76.37	TP5524	GBS				3	6,217,021	6,216,958	TGCAGCTTAGCTTAGGTAACTGGGATGTGTTTTAATTAGTTGATACTTAAATCTATGGCCAAGG
1,294	3	3002	76.37	74_6575	GBS				3	6,223,478		GAGGCAGATGGCAAATGAGCCCGGAACAGAACACACACACCAGGAAGAAAGCCATGAACACTGC
1,295	3	3002	76.37	89809769	F1Dsnp	PHR	T	C	3	6,225,238	+	CAATCAAAGACTACTTGAACGCCCACAACTATGCC[C/T]GAAGGGCGGTTGGTAACAAACCCTTGGAGTGGGAT
1,296	3	3002	76.37	89809770	F1Dsnp	PHR	T	C	3	6,231,204	+	CTATTGCACATATGGAGAACGATGCATGAATGCCA[C/T]CACTTTCAGAATTATGTTTCTCAGCAGTTGAATAA
1,297	3	3002	76.37	89809803	F1Dsnp	PHR	A	G	3	7,853,980	+	CTTTCAGATCCAACAGCAGCAATCGGAGATCGACC[A/G]ATTCATTGCCCATCATGTAAGTTTTAACTCTACCA
1,298	3	3002	76.37	89809805	F1Dsnp	PHR	T	C	3	7,954,949	+	TGAACACGAATTAATCAGGTTATGGTTGCTACTGT[C/T]CGGTGTGAAGAGATTGCTAATGAGAAATTTACTCA
1,299	3	3002	76.37	89809806	F1Dsnp	PHR	A	G	3	7,957,287	+	TTTACACTGAAACAGGTTTCTCCAAAAGATACACT[A/G]ATTACACCAGTGCAATGCAAATCACTTTGGAGACA
1,300	3	3002	76.37	5_1578922	GBS				3	8,012,244		CCGGATAAAGGACCTCAATGTGAAAAATTTCACTCGAACACAGACAAGAACAATTTTATTGCCA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,301	3	3002	76.37	5_1583227	GBS				3	8,016,551		CAAACTGAGTCCCAAGGTAGATTAGACACTCYGAATCCGAGACATTGGAGATAGCTAGGGACCT
1,302	3	3002	76.37	89865756	F1Dsnp	PHR	T	C	3	8,053,162	+	TCTTGACAATACTACTACTGCTGCTGGTAACGAGT[C/T]ATGCTCTGGCATTGGATGTTGCACAACTTCAGTCC
1,303	3	3002	76.37	TP3967	GBS				3	8,063,200	8,063,137	TGCAGCCATGTTCTTGACTTAACCCACTTGAGAGCTGCATAGCCATCTTCATAAGCACAAGGAT
1,304	3	3002	76.37	89865757	F1Dsnp	PHR	T	G	3	8,066,219	+	ATTTCTTCAATACTTGAATCTTATCCCAATATCTA[G/T]TAAAGACAGTAAACTCGTACTCCTCAGTGGTGTTA
1,305	3	3002	76.37	89809807	F1Dsnp	PHR	T	C	3	8,066,357	+	CCCGGACTATGCCGGTGAGGACCAAGTTCTTCAAG[C/T]TTTGGAAGTTGATTTCCGAGATGGCGAATTCCACA
1,306	3	3002	76.37	89865758	F1Dsnp	PHR	A	G	3	8,069,308	+	TGTAGCCGCAAAAGGACTGGTTATTGAAAACAGGT[A/G]TCCATATCAGGGTATTGAGAAACAATGTGATTCCT
1,307	3	3002	76.37	89865759	F1Dsnp	PHR	A	C	3	8,120,451	+	GTAACGGAGGCCTAGTACCTTCCTTGCTGATGCAG[A/C]CACTGAATCCCAAACATAGAGCTCTTGGCGGATCG
1,308	3	3002	76.37	89809809	F1Dsnp	PHR	A	G	3	8,120,973	+	AATCCATAAAGGTTATGCACATTATACTCTGTTAA[A/G]TTACCAAAGTGTAGAGCTGATGCCGGAACAGTCTT
1,309	3	3002	76.37	TP1876	GBS				3	8,225,010	8,225,073	TGCAGAGTCTTTGATCTTTTCAGTGATTTTCTGTAACTTCTTTGCTGTTTTACGCCTGAACCAA
1,310	3	3002	76.37	89809812	F1Dsnp	PHR	A	G	3	8,225,045	+	TGCAGAGTCTTTGATCTTTTCAGTGATTTTCTGTA[A/G]CTTCTTTTCTGTTTTACGCCTGAACCAAAGATTAC
1,311	3	3002	76.37	89809813	F1Dsnp	PHR	A	G	3	8,406,129	+	TTCTCAATGTCCTCAAACTCTTCTTTAACTGTTGA[A/G]CTACTCCCAACAGTTGCATTAACCGGAGACAGTAC
1,312	3	3002	76.37	89809814	F1Dsnp	PHR	A	G	3	8,441,953	+	GAAGTGTCATTCATTGGTTTCTTCTTGGGACAAAG[A/G]GATGAGCTTCTTACATTGATAAATGGGAGTCTTCC
1,313	3	3002	76.37	89865767	F1Dsnp	PHR	A	G	3	8,449,683	+	TTTTTGGTTCAGTATAGTTAAAACAGTACCCTGGG[A/G]AACAAATTGGAGTCGAACTCGGCACAAAGAATGCC
1,314	3	3002	76.37	89865768	F1Dsnp	PHR	T	C	3	8,455,226	+	TGTACAACTTCAGATCCAATTCGCACAACTGACTT[C/T]CTCCACTGCCTTACAAATCATTCTCACTACTCCAC
1,315	3	3002	76.37	89809815	F1Dsnp	PHR	A	G	3	8,456,300	+	GTGAAAGAGCCGATTCCGAAACATGGAATAGAATC[A/G]ATATTGGACTTGATGTTAAAGCCGGGTCTGGATAA
1,316	3	3002	76.37	89865769	F1Dsnp	PHR	A	G	3	8,460,310	+	GAAACCATGTGGCAGAAGATACTTGCTATAGAGAC[A/G]CTTCAGATGCAGTGGAACCCTTATGGTGGAAGAAT
1,317	3	3002	76.37	89865770	F1Dsnp	PHR	A	C	3	8,463,381	+	TATTGTAACAGCTAAACATGAATCCCATGTCCAAG[A/C]AACCGTGATGTGTGCAAAACAGCATGGTTTACATA
1,318	3	3002	76.37	89809817	F1Dsnp	PHR	A	G	3	8,466,360	+	ATTGTTGTGCAGTGGCAGAAAGTTGCTGATAATAT[A/G]GACAATGATCTGTTCATTAGAGTGATGCTAGCACC
1,319	3	3002	76.37	89865771	F1Dsnp	PHR	T	C	3	8,472,373	+	ACCGACCCTTCATACACACCAATCTTACATTCATA[C/T]ATAAGAAACCTTAGATTCACAACCCCCAAAACCCC
1,320	3	3002	76.37	TP1812	GBS				3	8,473,243	8,473,180	TGCAGAGGTTCCAATTGGATAGTTAGACCAATACAGGACCGATTCGATCCAACCGATTTCGACA
1,321	3	3002	76.37	89865772	F1Dsnp	PHR	T	C	3	8,473,569	+	GCTTTACAAGTATATGGCACCTTATGTGTCAAAGT[C/T]ACCAAGGTGTTCATATCTAAATTACAGAGATGTTG
1,322	3	3002	76.37	89809818	F1Dsnp	PHR	A	G	3	8,473,663	+	AATGTGAGCTACTCAGAAGCTAGTGTTTGGGGGAC[A/G]AACTACTTTAAGGGAAACTTTGAGAGGTTGGTACA
1,323	3	3002	76.37	89865774	F1Dsnp	PHR	A	G	3	8,530,301	+	GTGGGCAGCGCCAAAGTTCAGTGTCACCCATACGG[A/G]CATTGTGGCACCTTCAGTGAATGTAGTCTTGACAA
1,324	3	3002	76.37	89865775	F1Dsnp	PHR	T	C	3	8,545,582	+	CAAATAAAACCAATGTGATCAAATGCTGCACATAG[C/T]GATGCCAATACAATGCTCCCTGCCACCAACTCATC
1,325	3	3002	76.37	89809820	F1Dsnp	PHR	A	G	3	8,545,795	+	AAACAACCAAATTCTGAAAATATCCTTCTGCCATC[A/G]CCATCAGAATTCACTGCACAGAAAGGAAATAATC
1,326	3	3002	76.37	89809821	F1Dsnp	PHR	A	G	3	8,551,965	+	GTAGTAATGGGTAACATCATACATGACATAACCCA[A/G]TAAACCACCAGCAAATAAAGCAGGAGCAACAGAGG
1,327	3	3003	78.88	TP7011	GBS				3[z]	27,664,221	27,664,172	TGCAGGGGCAGCAGCAGCACACCGCCGCGCACTCCGCCGCCGCCCCGCCGAGATCGGAAGAGCG
1,328	3	3003	78.88	TP5085	GBS				0	798,818	798,896	TGCAGCTCCGATGGGAGGCCACGGGTAGAGAGAGAAGCACAACAGTGCTCCTCTGCGTAAATCG
1,329	3	3003	78.88	346_130640	GBS				0	854,878	854,941	CACTACTGGCTCTAGAGATTGTTTCTTCTTCGCAACGCTTTATGCAGCAGCTGCATTTGACTCT
1,330	3	3003	78.88	346_65497	GBS				0	921,202	921,271	GGTGGTTGGGAGTTGGTGTATAGTATGTTGTCTGTGTTGTGATTGTTGTCGATCATATGGACTT
1,331	3	3003	78.88	TP1170	GBS				0	8,817,246	8,817,309	TGCAGACCTTTTCATTGAAGACATTATGCATTTTAATATGGAAAAGGAAACACATTTATCGCAA
1,332	3	3003	78.88	89865456	F1Dsnp	PHR	T	C	2	8,638,345	+	ATAGGGTTCTCTGAACAAGTTTTTTGTTTAGCAGG[C/T]GTCAAACCTTCTCTACATTGACCAACCTACTGGAA
1,333	3	3003	78.88	89865457	F1Dsnp	PHR	A	C	2	8,639,465	+	ACTTTGTACCTTGCAATTTAACAGTATATTCGGCT[A/C]TGCTCCAGGACTATATGAGAAATCTGGAATTGGGT
1,334	3	3003	78.88	89865253	F1Dsnp	PHR	T	G	2	14,161,159	+	GTTACTGTTGTGCTTTACAAACCAGTTCAAAGAAA[G/T]GGGGCTAGCAGCACTTAGAACATGCATTTTAGGAT
1,335	3	3003	78.88	89809436	F1Dsnp	PHR	A	G	2	23,039,982	+	GTGTATCTGCAACTACCACTCCTATAACCTGCATC[A/G]GATACAGAATAACACCATGGTCAAATACTTCATAA
1,336	3	3003	78.88	89809437	F1Dsnp	PHR	T	C	2	23,292,126	+	AACTTTGGAGCCTCTGATTTTGCATATGCAGCACT[C/T]TCTATGGCAAGTCTTCTACCCCCTTTCTTGCATTA
1,337	3	3003	78.88	89865407	F1Dsnp	PHR	T	C	2	23,442,597	+	ATTAGATACCCACTTAATGAAGAGATTTTAACGGA[C/T]GCTCCCAATATAAATGAAGCTGCTACCCAACTCAT
1,338	3	3003	78.88	TP5795	GBS				2	23,450,162	23,450,191	TGCAGGAAAATATCATCAACTGTTCATCCACGTCTGAACACCATCAATTCTGCCCAATAACCGA
1,339	3	3003	78.88	89879378	snp	PHR	T	C	2	23,500,424	+	AAATTCCAGGCCTGGCCTCGCACTGCAGGACCTCC[C/T]GTTGTAATGAACCCCATCAGTCGCCAGAATTTTAT
1,340	3	3003	78.88	TP236	GBS				2	23,517,820	23,517,757	TGCAGAAAGGTGGTATAACTCGCTGGCTCGTAGCTGAAGTGGTCTAGTGTTTGAGCATAAAAGT
1,341	3	3003	78.88	TP8902	GBS				2	23,522,986	23,523,052	TGCAGTGGAGACATTATACAGAATTAATGTATTAACATTAACAACTACATGTAAAATGTGAAGT
1,342	3	3003	78.88	TP1103	GBS				2	23,553,287	23,553,349	TGCAGACCATCAGATGATGGTAATAACAAAGGCTTACCAATTTCTTGTTGAATGCTCGTTTGAC
1,343	3	3003	78.88	89865408	F1Dsnp	PHR	A	G	2	23,598,189	+	GCCACCAGAGGGTAACTCAAAATATAACCAGCTCC[A/G]CCGAATGCCATATCAAACGAAAAATCGGAATTAGA
1,344	3	3003	78.88	89809439	F1Dsnp	PHR	A	G	2	23,671,930	+	CTTGCAGACCCATATCGGTGATTGTGGCATCAACA[A/G]TGTCATTGACCTCTTGTTTGGTAAGACTAGTTGGG
1,345	3	3003	78.88	TP6919	GBS				2	23,702,637	23,702,680	TGCAGGGCATCCTGATGATGACTGCTGGTTTCTTCCGCTTACTGCCGAGATCGGAAGAGCGGTT
1,346	3	3003	78.88	89865410	F1Dsnp	PHR	A	G	2	23,839,377	+	TGGCCGCGAACATCGACATTGGGATGAAAGCAGAA[A/G]GTCTCGAACTTGACCTTGGGAGGCTTAAAGGGATA
1,347	3	3003	78.88	89809441	F1Dsnp	PHR	A	G	2	23,839,404	+	AAGCAGAAAGTCTCGAACTTGACCTTGGGAGGCTT[A/G]AAGGGATAGTCATTGGGGAAAGAGAGCAACAATCT
1,348	3	3003	78.88	41_109035	GBS				2	23,858,934		TTCTGCACTAGTTGATGTTTCAACAGTAGCTYGCCAGGCAATATATTTGCTTCTCTTTGCATAT
1,349	3	3003	78.88	41_108979	GBS				2	23,858,990		CATCAGCATTTAAAAGAAACCGGAGCATAAAMCAAGATTACCTGCAAAGCCAGATGTTCTGCAC
1,350	3	3003	78.88	89809442	F1Dsnp	PHR	A	C	2	23,875,644	+	TCTCAAATCAAACTGCTTAGGCTGTAAGGGTTGGG[A/C]TAAATGCAGAGAAGAGTGGTGATGTTGGACGTGTA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,351	3	3003	78.88	89865412	F1Dsnp	PHR	A	C	2	24,002,148	+	CAGGTTGGAAACCAGTTTCCCATTCATCCTGCAAT[A/C]TGTTCCCTATCAAGACTACTATAGTTTATATAGTC
1,352	3	3003	78.88	89809443	F1Dsnp	PHR	A	G	2	24,023,962	+	ACTGCAAAATGAGGCAGCTGCTGATGAGGGTACTG[A/G]TCCAGGAGTGTCCAATTCCAAGTCATCTGGGAGGA
1,353	3	3003	78.88	89809445	F1Dsnp	PHR	A	G	2	24,118,480	+	TCACCAGAAAGGGTAACAGCACTTGTATGGTACTC[A/G]CCACAAGCAACAAAATCAATGTTCACATTACTAAG
1,354	3	3003	78.88	89865719	F1Dsnp	PHR	T	C	3	6,032,258	+	ATGGTGTTGGATCGTGCAATGGTGGGATGGAGCAG[C/T]TGGAGGTTATGCATAATGGTGTTGAAAAGTGCAAC
1,355	3	3003	78.88	492_105731	GBS				3	6,326,857		ACGTGCTAGAGAATGGCATCAGCTGACCAGCGCACCTCCAAAAAGAAGAAAAATGATCATAGTG
1,356	3	3003	78.88	89865725	F1Dsnp	PHR	T	C	3	6,328,542	+	ACCTTCCTTAACGTCTTCAAGCACTGAGGTGGATT[C/T]ATTTTCAAAACTTGAATTGAATTTCCGGCTCAACG
1,357	3	3003	78.88	89809775	F1Dsnp	PHR	T	C	3	6,582,903	+	AAGTGGCACTGTACTAGTTCATCATGCAACTCATC[C/T]TTCTCAAACCTTTGCCAACTTCCCAAGTCCTCCTG
1,358	3	3003	78.88	TP9709	GBS				3	6,613,867	6,613,804	TGCAGTTTCCTCCGCAAGTTCTATGTTGTTGTGTATCCTACAAGCTCCAAGTAATGCACCGTAT
1,359	3	3003	78.88	5_137828	GBS				3	6,618,066		GAGGACGTCTTTGAAGCATTTCGTCGAACACYTTCAAGGCATCCTCAACATTACTCGCTAGATG
1,360	3	3003	78.88	89865727	F1Dsnp	PHR	A	G	3	6,620,133	+	GATACTTGTTTAGCCATTATGTCCGTAAAATTAAC[A/G]AACTACCAACAGAAAGAAGCTAGTTAGAGATTTCA
1,361	3	3003	78.88	89865728	F1Dsnp	PHR	T	C	3	6,691,768	+	CATAGCTAATGAAGAGAGATCTAATGCCGAACTCT[C/T]GACGGTCAGTTTCTTGAAATGTCCATCCATATTAA
1,362	3	3003	78.88	89865729	F1Dsnp	PHR	A	G	3	6,704,353	+	TAAAAAAGACATTGAAATGCAAAAGATGGAGAAAG[A/G]TCACTTGGAAAAGAGGCTTAATGAGGTATTGATCT
1,363	3	3003	78.88	TP3772	GBS				3	6,731,487	6,731,445	TGCAGCCAACGCCGCCGCCGATGTGGGTCCGCTCGCGCCGCCGAGATCGGAAGAGCGGTTCAGC
1,364	3	3003	78.88	89809779	F1Dsnp	PHR	T	C	3	6,747,961	+	AAGAAGAGCCGCAAATCTAGATCAGATTTTGGCCT[C/T]TCTGCTACCAACTCCCTCCCAGAACTGATGGCAGA
1,365	3	3003	78.88	89809780	F1Dsnp	PHR	T	C	3	6,780,406	+	AACCAGGCAGACAAACTTTGTACTATTCACCTCTA[C/T]GCTGATCAAGACACCAGAAACAGAGCTCCTGTTCT
1,366	3	3003	78.88	89809781	F1Dsnp	PHR	T	C	3	6,786,767	+	CTCCAGAGTATAATGGAAAATATTTATTGCCAGGT[C/T]CAAATTCCCTTCTCTGCATAGACCATCTATCAGGT
1,367	3	3003	78.88	TP2091	GBS				3	6,813,596	6,813,533	TGCAGATATGAAGATGCCAGAAAAAGAAAGAACAAGTAGTGAGCAACAATTTTGACGAGGAAGC
1,368	3	3003	78.88	89865732	F1Dsnp	PHR	T	G	3	6,859,451	+	ACGGCCCTATCGTTCTCTTTAACACTCTTCAATGC[G/T]GTGATAGATCTCATATCATTCAGCAACATCTTGTT
1,369	3	3003	78.88	89865733	F1Dsnp	PHR	A	G	3	6,865,898	+	TCACCAAATCCTCCTGGAACTAGAACACCATCAGC[A/G]CCCTGAAATTAAAGGATCAAAGTCTGAATAAGCAT
1,370	3	3003	78.88	89865734	F1Dsnp	PHR	A	G	3	6,886,380	+	ACAATTCACCATAAGACGACCTTCAGGCATCAGCA[A/G]GGTCTCCAAATCCAACCAAGTAGTAACCTTTCACA
1,371	3	3003	78.88	89865735	F1Dsnp	PHR	T	G	3	7,006,095	+	CACAAAATCATAATTATTTTTCTCGTTCTGCTGAC[G/T]CACATACCACTGAATCAAGTCCCTCTGCCTCATTC
1,372	3	3003	78.88	89809783	F1Dsnp	PHR	T	C	3	7,059,861	+	AACCTTTTCTTTTTCTTTAGCATCTAAATTCCGGC[C/T]ATCATCTGCAATACCTTTGGCATCTTCAAAGGAAT
1,373	3	3003	78.88	89865737	F1Dsnp	PHR	T	C	3	7,082,985	+	TTCTATGACTAGCATGTCTCGCAGAAAACCCTTCC[C/T]GTTTCTCACGAACATCAACTGTTACAATCGCTCCA
1,374	3	3003	78.88	89865739	F1Dsnp	PHR	A	C	3	7,090,486	+	CATTGGGTTATCTATCGGTTTAGTTGGTCTCGGAG[A/C]AATTGGTCTAGGGTTGAAAGTCTGGGAAATCAAGC
1,375	3	3003	78.88	89809784	F1Dsnp	PHR	T	C	3	7,114,372	+	TCATAGGTAATCAAAGGGTGGGACCAAGGTATTCT[C/T]GGTGGCGATGGAATTCCTCCCATGCTTGCTGGTAT
1,376	3	3003	78.88	89809785	F1Dsnp	PHR	T	C	3	7,123,920	+	ATGGACTCAGAAATCATGGCTATCATGTCACAATA[C/T]ATGCCTCTAGACAGCCAACAGGCCAATCAAGTCCA
1,377	3	3003	78.88	89787636	snp	Other	A	G	3	7,140,685	+	CCTTAGCCAAATCCGTTGGTTTCATCGAGACAAAG[A/G]CTTTTCCGATTTGCCATGGAACTTGTGTCATCGAG
1,378	3	3003	78.88	89865741	F1Dsnp	PHR	A	C	3	7,150,191	+	CCAGAAGTAATTGAGAATACCCTAGAAACAAAAAC[A/C]ATGCTACTACCCGCTGACATTGCGATGATGACCTT
1,379	3	3003	78.88	89809786	F1Dsnp	PHR	T	C	3	7,158,215	+	AGTCACAGCACCTCTGTCTGCACATTCACTGGTCG[C/T]AAGTTGTCATCTGCCACAATCCCGACATGTACGAG
1,380	3	3003	78.88	89865742	F1Dsnp	PHR	A	C	3	7,158,238	+	ATTCACTGGTCGCAAGTTGTCATCTGCCACAATCC[A/C]GACATGTACGAGAGATTTATCATTTTGCAGGGGCA
1,381	3	3003	78.88	89809787	F1Dsnp	PHR	A	G	3	7,173,086	+	TCCCTCTCAGTCATTCCATCAAACACCTTGTATGC[A/G]TCCCCAATATCGCCGCATTTCCCATACACATTAAC
1,382	3	3003	78.88	89865744	F1Dsnp	PHR	A	G	3	7,189,797	+	CCAACAGCAAGGAGACCAGAGACAGCCTGTCGTGC[A/G]CTTGAGACCATTACCTTTCGCTTCAGAATTGTCTG
1,383	3	3003	78.88	89809788	F1Dsnp	PHR	A	C	3	7,236,585	+	CCCATTAAGACTTCCCATGCTCCCAAAGCACAACA[A/C]CACCACCGATGACGGAGGCTGGTCATCGAGCCACT
1,384	3	3003	78.88	89809789	F1Dsnp	PHR	A	G	3	7,258,428	+	ACTCACCATGGACATAGCCTCATCATCCCAAACTA[A/G]ATACACCTCATTAGTGGCTGGCTGGGGAGCTTTGT
1,385	3	3003	78.88	TP7955	GBS				3	7,259,853	7,259,790	TGCAGTAGAATGCATGATTATCTTACTGTAGATTTATAAACAACATATTTACATGCTTCTGTTC
1,386	3	3003	78.88	89809793	F1Dsnp	PHR	A	G	3	7,422,894	+	TTACCCCCCAAGCAAGATTCTTCAAATTTAGTGAC[A/G]TTCGGGTGCAATGGATATGGATTGCGGAGATCAAG
1,387	3	3003	78.88	89865747	F1Dsnp	PHR	T	C	3	7,446,770	+	AGCCATGAATCTGAGTGCGTCCCACAGTGGAATGA[C/T]CCTGGAACATGAGTGAAAGACCATATAAATAATCA
1,388	3	3003	78.88	5_1059346	GBS				3	7,478,878		GGGCTGCAGATACGAGAAAGAGAGAGAGAGAAAGCGAAGGGAGACAAATGGAAATAAATAGGAG
1,389	3	3003	78.88	5_1059429	GBS				3	7,478,958		TTTTTTCTCTTTTTTCTTAATTTTCTTTTTGAGTTGTAGAGAGAGAAACAGAGTTGAGATTTCT
1,390	3	3003	78.88	89865749	F1Dsnp	PHR	T	G	3	7,622,264	+	GGATTGGGCTCAAGCCACATCATTCTATCCGACCT[G/T]TCTTCATTAATGAGCTGGTATGTTATCACTTTCTA
1,391	3	3003	78.88	89809795	F1Dsnp	PHR	A	G	3	7,622,640	+	GGGGTGCTAAACTAGATGGAGATGATGCACTTAAA[A/G]CTGCAATTTTGGAGGAGGCTGTAATTGTAGGTTAC
1,392	3	3003	78.88	89809796	F1Dsnp	PHR	A	C	3	7,625,709	+	ATATTTTCTTGTGTCAGGGCAAGCAAGAAAGGAGG[A/C]ATTGGGCATGTGGAAAATTTTCGGCGAATGAATGT
1,393	3	3003	78.88	89809797	F1Dsnp	PHR	T	C	3	7,630,120	+	TGCAATGATTAGCAGCGGGATACTCAATTGGGTTA[C/T]CTTTTCCAGCAAAGGAACAATTTCTTTAACAGATG
1,394	3	3003	78.88	5_1268973	GBS				3	7,725,177		CTTCCGACGACATCGTTTTGGTCCTCTTCTTCTCTTTCTTCTTCAGCTCGTTACCGGAGACCGG
1,395	3	3003	78.88	89809800	F1Dsnp	PHR	A	G	3	7,782,164	+	GATATCTGGTAAAAGTTGTAAACGTACTTTCCAGC[A/G]TGTACACCAGCTCTGTGGTCAGTGAATATGTGAAC
1,396	3	3003	78.88	89865754	F1Dsnp	PHR	A	G	3	7,782,293	+	TGTGAAGACACTCTTGTTGAGAATGTAACCCCTCT[A/G]ATCCTCTTAACCATCCCCTCATCAGTCCACTTTAC
1,397	3	3003	78.88	89865755	F1Dsnp	PHR	A	G	3	7,807,379	+	AGGAGGAGATGTGCCTGTATATCCCAATCTGGCTA[A/G]GAATGCAGCCATCTCATTTAACCTCCTTCCCTGAT
1,398	3	3003	78.88	391_20567	GBS				3	8,819,971		TATATGAAGACTCCAATTACTTAAGATATGAAGCAGCAATGCACTATACAAATATCTAGGGGAG
1,399	3	3003	78.88	89865777	F1Dsnp	PHR	T	G	3	8,847,982	+	ACTCTCTCATCACCCAGATATCAAGAAAGCAATCG[G/T]TCTCACTCTTACACCTCACGAACAGACCAATGGAC
1,400	3	3003	78.88	9_833054	GBS				3	8,959,180		AATCTTCCATCGATCCTGGTGGCAGTAATGTCTCAACTTTTACTATGGTACCAGGCACTAGCAG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,401	3	3003	78.88	89809825	F1Dsnp	PHR	A	G	3	9,419,000	+	TCATCTACTGGTCTTATGTTTATTCTGTAGCTGAT[A/G]TTGTAGCGATTGTTATTGTATCTATCGCCCACAGA
1,402	3	3003	78.88	241_204984	GBS				3	9,436,094		TCAGTGGTGTGAGCATGGCGTTGAAGTTTAGTGTAAGAGGAAACAGGTAGCCTAGACCAAGAAT
1,403	3	3003	78.88	89809826	F1Dsnp	PHR	T	C	3	9,485,449	+	GGCTTTTATCCTTGAAAATTTCATCTTCATTGGTA[C/T]GGACACTAGGGCTACCGATTATTCAGGCTCTGTGA
1,404	3	3003	78.88	89865782	F1Dsnp	PHR	A	G	3	9,486,870	+	AAAAAAGCATATGAAGATTGTTGTTTTCAGTATGA[A/G]AGGGACACCATAAGTAATACTAGAAGGGGAAACCC
1,405	3	3003	78.88	241_287417	GBS				3	9,504,385		CGACCAGACCCCATTTAGCCTAAATCTTGTCMGATATTTTGGATTAGGAACTGATGCGGAAGAG
1,406	3	3003	78.88	89865783	F1Dsnp	PHR	T	C	3	9,516,839	+	TATAGATATGTTTGTACCTGAGTAACCAAAGCATA[C/T]AGTGGCAAGGTGCTGTAGCTGCATAGGAATTGCCC
1,407	3	3003	78.88	89809827	F1Dsnp	PHR	A	G	3	9,548,247	+	CCAAAGCTGTTCTGCAATATCTCAAGGACAAAATC[A/G]TGGAATGACTTCTGCCTCTCCCTCGTCCGGACATG
1,408	3	3003	78.88	89865784	F1Dsnp	PHR	A	G	3	9,548,847	+	AAATAAAAATTTACTACTCCGTAAATTCAGGACTC[A/G]GGAGACCTTCACCGCTTCACCTCAAAACTATTTGT
1,409	3	3003	78.88	89865785	F1Dsnp	PHR	A	G	3	9,641,595	+	GCTGGGTACCTGTGGGCCTGTTCATTCTTAAACAA[A/G]AATATCGGAAATGGAACTGTTTCTACTACTCGCAT
1,410	3	3003	78.88	89865786	F1Dsnp	PHR	A	G	3	9,644,451	+	AGCTGAAATCAGCCTTGAGATTTTCAGAGAATGAG[A/G]CTCCAAACAGGGTTGAATCCTTGAAAGAAGCACAC
1,411	3	3003	78.88	89809828	F1Dsnp	PHR	A	G	3	9,664,586	+	CCAGGGCTCAATGGCTTTCCACAACAAAAGCATCG[A/G]CTTACCAACATTACGATGACCTGAGAAACCAAGAG
1,412	3	3003	78.88	89865471	F1Dsnp	PHR	A	G	3	11,297,192	+	GAAGGGATGAACCTTGAAATTTTGGCTACACAATT[A/G]ATTATCATAAAATCCCTCCTAATTGCATCACCAAC
1,413	3	3003	78.88	89865472	F1Dsnp	PHR	A	C	3	11,469,590	+	AATAGGGACAATCTCCAAGGGATATGGAAACAGGT[A/C]CAACACCTGTAGGAACAAGTGTGAAAACAGATCAG
1,414	3	3003	78.88	282_10889	GBS				3	11,937,429		CATGAACCCTAAGATGCGTTGCTTCATACAARCTTAGCATCCCCGGAACATCAGCAATTGAGCT
1,415	3	3003	78.88	TP2268	GBS				3	11,958,113	11,958,050	TGCAGATGAAAGTTTACTGAAACAGATGAAGAGAAGAATGAAGCAAAGGTTGTTCATCGTCTCA
1,416	3	3003	78.88	89809515	F1Dsnp	PHR	T	C	3	12,256,312	+	CATCACCTTAATGGTCTTTAATTTGCCAAGGCATC[C/T]TCTAGGGAGTATCCTCTCTGCCATGGTATCCAAGT
1,417	3	3003	78.88	89809517	F1Dsnp	PHR	T	C	3	12,394,371	+	ATGAGCAGGATATTAAGAACTACAACTTGAGAATG[C/T]TGAGGGCACATGTAGCCTTGGTTAGTCAGGAGCCA
1,418	3	3003	78.88	89809518	F1Dsnp	PHR	T	C	3	12,702,476	+	GAATATATACTGAAGCATATTATCTGTCCATGATC[C/T]ACAGGTGTTTCTTTCTTAACATCTATCTCGGCCAC
1,419	3	3003	78.88	89809520	F1Dsnp	PHR	A	G	3	12,987,522	+	CTGCCCAAGACCCTAACTTGTACTATGGAGGGTAT[A/G]CTGGATATGGAAATTACCAGCAGCCAGGTGCAGCG
1,420	3	3003	78.88	89865481	F1Dsnp	PHR	A	G	3	13,139,618	+	GACCAACAAGCGAGTGCTGCATCAGTGGTGAATGT[A/G]CTTGAATCTGAATTAGAGCAGGCTCGAGCCCGCAT
1,421	3	3003	78.88	89809528	F1Dsnp	PHR	A	G	3	14,352,519	+	ATGGCAACCATTTGGCCTGTTGGAAGAATTGCCTT[A/G]TACACCTGTAAAATGTTTCCAGAAGTCATATGGTG
1,422	3	3003	78.88	89865494	F1Dsnp	PHR	A	G	3	14,430,799	+	ACCACTGAAATCTCGATATGAACCACTTTTTCGTA[A/G]TTGGATAGATCTTGACAATAAGGAGGATCTCAGTT
1,423	3	3003	78.88	89865500	F1Dsnp	PHR	A	G	3	14,582,884	+	AAACAATGTCTGCGGCAAGGAGATGGGGCCTGGAT[A/G]CAAAAGTAGCGTCGTGGGTCTTCATCACCTCTTTG
1,424	3	3003	78.88	89865506	F1Dsnp	PHR	A	G	3	15,927,103	+	TTAGAGAGAAGTAATCTCGTTTCATGAGCTCGAAA[A/G]CTGTCACAAGATCAGTTTGGTTGATTGTGTTATTG
1,425	3	3003	78.88	89865509	F1Dsnp	PHR	T	C	3	16,494,414	+	ATTTCAGCGGCACGCTTCTCTGCAGTTGCTGCATC[C/T]AGAGCTTCAAGACGCTCATAAATGCGTTCAAGCTG
1,426	3	3003	78.88	89865510	F1Dsnp	PHR	T	C	3	16,567,638	+	GACGGCGCGGAGAAGAAGAAGGAGAACAACCCCAT[C/T]ACTGTGGTCTTGAAGATTGACATGCACTGTGACGG
1,427	3	3003	78.88	89865511	F1Dsnp	PHR	T	C	3	16,766,198	+	AATCTAGCCAAAGATGCCAAAATTCGTGCAAGCAG[C/T]ACGCGAGGGAGTGCCAATAATTCTTGGTTCAACCC
1,428	3	3003	78.88	TP5173	GBS				3	16,785,611	16,785,670	TGCAGCTCTCGTCTTCGGATACAGATTGCTGCTTCTGCTTGTAGTACTTCTTCATCCTTCTGAT
1,429	3	3003	78.88	89809540	F1Dsnp	PHR	T	C	3	16,785,620	+	ATGTTCTGGAAGTTCCATATTCCAGCTGCAGCTCT[C/T]ATCTTCGGATACAGATTGCTGCTTCTGCTTGTAGT
1,430	3	3003	78.88	9_1492624	GBS				3	17,149,925		CTAGAAGTGAGGACACTGTGTCAGCCCCAAAGAAGGTTAGGTATTCCCGGAAGGCTAAGTAGTT
1,431	3	3003	78.88	89865514	F1Dsnp	PHR	A	C	3	17,499,120	+	TGGACAAAGAGGACCAGACTGGAGTCAAGGTACTG[A/C]GGGATGAAAAGAGAGTTAGGTTCCATGGAGAGAAA
1,432	3	3003	78.88	89865515	F1Dsnp	CRBT	A	G	3	17,521,609	+	TGATCCAGCCTCATTTAGCCTATGATCCATATCAA[A/G]TGCCAGTAGAAGAGTGTCATATGTTGCCATTGTTG
1,433	3	3003	78.88	89865516	F1Dsnp	PHR	T	C	3	17,532,117	+	GTTAGGGTTTTCTCCGGTTCTTCTGAGAGGTCCAC[C/T]AATTTCTTCAACTCTTGTAGTCTGTCCTGCTCTTT
1,434	3	3003	78.88	89809544	F1Dsnp	PHR	T	G	3	17,638,132	+	AGGAGCAAGCAGGAGAGAAGTAATATTCTAGCACT[G/T]GATCTAAACCTTCCAGCACCAGAAGACCATGATCA
1,435	3	3003	78.88	89865518	F1Dsnp	PHR	A	G	3	18,327,618	+	ACAAACTCATGAAATTCATGGCCACAGTAGGTAAC[A/G]GTCCCACTTACCTGTTAGAAATTCCAACTAGTCAA
1,436	3	3003	78.88	89809547	F1Dsnp	PHR	T	C	3	19,099,027	+	GAAAATGAAATGCTGCGAGTGGAAATCAATAAAAC[C/T]GAAATGGACAAGAACAAAGCGAATGAGGAGGTAGT
1,437	3	3003	78.88	89809548	F1Dsnp	PHR	T	C	3	19,175,567	+	GGCATTGGTGATGTGGATGACAGAACCTTGATGAT[C/T]AATTTCACGCTAAGAGACCCTGTTCCAAGAGCAGA
1,438	3	3003	78.88	89865522	F1Dsnp	PHR	T	C	3	19,196,568	+	TATGCGGAAACGGATGATCTTGTTATAGATCAGTA[C/T]GATGCTTGTGGAAGTGAACCCAAGTGTTCAAATGC
1,439	3	3003	78.88	378_47601	GBS				3	21,625,366		TGACTCCTCGGATGATTTTTCCGATGACTCCTCGGATGATTTTTCCGATGACTCCCCAGATGGA
1,440	3	3003	78.88	89809575	F1Dsnp	PHR	A	C	3	21,711,437	+	ATAGTATTGATAACAAGGTCATACTGCAGCGACTT[A/C]AACATGTCAAAAAATTTCCATGGAAGTTGAAATGA
1,441	3	3003	78.88	89865545	F1Dsnp	PHR	T	G	3	21,712,607	+	TTGTTTGTTACTGTAAGGTAGTTTTGAAGTGATGG[G/T]TGCTGAAGGGAAAGGATTGGCCAAGTATAAATAAG
1,442	3	3003	78.88	249_300090	GBS				3	21,712,738		GACAAAGCAGGCCTCATCATATAAGAGGAATGCATGTTTTCAATCTGGATACACGAATTACCAG
1,443	3	3003	78.88	89809577	F1Dsnp	PHR	A	G	3	21,816,376	+	TGATACCAGATGGCTGTCCAGTTGCTCCCTGTTCC[A/G]TCTGAAAAGCTGGCCTCTGTAGGCCCATCTGACCT
1,444	3	3003	78.88	89865546	F1Dsnp	PHR	T	C	3	21,860,444	+	ATCTTCAACAGCAAACATCTGACCAGTATGACAAG[C/T]TGAGCATGTTGAAGAACAAGCTGGAGGACCTCATA
1,445	3	3003	78.88	89809578	F1Dsnp	PHR	A	G	3	21,860,470	+	TATGACAAGCTGAGCATGTTGAAGAACAAGCTGGA[A/G]GACCTCATAATAGTCTTGCACTATTCCAAAACTGA
1,446	3	3003	78.88	89809579	F1Dsnp	PHR	T	C	3	21,892,699	+	CTTGCTACTCGAACTGCCCAAGCTACTAAATCTAT[C/T]AGGTCATACTGCAGTCAAGAAAGTGCGCTCACTTC
1,447	3	3003	78.88	89809580	F1Dsnp	PHR	T	C	3	21,900,608	+	TAAAGCCTGAGCACTTGGATATTTCAGAAGTTCTA[C/T]GGAATGAAGCTTCATTATATCATGCAATAAAGGAA
1,448	3	3003	78.88	89865549	F1Dsnp	PHR	A	C	3	22,019,213	+	GTGGATGATGAAGGATCATGCAATGTTCTATCATC[A/C]TCAGCATTAGGTGTCTCCACACTGCTTGCTTGATC
1,449	3	3003	78.88	89865550	F1Dsnp	PHR	A	G	3	22,129,977	+	CTCAGGATTTTCTCCATTGCCATGGTTGATGCTGC[A/G]TTTCTCCGTAGCCTTGGATCCATGACAAGTACAGC
1,450	3	3003	78.88	89825301	snp	PHR	T	C	3	22,166,730	+	GGCGAAATCCTCGTAGAAGCTCGAGTTGCCTGGTT[C/T]CTGGGGTGGAACCACGATTTGTGAGACGGCCTCTG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,451	3	3003	78.88	89865551	F1Dsnp	PHR	T	G	3	22,177,269	+	GGAAGTTTATGAATGCACAAAACTGAGAAGTCTCT[G/T]CACATTGGATGTAGCTGAATGTCTTCTGCAATTGG
1,452	3	3003	78.88	89809582	F1Dsnp	PHR	T	C	3	22,204,207	+	GTGTATACATCATCATCTTCTGCAATGGGTTCAAC[C/T]CTCCCATCTTTTGCATACACATCATCTTCTCCCAT
1,453	3	3003	78.88	89865552	F1Dsnp	PHR	T	C	3	22,228,708	+	ATGTCTTGACGTGCTAAGGTGTCTGTTGATGGATG[C/T]GGTTCATAAATTATTTCTGTTTCTTCTCCAACTGC
1,454	3	3003	78.88	89865553	F1Dsnp	PHR	T	C	3	22,229,388	+	GACTTGCGGACAGCTTCGCGTGCTAAATCTCTATG[C/T]GGCTACAAAACATATAGTGATTTCAGTAAAAAATA
1,455	3	3003	78.88	89809583	F1Dsnp	PHR	A	G	3	22,230,556	+	ATGACAGTTGAAACTCCTTGAGAGATACAGTCCAG[A/G]TATGGTGCCATATGAATCCTCTCCAAGTCATCATA
1,456	3	3003	78.88	89865555	F1Dsnp	PHR	A	G	3	22,243,208	+	ACACGTCTGTGTGTATATAAATGTTAGGTTGAAAC[A/G]CCTGATAGGATTGGAAGAGAATCAATTCTCAAAGT
1,457	3	3003	78.88	TP1129	GBS				3	22,257,461	22,257,398	TGCAGACCCTAAAGAAATTTTGCAGTCACGACCATCTTTGTTACGATACTGAACTACTGGTATA
1,458	3	3003	78.88	343_81809	GBS				3	22,265,478		CCTCATCTTGAGTCACTTGATCTTCGCTCTTRTTTCAATCTTAATCTGGAGGGAGATTTGGGCA
1,459	3	3003	78.88	89865556	F1Dsnp	PHR	A	G	3	22,270,372	+	CGGAATATTGGGACTTTGAAGATGTTGACTCCCAG[A/G]ACGTTGAATTTGTTTGATATTTTGAATGCTGATAA
1,460	3	3003	78.88	TP4774	GBS				3	22,313,303	22,313,366	TGCAGCGTTTGCGGGATCATCAAGTCAGGGTTCTCCCCCAAGATGGACGGAATCTCCACGCTGT
1,461	3	3003	78.88	89865557	F1Dsnp	PHR	A	G	3	22,375,573	+	TCCGACTCCGAACTAACGGCGGTAACGTCGTCGGA[A/G]AGCTGGAATCTGAGAGCCAATTCCTGAATCTTCTT
1,462	3	3003	78.88	245_297927	GBS				3	22,441,176		TTTATCCATACGAACGATTAACTGTCAATTCCAAAGACCCGGAAACCAGCATAGACATAACCAA
1,463	3	3003	78.88	89865558	F1Dsnp	PHR	A	C	3	23,171,849	+	GAAAACGATGGGGTTCTGACACCAGTAAGGCGCGC[A/C]TCTAGGCCATTGGCAAAGTAGTGAGCTAACCTTTG
1,464	3	3003	78.88	TP2325	GBS				3	23,200,352	23,200,415	TGCAGATGCAAGGCAACTCTCTAGTGATGTGAATTTCAGTCCAGACAAGGGTGAGAGTGAGTCA
1,465	3	3003	78.88	TP4701	GBS				3	23,200,615	23,200,673	TGCAGCGTAACGGCAAGGCGAAAGGATCCAAGGCCAAAAAAACAGGCAAGAAAAAGCCGAGATC
1,466	3	3003	78.88	89865559	F1Dsnp	PHR	T	C	3	23,234,360	+	TGGCCTTGGTTTCTGGCTGTTTCGGTAGGCCTTTA[C/T]GGGTTGTACTGTTTTCGAAAGCATTTAGTTGGTGA
1,467	3	3003	78.88	89865561	F1Dsnp	PHR	T	C	3	23,331,025	+	AGTTCCGCGAATTTGAGATGGACATGTTTCAGCAA[C/T]ATAGAGTGGAGCCCCATGCATGGCCTGTCAAAACA
1,468	3	3003	78.88	89865562	F1Dsnp	PHR	T	G	3	23,434,335	+	TCCACAAGGTCCGGAAAGAAGTCTACCCAGGGCAT[G/T]GGCATTTTGTTTAAAGAGGAGTGGTGAAGTGATAT
1,469	3	3003	78.88	TP1114	GBS				3	23,575,804	23,575,745	TGCAGACCCAAGTCTCCTTGGAGACCTCCATGGACAGCTTCGGCTCACACATCATTAGCAGGAG
1,470	3	3003	78.88	89865565	F1Dsnp	PHR	T	C	3	23,810,279	+	AGTTCTGACTCTTCTCGGCGGCTTGACAATTCTTT[C/T]TTCATTTTCAGTGATTCAGGCACAACCCAGTTTCC
1,471	3	3003	78.88	89809590	F1Dsnp	PHR	A	G	3	23,811,754	+	TCATAATCCAATTCCTTTGATTTAACTTCCTCCAC[A/G]ACATCAGCAGAGGAACTGAAATCATGAGTGTCAAC
1,472	3	3003	78.88	89809591	F1Dsnp	PHR	T	C	3	23,942,073	+	TTGACACGATCAGTTCTCGAATTTTTTCTTAAATT[C/T]GTCTGGCATGTCTTCTGGGAATAATTCCTCAATAA
1,473	3	3003	78.88	89809593	F1Dsnp	PHR	A	G	3	23,955,212	+	TGCATGTTATCATTCAATTTCACATCAAATTTATA[A/G]GCTCCATTCTTAGCGGTCTTCACTTTAAGGGAGTA
1,474	3	3003	78.88	89809594	F1Dsnp	PHR	T	C	3	24,030,930	+	AGAAAGAAAATACCCTTTTGCGCTTTCCAGTAACC[C/T]TAAGGCCACTGCGATCTGATTTTCCAACATTGAAA
1,475	3	3003	78.88	89809595	F1Dsnp	PHR	A	G	3	24,050,632	+	ATAAAGGGGAAATGTTTTGTTTGATCTGAGAGAAT[A/G]AACATAGGAGTATGGTGTCTCGATAAGAACAGTGT
1,476	3	3003	78.88	89809596	F1Dsnp	PHR	T	C	3	24,058,422	+	TTCTCTTCTAATTTCTTAGGTGAAGTCTGTTCACT[C/T]CGCCAAAGTAGTTTTGAGAATGTGGCTATTGTTGA
1,477	3	3003	78.88	89809597	F1Dsnp	PHR	A	G	3	24,065,775	+	ATGAGAAGTATTGGGAGGATGAGTTTAGAAAGGCC[A/G]CGACTAGTGCTGAAGCAATGGAAAAGCTAGCAAAA
1,478	3	3003	78.88	89809599	F1Dsnp	PHR	T	C	3	24,111,503	+	CCATGATGCTTGCAAGAGCAAAAATGAAGGGAGCA[C/T]GCACGAGACCAGACAAATATTTTCATCCTCGCACT
1,479	3	3003	78.88	89809600	F1Dsnp	PHR	T	G	3	24,204,279	+	TGAGCAGAAGTGAAAACTTGCCCACTTGAAGCAAT[G/T]TACTCGGCCAAAACTAGCCTCATTTTCTGGTGAGA
1,480	3	3003	78.88	89865568	F1Dsnp	PHR	A	G	3	24,208,590	+	TTTGGAATGGAAGGTTGCACACTGTAAACCCCAAC[A/G]GAGAAGTTGCCATCAAATTCTTCTTTTGCTTCTGC
1,481	3	3003	78.88	89865569	F1Dsnp	PHR	A	G	3	24,283,436	+	GAAGCACAGATGAGTCTCCGATAGCCAAGACTAAA[A/G]AATAAGGTTCCAGACATGGATGAGAATATACGTGA
1,482	3	3003	78.88	89865570	F1Dsnp	PHR	A	G	3	24,285,745	+	TACCTTTTCTTAATTTTAATCCCACAACAGCCATG[A/G]TGAAGTTGATGAACGTCTTCTTTACAGTACTACTG
1,483	3	3003	78.88	23_149629	GBS				3	24,388,680		CCAGCTCTTACCCAGTGTCTCCCCAATGTCCATTAAAGCTTGTACTACAGGCAAATCCATCAGC
1,484	3	3003	78.88	89809602	F1Dsnp	PHR	T	C	3	24,391,910	+	ATTCAGGCTAGTGGTTTTACAGGCCCAATTCCTTC[C/T]GGCATTTCTCTCTTGACAAGTATAATTGACCTGTT
1,485	3	3003	78.88	89865572	F1Dsnp	PHR	A	G	3	24,434,259	+	GGACAAAAGGTAGTGAAAGAAATGGATCACTTGGA[A/G]GCATACAAGATTGCATTAACAACTTGGGCTAAATG
1,486	3	3003	78.88	89865573	F1Dsnp	PHR	T	C	3	24,436,656	+	GTAGCTATTACCATCCACCTCCGGCTGTGATCTAG[C/T]AATCCTGAAGTATATACTATCTGGCACTTTTCCTC
1,487	3	3003	78.88	89865574	F1Dsnp	Other	T	G	3	24,600,064	+	CTACATCAAACCCGCCATCACCGACAACGGCGGCC[G/T]TTTCACTTTGATCGACCGAAACAACTCGTGTCCTT
1,488	3	3003	78.88	89865575	F1Dsnp	PHR	A	G	3	24,711,659	+	CCAAAATCTCGAGTGCCTCCCTCGGACAGCATTTC[A/G]ATTAGCTCTACAGGACATGGTGATGTTTAATCTTG
1,489	3	3003	78.88	89809604	F1Dsnp	PHR	A	C	3	24,733,488	+	ATCACTAGGTTTTGCAAACACATCTTTCAGATCTT[A/C]CGGATTCATAATGTTCACCCGTGGTAGAGGGCCAA
1,490	3	3003	78.88	89865576	F1Dsnp	PHR	A	G	3	24,864,204	+	CTCAAACAGATGCCTCCATGGATCCTTTTCCATCT[A/G]TTATCAATTTGTCAATATCTGGTTCAGGCCGTCCA
1,491	3	3003	78.88	89809605	F1Dsnp	PHR	A	G	3	24,942,745	+	GATAAATTAGCATCATCCTGGAGAACTATCATCAG[A/G]TACTCAGCCAAACCTCTAACTGCTTGATCAATTGC
1,492	3	3003	78.88	89809607	F1Dsnp	PHR	A	G	3	25,254,847	+	CAGCTTGTTCAAGACATCCGCAAGAGGAAGGGCCT[A/G]AAGGAGCAAATGACCCCGCTATCTGAGTTTGAGGA
1,493	3	3003	78.88	89865577	F1Dsnp	PHR	A	G	3	25,377,456	+	TTGCAGTTGCTGACACACTCCGTTGTTCTTGTACA[A/G]CCACTGCATGAAGCATTTACACAGAATTATTGTAT
1,494	3	3003	78.88	89825899	snp	PHR	T	C	3	25,381,644	+	CAGGGAACTGCGTGGAGAATCCGGTTGATGGGTTC[C/T]AGATGTAGAAGTAGGTATCATCAAGGGCTACAAAG
1,495	3	3003	78.88	89865578	F1Dsnp	PHR	A	G	3	25,390,312	+	TGTTGAGATCGCCCTTCAGAGGAAAATCAAGCACA[A/G]AGGGTAACATATCATCATCTATAGGTGCTTCTTGG
1,496	3	3003	78.88	89809608	F1Dsnp	PHR	A	G	3	25,434,893	+	ATAACTAAAGAAACTTACGATCTGTCACGTCAATG[A/G]TCATGGCTATTTTGTCAAGTACAGCAATAGCATCT
1,497	3	3003	78.88	89865579	F1Dsnp	PHR	A	C	3	25,467,625	+	TAGCGATTGAGTTCCCGAAAGCAGGGACCGGGCCT[A/C]TGCTTCTTGTTCAGGAGAGCTTCTTTGATTGTGGT
1,498	3	3003	78.88	89809610	F1Dsnp	PHR	T	C	3	25,471,538	+	AAATTCGGACCTCATCTCAACACACTGCTCATATT[C/T]AACAGAAGCTATAGTCAAAGGAACTCTTTCACTAA
1,499	3	3003	78.88	89809611	F1Dsnp	PHR	A	C	3	25,613,411	+	GAATAGCTGCTTTACATGGAAACACATCTTTCCAA[A/C]TGTTTATGATCTGCAACGCATTCTCCTTTTTTTCG
1,500	3	3003	78.88	89809612	F1Dsnp	PHR	A	G	3	25,641,099	+	CAATTGATTTCAAGTTCCCAATTTGTTCAGGAATG[A/G]TTCCAGATAGGTTATTTCGATACAGATACAGAGAG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,501	3	3003	78.88	89883134	snp	PHR	A	G	3	25,641,455	+	ACCTCAAGATTTTTTAGAAGACCAATTTCTGGTGG[A/G]ATATGACCGGAAAAGTGATTCCTAGACAGATCAAG
1,502	3	3003	78.88	310_136508	GBS				3	25,641,461		ACCGGAAAAGTGATTCCTAGACAGATCAAGACAGATGAGTTTGGAGAGGGAACTAATCTGAGGT
1,503	3	3003	78.88	89786118	snp	PHR	T	C	3	25,641,492	+	TATGACCGGAAAAGTGATTCCTAGACAGATCAAGA[C/T]AGATGAGTTTGGAGAGGGAACTAATCTGAGGTGGG
1,504	3	3003	78.88	TP5929	GBS				3	25,641,656	25,641,593	TGCAGGAAGTGTAAACAGGATAAACCTCACCAATTCTGGTATTCAAGGTACGCTTCATGATCTA
1,505	3	3003	78.88	9_1005867	GBS				3	25,774,099		TAACCGAATTTGAAACTGAGAACTTTCACACGTGTGTCGTCACATATGACTGATATGAGGCTGA
1,506	3	3003	78.88	89865581	F1Dsnp	PHR	A	G	3	25,816,127	+	GATTAATTTGAGAGCGGTGGAGCTACGAGATGGAG[A/G]TAGACATGCCTTGCCAGTGCAGTGAAGTAATTTCT
1,507	3	3003	78.88	570_40143	GBS				3	25,880,539		GGCCCATGAAATTAGTTGAAGTGAGAAACACRTAATCATATTTAAAATGAAAATCACTGTTTAT
1,508	3	3003	78.88	89865582	F1Dsnp	PHR	A	C	3	25,909,289	+	TGTCCAGAGTCTTTTCTGAGGACTATGAAAGAGTA[A/C]AGAAGAAGATATTGGATCCTCGAGGACCAACAATT
1,509	3	3003	78.88	89809613	F1Dsnp	PHR	T	C	3	25,964,140	+	GAAACTTCTATCTGTGTGTTTGTTAACACCGATGG[C/T]CAATTCAGGCTGCGGGCATGCTGGATAGTATGAAC
1,510	3	3003	78.88	89809614	F1Dsnp	PHR	A	G	3	26,199,131	+	CAGGCACGCCTCCAGGTTTCTGAAGTGGTTCTCGA[A/G]CAGATAAAGCAACTTAACCACCTTGATTTGGAGCT
1,511	3	3003	78.88	89809615	F1Dsnp	PHR	T	C	3	26,286,869	+	TGGTACAGCACCTGTTTTTTGGGTTGCATCACTGC[C/T]CTCTGACCCTTCACTCGAAGTATTAGTGGTGGTTG
1,512	3	3003	78.88	89865584	F1Dsnp	PHR	T	G	3	26,660,269	+	TAACCAGAGTTCTTCAGCAAGAGTGAGTTGGCCAA[G/T]CTACCAAATGCTTCAATTGCCATCACATAACTCT
1,513	3	3003	78.88	89809616	F1Dsnp	PHR	T	C	3	26,735,898	+	TCAATTTCAAAGGCTGCTTTTGAACTTGACGACTT[C/T]ACACGAATAGTAGAGATTTTGCACAAAAGGTTTCT
1,514	3	3003	78.88	89826159	snp	PHR	T	C	3	27,053,464	+	TGCTCACATTTAAGCAATACAACAATGTACGTGGA[C/T]GTCTCCGACGGCGGGCTACGTAAGTGAGCGGAAGA
1,515	3	3003	78.88	89865586	F1Dsnp	PHR	T	G	3	27,211,130	+	TCGCCGGGATGATTTGGAGTCACTTGGCCATGTTC[G/T]TCTGTATTTCTTAAGAGGAAGCCTTCCTTGGCAGG
1,516	3	3003	78.88	TP2958	GBS				3	27,244,125	27,244,181	TGCAGCAATGACAGTAAATACTGAAGTAGATCTTCAAAGCTTGGTTGCTACATTCCGAGATCGG
1,517	3	3003	78.88	89865587	F1Dsnp	PHR	T	C	3	27,295,811	+	CATCTGATCCGAATTGGTCATCGATACCCTTTGTT[C/T]TTATGCTCCAATCATCTGATCCAACAGGAGACACG
1,518	3	3003	78.88	89809619	F1Dsnp	PHR	T	G	3	27,361,179	+	ATCCCCAATTATGTATTCCCTTATATCAAATCCTC[G/T]GGAGAGCTCTAATACTTTCCCATTTAACCTCTCCC
1,519	3	3003	78.88	68_605340	GBS				3	27,448,217		CAGAGTTGACAATGTGAAAGACTAAAGCAAASAGTTGAAAGAATCAATCTTTGAAGATTAAAGA
1,520	3	3003	78.88	89809620	F1Dsnp	PHR	A	G	3	27,471,570	+	CCTATGGTGCTCGAGTCTGCTTTCAATGTGGATTC[A/G]GAGACTGAGCACCTATTCCGTTCTAAGAGGACTTC
1,521	3	3003	78.88	89809622	F1Dsnp	PHR	T	C	3	27,632,617	+	CTCTCAGTCTTGGTTGCCATTGAGATGTTCAACTC[C/T]CTCAATGCCCTGTCCGAGGACAGTAGCCTCCTGAT
1,522	3	3003	78.88	89809623	F1Dsnp	PHR	A	C	3	27,642,111	+	TGTATTCATCTTGTGATACTACCAAAGCTGTTACC[A/C]GTGTTATTGCAATTGAAGATCGTACGATAACCACT
1,523	3	3003	78.88	89865588	F1Dsnp	PHR	T	C	3	27,719,286	+	GATGATGCTGAAGAAGAAGAAGCTGAAAAATTCGC[C/T]GCAGGAGGCATTGATCTTGACCAAGTTGTTAATTT
1,524	3	3003	78.88	89809624	F1Dsnp	PHR	T	C	3	27,734,495	+	CTATAACAAAATCCAAAAGCAGACATTACCAGGAG[C/T]GAGGTTGGGGCACTGAAAAGTCGGGTGCCAATCTG
1,525	3	3003	78.88	89809625	F1Dsnp	PHR	A	C	3	27,751,454	+	AAAGAGCCTAAAAAATGCTTGCAATGAAAGAATAG[A/C]GAAACCCATTTTACTCTATCTCTCTCTCTCTCTCT
1,526	3	3003	78.88	89865589	F1Dsnp	PHR	A	C	3	27,781,363	+	TCTCACGAGAAGGATAGAAGAAAACTTCATTTTCA[A/C]CTCTACTATTTGAAGAGTATACTCCCCAATGTTAT
1,527	3	3003	78.88	89809626	F1Dsnp	PHR	A	G	3	27,810,350	+	AGCGGCGTCTAGGTTTTTTCTGTTTCTTTTCAGGA[A/G]CCTCCTTGATGCTATGCATTGAGAAGTTAGCATCA
1,528	3	3003	78.88	89865660	F1Dsnp	PHR	A	C	3	31,538,685	+	GTTTCTATAGGTCCGATTCATCGCTGCATGGAAGG[A/C]TTGCTAGTCACGGCAGAGGAGAAAGACAACTACCT
1,529	3	3003	78.88	312_127000	GBS				3	31,598,991		ATTCATTGGCTCTTCCTGCTTCGAATAGGCCAATTAAAGTTGCCTTGGTCCGGTGCAAGGACAT
1,530	3	3003	78.88	89865662	F1Dsnp	PHR	A	C	3	31,694,156	+	AGCAAATCATCTGCTAAAATCCTGTTTGCGGCCTC[A/C]GAAGGATGAAACCCGTCCCAAAACACATACTGAGA
1,531	3	3003	78.88	89865663	F1Dsnp	PHR	T	C	3	31,694,344	+	GAGGTCGTAGAGAGGCTGGTAGATGTCAAAGACGA[C/T]CAGCTTGAGTCCGGGCAGCTTAGTTTGCAAATTCT
1,532	3	3003	78.88	89865664	F1Dsnp	PHR	T	C	3	31,709,131	+	GGGTCCAGCCCTGTTTCATTATCCAGTGATAGATG[C/T]TCCAACACACACATAGGCCTAAATTATAAACACAA
1,533	3	3003	78.88	89865665	F1Dsnp	PHR	A	G	3	31,815,106	+	GTCCGTGAGAATGCTATTCTGTTGAATTTGGGCAC[A/G]TTACGTGCAATTGCAATGCAAGAGCGTGTCCTTAT
1,534	3	3003	78.88	89810086	F1Dsnp	PHR	T	C	4	6,603,050	+	ATGACCTTCTTTCGGCCCAAAACTCTCCAGATACA[C/T]GGCAGCACTCTTTCCTTCTCCCTACTTGCAAGTAA
1,535	3	3003	78.88	89810087	F1Dsnp	PHR	A	G	4	6,635,081	+	AATTTCTCATGCTTGTAAAACAAAGGAAGCAGGAA[A/G]CAGCAGATAAGTTACAAAACACTGTTTCATTTCTG
1,536	3	3003	78.88	89866042	F1Dsnp	PHR	A	G	4	6,701,138	+	AACCGCCAGCATTGTTGTTATTGTACTGGTTTACA[A/G]CTGCTACTGCCATTTTTCTTGCTACTTCGCTGCTG
1,537	3	3003	78.88	89889056	snp	PHR	T	C	4	6,774,600	+	TTCTGGACTTGCTCTTGCTGAAAAAAAGACACATC[C/T]GGCACGGTTCTTGGGCAATCAACAGAAATCTAACA
1,538	3	3003	78.88	89866043	F1Dsnp	PHR	A	G	4	6,844,256	+	ACATTACTCGTTTGTGGAAACCAATTTGTTGGTGA[A/G]CTTCCTAATGTGTTTGGGAACCTTAGTCGACTAGA
1,539	3	3003	78.88	89810088	F1Dsnp	PHR	T	C	4	6,846,218	+	TTGGTTGGGACTTTGGGTTATATTCCTCCAGAGTA[C/T]AGTCAGACGTTAACTGCAACCTGCAGGGGCGATGT
1,540	3	3003	78.88	89865934	F1Dsnp	PHR	T	C	4	21,365,621	+	TAAAGAAAACTCACATAGGTGCTTGTAAGCAAGAG[C/T]CTTCTTGCGATCCCTAACACAACATTTATGGGCAT
1,541	3	3003	78.88	89865935	F1Dsnp	PHR	T	C	4	21,558,771	+	GTTTTTACCCCATTGGTTGAAAAATGCAAGAAATA[C/T]GGAAGAGCAATGCGTATTGGCACAAACCATGGGAG
1,542	3	3003	78.88	89809989	F1Dsnp	PHR	T	C	4	21,667,310	+	CTGCAATGGTTTGGTTTGTGCACTGCTTCTTCCAC[C/T]AAAGCACTTCTACATCTGGAACCCATCAACTGGCT
1,543	3	3003	78.88	89890194	snp	PHR	T	G	5	14,491,063	+	TAAAACCGACAACTATAATAAACAGAATGACCAAT[G/T]CACTTGCAATAGAAGCGATCCAGTTAAGCATGGAA
1,544	3	3003	78.88	89866122	F1Dsnp	PHR	A	G	5	14,537,500	+	TCTTCACCAAACACAGTGTGGAGTAGTAGGAGGTG[A/G]GTGGCATTCTGGGTATTGAAGCTACGTTTGTGGGT
1,545	3	3003	78.88	89810161	F1Dsnp	PHR	A	C	5	14,674,741	+	GATCATACGGAGGATCATTTTGAACTACCTCAAAG[A/C]CTTTTCATGTGCACTACACTGGAGAAGCTGACAGT
1,546	3	3003	78.88	89866124	F1Dsnp	PHR	A	C	5	14,701,704	+	GGCTTTGTTTGAGGGGTGATGATGTGGACCACACT[A/C]GTATTACTGCTTGGATCAACACTGCCATTAGGCGC
1,547	3	3003	78.88	89866125	F1Dsnp	PHR	T	G	5	14,703,402	+	ATATCTATGGATGATCTTGATGTGAATGAAAAAGA[G/T]AAGATTTATAAGGAGATTTTGATGGTTCCAAGGGG
1,548	3	3003	78.88	89866126	F1Dsnp	PHR	A	C	5	14,740,648	+	GTGGAACTTGATCTTTCTGTTGTTTCAGATGGAGA[A/C]GAGATGCTTGAGTTGCCAAACAGTCTTTTGACTTG
1,549	3	3003	78.88	89810164	F1Dsnp	PHR	T	C	5	14,741,131	+	CGTGCAACTAAGTTTCTGGCTGGAATTTCTGGTGT[C/T]AAATGTCTGACTCTTTCTCCTTTCTCTATGGTGAG
1,550	3	3003	78.88	288_97570	GBS				6	30,128,644		GGTGTCATTCCCAATTTGACAAGCAATTGAGMATCTAAAACACCACTGCAGTCACCGGGAGCAT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,551	3	3003	78.88	89810917	F1Dsnp	PHR	T	G	7	184,665	+	GGGAAGAACAGTGATGAGTGGACTGAGGAGATTGA[G/T]TATTTGGATGAATCAGGCAGTGTTATTTACACTGG
1,552	3	3003	78.88	89866956	F1Dsnp	CRBT	T	C	7	318,773	+	CATTGAAAATGTCTGCATGCCATCTTGGAAGTAAT[C/T]AAAACTACTTTGTTGTTTCTCCAGGGATTGATGAT
1,553	3	3003	78.88	TP3322	GBS				7	324,717	324,776	TGCAGCAGCAGCAGCAACAACAACAACACCACCACCAACAACAGCCGCCTGTGGTTGGTGTTGT
1,554	3	3003	78.88	89866957	F1Dsnp	PHR	A	G	7	328,313	+	TGTGAGTGTGGTGGAACTGGTGAACAGAAAGGAGG[A/G]ACATTGTATAGGGATGTGTGTGATTCCTCTAAGCG
1,555	3	3003	78.88	89866962	F1Dsnp	PHR	T	C	7	373,646	+	GGAAAAGATGCGACTCTTCTATCATAATCTTCCAT[C/T]AGGTAGACTTTAAAGCAAGGATATTTATTCCTACA
1,556	3	3003	78.88	89811008	F1Dsnp	PHR	A	C	7	447,799	+	GCATCAGGATTTGGTGAGGGCATTCTTTGCCAGTG[A/C]ATGTGATATGCTGAATGAAAGTGGGGAAGTTCATG
1,557	3	3003	78.88	89811012	F1Dsnp	PHR	A	G	7	499,276	+	AGAAAGCCATAAGCTTTACCCACAAGCTTCATGTT[A/G]TCAGCATTAAGACACGTGTCCAGGACCTCCCAATC
1,558	3	3003	78.88	89866971	F1Dsnp	PHR	T	C	7	531,567	+	GTCAATGATGCATTCGGAACTGCACACAGAGCCCA[C/T]GCTTCAACTGAGGGTGTAACAAAATTCTTGAGGCC
1,559	3	3003	78.88	89811014	F1Dsnp	PHR	A	G	7	532,211	+	TCTCTGGTGGAAGAGGATAAGCTAGAACTTGCTAC[A/G]TCACTCATTGCGAAGGCCAAGGCAAAGGGAGTGTC
1,560	3	3003	78.88	89866972	F1Dsnp	PHR	T	G	7	536,588	+	TATTGTTGGTGGCTCGAAGGTGTCATCCAAGATTG[G/T]AGTCATAGAGTCCTTATTGGAGAAGGTTAACATTC
1,561	3	3003	78.88	127_476391	GBS				7	573,017		TCTTGTGGGCTGCAGACTTACACACGCATATGTATGCATGTACGATCAGTGTTTATATAATTTG
1,562	3	3003	78.88	89866973	F1Dsnp	PHR	A	G	7	586,048	+	AGTCCCTCTCAGACATTGCCTCAAAAACACAACAA[A/G]CATCTTCCATCTTCCCACACTTGGCATGAAAATCA
1,563	3	3003	78.88	TP8076	GBS				7	588,523	588,500	TGCAGTATACATCAAGTAATCTTCATTCTCATTTGAAACAATGGTAAAGTTGTACCTCATCTTC
1,564	3	3003	78.88	244_324861	GBS				7	4,014,215		TTTTCAGCACAATAGGTCGCCGAGGCTTTTTTGGTGTTGCAACCGGGAAGAAGAGTTTGCTGTT
1,565	3	3003	78.88	TP5092	GBS				7	13,147,562	13,147,620	TGCAGCTCCGCCGCTTCGTGGCAGCTTCCAGGCGGCGCAACAGCGAGCGGGACTGCTCCATAAA
1,566	3	3003	78.88	89866796	F1Dsnp	PHR	A	G	7	13,250,543	+	TTTGTCTTCTCAACCTCACAAATCCCCCACTCCCC[A/G]ATACAACTCTTCTGCAAACATCAACCTCAATCAAA
1,567	3	3003	78.88	89810835	F1Dsnp	PHR	T	C	7	13,258,088	+	GTTGAGCATTTGCAAGCAACTGTCTTCCCACAAGA[C/T]TGGTCGCAGCATTCTATTGGAAATTATGGCTCTGG
1,568	3	3003	78.88	89866797	F1Dsnp	PHR	T	C	7	13,390,648	+	CATTCCCAAGCTTCATCTCCATATCAATGCACCTC[C/T]TAAATATCTTGTGTTTGGGTGCCACTCTCATTGTA
1,569	3	3003	78.88	89866798	F1Dsnp	PHR	T	C	7	13,390,737	+	GCACCCTTGAGATTCCTCTGTCGTAACTCCAACCC[C/T]GCAGCAAGAAGCCATACTTTTGCAAATGAGAACTT
1,570	3	3003	78.88	288_251385	GBS				NGH			CAGGCCCGTGATCCTCCGGTGACACCAAATAAAAGCACTACGGAAATAGCACAAGCTAGTGCAC
1,571	3	3003	78.88	TP4584	GBS				NGH			TGCAGCGGAGGAGCTCGGAGGAGTTCTCCGTCGTCAGACCATCTCTTTGCGTCCAACCGAGATC
1,572	3	3003	78.88	TP2198	GBS				NGH			TGCAGATCCTCATCTACACACCTCCTCATTCCCACCCCCATCTTTCCTCGTAGTCTCACACCAT
1,573	3	3003	78.88	TP7269	GBS				NGH			TGCAGGTCAAAGCAGGGAGGGAGACCTTTGCTTTAGCCCTTCTCAGATTCTTTGTCTTGAGATT
1,574	3	3003	78.88	TP6477	GBS				NGH			TGCAGGCATTCATTTCACTCTCTACTAAGGAGTTTAAGATAGAAGATTTAGATTGTCAGATGCA
1,575	3	3003	78.88	TP898	GBS				NGH			TGCAGAATTAGTAGAATCGAAACAGGAACCAAAGCCAAAGCGTTAGTCCTGTTACCCTCCTCCG
1,576	3	3003	78.88	TP8995	GBS				NGH			TGCAGTGGTGTTTTAGATGCTCAATTGCTTGTCAAATTGGGAATGACACCTACCTCTAGAACCC
1,577	3	3003	78.88	TP8364	GBS				NGH			TGCAGTCCGACTTCAGGAACTTCGTCTGGTACAACTCCAATGCCAAATCCTCGCATCCGTCCGA
1,578	3	3003	78.88	244_324778	GBS				NGH			GTAGAATCGAAACAGGAACCAAAGCCAAAGCTTTAGTCCTGTTACCCTCCTCCGAGTTCTCTTC
1,579	3	3004	83.99	89865063	F1Dsnp	PHR	A	G	1	18,952,671	+	CCTTGCACACAAACGGCCGTTTGAAGGTGAGTTCA[A/G]CCGCATTTATTTCGGCCATATCATCATCACTGCTC
1,580	3	3004	83.99	TP2422	GBS				3	19,853,385	19,853,445	TGCAGATGTGTTTACTATGGAATTGATAGGTGGTTTATTGTGTAAGGATGTAGTAGATCCGAGA
1,581	3	3004	83.99	89809551	F1Dsnp	PHR	T	C	3	20,005,263	+	AACAGCCAGGCCAAGATTAACAACACAATCATCTC[C/T]TTGCTGCTTATTCTGCGCAACTATGGAGGTGTTAA
1,582	3	3004	83.99	35_831787	GBS				3	20,053,834		GATTGCAGAATATGCGCAAGAGCTGACGATTGCAAATGAAAAATTACAGGGCTCAAAAGAACAG
1,583	3	3004	83.99	89809553	F1Dsnp	PHR	A	G	3	20,101,652	+	GATGTATTGCTAAATGCAGGACACAGTAATGCAAG[A/G]TGTCACTATGCCCCTTACTACCAATGATTTAGAGT
1,584	3	3004	83.99	TP7807	GBS				3	20,120,569	20,120,632	TGCAGTAATCGGCTGTTCTTGTTTCTTTAGATACGCGTTAAATTTGACAGGTTTCTTCTGTTAA
1,585	3	3004	83.99	89809554	F1Dsnp	PHR	A	C	3	20,150,573	+	CCATTCATCCTTTGCGCCTTGTGTTCAGACTTATC[A/C]GTAACATCATTTGCTCCATTCACCGTTTGTGGCTG
1,586	3	3004	83.99	89809555	F1Dsnp	PHR	A	C	3	20,187,581	+	GCATATAATACTTCCAAGGCTTTACTTAGCGCTTC[A/C]GCCTCTGGAGGGTCCAAAAAATCAAAATGTGTCAA
1,587	3	3004	83.99	89809556	F1Dsnp	PHR	A	G	3	20,190,499	+	CATACACTGCAGCAGAGCATACTAGCTACTTCTTT[A/G]ATGTGAAACGAGAATTTCTCAAGGGTGCCCTGGAA
1,588	3	3004	83.99	89865524	F1Dsnp	PHR	T	G	3	20,191,307	+	TTTATTTGGAATCTTTGATCTTTCAGATTTTCTCA[G/T]TTCTTTGTTTCACCTCTTATGAAAAGTGAAGCCAT
1,589	3	3004	83.99	89809557	F1Dsnp	PHR	T	C	3	20,351,499	+	TTTGTTCACCGCCTTTTTAATATCATCGATCACAT[C/T]GAATCCCCTGACTGAATTCGCATTTGGGAGAGCTG
1,590	3	3004	83.99	89865526	F1Dsnp	PHR	T	C	3	20,351,506	+	ACCGCCTTTTTAATATCATCGATCACATTGAATCC[C/T]CTGACTGAATTCGCATTTGGGAGAGCTGTCTTCTC
1,591	3	3004	83.99	89809558	F1Dsnp	PHR	A	G	3	20,382,244	+	AGAGACATAATTAGTGATAGGTAAACTATGTGGGG[A/G]AAGCTTCCATAGACGAGGACCAAAGGCTGGAATGA
1,592	3	3004	83.99	49_345349	GBS				3	20,391,601		ATATTAAGCTAACGTAGAAGAGAAAGAGAGGRGGAAGGAACATGCATTAACAAAGCAATCGTGA
1,593	3	3004	83.99	89809561	F1Dsnp	PHR	A	G	3	20,627,913	+	CCACCTTTTGCAATTGCTCCTTGACACAAATTGCT[A/G]AGTTCCTTCACTTTTTTTCTCATCTCCTTTCCGTC
1,594	3	3004	83.99	89865530	F1Dsnp	PHR	T	C	3	20,628,351	+	CCGGCAGCAATTTCATCCATTTGGGCACTCGAAAC[C/T]GATAGAAAACTCCCCAATGAAATGTACAAGACAGA
1,595	3	3004	83.99	89865531	F1Dsnp	PHR	T	C	3	20,635,021	+	TGTTGGAGTTCACTCGCTCTCCTTCTCATTCCTTT[C/T]CCTTCATCATCCTCCAAATCCATAAATTTTTTCAC
1,596	3	3004	83.99	89865532	F1Dsnp	PHR	A	G	3	20,642,204	+	TCACTGATAAAACCATCAAGGTTCTTATCAGATGA[A/G]CCACCTTTTGCAATTGCTTGGTGACACAAATCCCC
1,597	3	3004	83.99	89865533	F1Dsnp	PHR	A	G	3	20,642,279	+	TCTATCGCTCTCTTCCTCATTTCCTTTCCATCTTC[A/G]CTTTCAAGATCCATAAATCTCCGCACCAGCTTGGC
1,598	3	3004	83.99	TP9721	GBS				3	20,696,312	20,696,255	TGCAGTTTCGATTCCTTCCTGTCAGAGACTAGCCTTCCTTCAAAAGGACATTTCCGAGATCGGA
1,599	3	3004	83.99	89809563	F1Dsnp	PHR	A	G	3	20,704,176	+	AGCTATAGATTGTTTAAATGGTGCAGATGGGAATG[A/G]GAAACCAAAGTATGACACTGTTTATGGGGTAAAAC
1,600	3	3004	83.99	89865534	F1Dsnp	PHR	A	G	3	20,706,492	+	ACCTTTGCCTCCTCATCCCTGATCGAATGGAGACG[A/G]AAACGACCCTTGGTGTCATACAGCAGACGGAAATT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,601	3	3004	83.99	89809564	F1Dsnp	PHR	T	G	3	20,710,749	+	AGGGAGCAATTTGTTTACACAGCTAAGCAGATGGG[G/T]TCAAGGGCTTGGGGTTCTGCTAAGGCATTTGCAGT
1,602	3	3004	83.99	89809565	F1Dsnp	PHR	A	G	3	20,728,521	+	GCAGCAACCTTATCTGCCGGAGTAGATATATGGAC[A/G]GAGAACTCAATAGCATCTTGTGTGTCCGGACTGCG
1,603	3	3004	83.99	240_241980	GBS				3	20,846,602		TCAAACTCAACATAATCTGTTTTCTTTTTTTCTTCAACTGCAATTTGCTAAAGCTTTCAACTTT
1,604	3	3004	83.99	89809587	F1Dsnp	PHR	A	C	3	23,014,976	+	AGCAGAAAATGATCAAATCCAGCAAAAGATTGCAA[A/C]TGTTACCGGAAAGCTTATGGTGAAAGAAGGTATTA
1,605	3	3004	83.99	89809637	F1Dsnp	PHR	T	C	3	28,661,847	+	CTGGAAACACAACAATACTAGGACATGCCTACCTC[C/T]TGTGCTTCTACAAATTCAGATCGTGTCAACTCCAT
1,606	3	3004	83.99	89809638	F1Dsnp	PHR	A	G	3	28,662,731	+	AATATATGCAGCAGTTCATTGTAGAAGAATAAGCC[A/G]AGGCATTGTTGTCTCTGCATCAGCATAAGAAAGCA
1,607	3	3004	83.99	89865599	F1Dsnp	PHR	T	C	3	28,829,188	+	GGAAATCTCATTAAGCTTGCTATACTCCAGTTGGG[C/T]AATAATTCACTGTCTGGTCAGATTCCACCTGAGCT
1,608	3	3004	83.99	89809641	F1Dsnp	PHR	T	C	3	28,970,947	+	TTACAAGATCTAGATACCGACTTGTCATGGGTGGG[C/T]AAGCTAGACAAAAAGAAGAAGCATGGGTCTTTTGC
1,609	3	3004	83.99	89865600	F1Dsnp	PHR	A	G	3	28,977,500	+	TTCTTGGAAAACTGAGTAGGAGGCTCAATCCCCCT[A/G]TAAGGCCTATCCGGGTGTGACCTCATGTGTCCATA
1,610	3	3004	83.99	89865601	F1Dsnp	PHR	A	G	3	29,004,192	+	TGTAATCTTATGGCTGGTAGGCGTACCATGGGTTT[A/G]CACCAGGCTGTCGCTCTTTGTATGGACCATTGCCA
1,611	3	3004	83.99	89883660	snp	PHR	T	C	3	29,007,435	+	AATGGAGATGGAGAGGAGGTGGTATGAACCCCGTT[C/T]ACATCATCAGCCACAGTTGAAGGCGGTAATGCAGG
1,612	3	3004	83.99	89809642	F1Dsnp	PHR	A	G	3	29,007,637	+	AAGGGCATGCCAATTCCTTGAATGAAGCACAACAC[A/G]GATCGGCAGGGTACCGTGGTCCTTTGCATTGGCTT
1,613	3	3004	83.99	89865602	F1Dsnp	PHR	T	G	3	29,011,298	+	GATTATTAGAACAAGTACCTTCTGAATTTAATGTT[G/T]CCTCACAAGAACTATTGTTCATACAACAATCAACT
1,614	3	3004	83.99	TP5666	GBS				3	29,025,974	29,025,915	TGCAGCTTGATTCTTAGCCACCTTCTTGCCCTTATTTGCTGGCGCCTCATCGATGAGCTCCTCA
1,615	3	3004	83.99	89809643	F1Dsnp	PHR	A	G	3	29,026,313	+	TGTTATTTTCTGTTGTAATGTCTTTAGGGTTTGGC[A/G]AATGCATGGAGAGATGCATGTTCATCAGAGTCGGC
1,616	3	3004	83.99	TP3541	GBS				3	29,053,687	29,053,750	TGCAGCATAACACACATTGATCATAAGTCCTTAGTTACTGCAACACAAATGCATTACTAACAAC
1,617	3	3004	83.99	89865605	F1Dsnp	PHR	T	C	3	29,104,073	+	TTTCTTGATTTTTCACCGTGATCCAATGGATTACT[C/T]CATTTGCAAGAACCCCCTTCCTACTGAAGATCCAG
1,618	3	3004	83.99	89809648	F1Dsnp	PHR	T	G	3	29,111,952	+	CGATATCCATACGAAGATCAGACACTTGAGACCCT[G/T]CTGGGATTTCGAGTTCGAGCATCTGTACGGTTACA
1,619	3	3004	83.99	89809649	F1Dsnp	PHR	A	G	3	29,124,505	+	CGCAGTGAACAACAGGAGAGGACTGAAGATCAACA[A/G]GAGTGGGGAGATGAAGAGTAGTAGTGTCAATGATG
1,620	3	3004	83.99	89809650	F1Dsnp	PHR	T	C	3	29,126,307	+	AGTGGTTTCATGTCAAGAACATCTTCAGGGATCCA[C/T]GTGTCTCCCATCTTTGGAAAAGTGTTATAAGCATG
1,621	3	3004	83.99	89865609	F1Dsnp	PHR	A	C	3	29,229,103	+	ACTTCTTCAACACTTACTATAACAGCGTATTTGAG[A/C]TTCTTCCTTAACGACTTGGCCAAGCAAACCGAATC
1,622	3	3004	83.99	89809653	F1Dsnp	PHR	T	C	3	29,244,393	+	TTGGTATCGAGCTTGGTTTACTTACCTCAGAATCA[C/T]GCTCTGGCGCTTCGAACCCAGGTGCAGAACAATCG
1,623	3	3004	83.99	89809925	F1Dsnp	PHR	A	G	4	16,952,213	+	CCTCCAGTAAAGTTTTGGGTAATTTTAAATACTAC[A/G]CAGATAACCAACCCTATTCTCTTGCCCTTCAAAGT
1,624	3	3005	86.46	TP2267	GBS				3	29,380,285	29,380,347	TGCAGATGAAAGTGCTTTTATGTTTAACATGAAAATTTAGGATCCTAAGAGCTAAGGAAATACA
1,625	3	3005	86.46	106_306382	GBS				3	29,419,142		ATAAAGAAGACATAGAATTTTGCTGCAATCCCGTCATATTGTTCTGCTGCATTGTTGGCACAGA
1,626	3	3005	86.46	89865612	F1Dsnp	PHR	T	C	3	29,427,227	+	AATTTTGTCTCTCTGCAATTGCAGCAATGTCGGAC[C/T]ATCTCCCTCAGGAAGTCATAACCAATATATTACTT
1,627	3	3005	86.46	TP6687	GBS				3	29,427,853	29,427,902	TGCAGGCTCATGGAGTAATCCTAGACTTGTAGATCCCAAATTTTTGTTATGTGGCCAACGGTCA
1,628	3	3005	86.46	89865614	F1Dsnp	PHR	T	C	3	29,460,432	+	AATTAGTAGTTGGGCTGTAGCTGCCCGATGGCCAG[C/T]GAGAAGCTTGCCTGAGTTTCCAAGAGTTCTCTCTA
1,629	3	3005	86.46	89865615	F1Dsnp	PHR	A	G	3	29,463,905	+	AAGGCAGAGGCATCCTCCTGAATGATCAATAGTCT[A/G]CATTTTTCTGTTAACATGAGGATTATCATTTTGGT
1,630	3	3005	86.46	89865617	F1Dsnp	PHR	T	C	3	29,466,457	+	TAAATTTAAAAAGATTCATCCATGAATTACACACC[C/T]CATAATCTCTCATAATCCACAATTCGATTTCCCCA
1,631	3	3005	86.46	89865619	F1Dsnp	PHR	T	G	3	29,635,315	+	AATACGGCAAATGAAAAGAACACCATTGTTTTTGG[G/T]CTCAAAGTGAGGTGTGAAAAGCAAGGCAAACGAAA
1,632	3	3005	86.46	89809657	F1Dsnp	PHR	T	C	3	29,663,145	+	TTCAGACTTCTGAAGAAGTTGGGCTGTGGGGATAT[C/T]GGAAGTGTCTATCTTTCAGAGTTGAGTGGAACAAA
1,633	3	3005	86.46	TP7398	GBS				3	29,708,276	29,708,213	TGCAGGTGACCTTGGCTCCACATTGTACTTCTTGCAATATGGTATCCAATGCTTAGCAAACTCC
1,634	3	3005	86.46	106_119087	GBS				3	29,716,319		CGGGGTCCTTCCCTATATATTAAATCATCTCMACTAGAGAAAGAAAGCTTGAGCAATCAGAGTT
1,635	3	3005	86.46	106_114741	GBS				3	29,720,404		TGCTTGATTTGGGTTTATAGAGTGACTCATAYACCAAAAGCTGGAGAAGATGGAAGATTTGGCT
1,636	3	3005	86.46	TP9039	GBS				3	29,746,783	29,746,720	TGCAGTGTCAGTATCTGTTGGTATATGCTTGATTTGGGTTTATAGAGTGACTCATACACCAAAA
1,637	3	3005	86.46	89865621	F1Dsnp	PHR	A	G	3	29,754,333	+	AAGAATTGCAAGAGCATATGACAATGAGGAAGAAG[A/G]CCATAAAAGACAATGCTGATGCTCTGCAGTTGGCT
1,638	3	3005	86.46	89809659	F1Dsnp	PHR	T	C	3	29,792,753	+	GGAGATGGAGATGTTATCGCTAGCAGCTGTTTACG[C/T]ATAGAACAAAAACTATTAGAAGGTTACATCCAAGC
1,639	3	3005	86.46	89809660	F1Dsnp	PHR	T	C	3	29,830,945	+	CTATAGTGAGAATCGAGTATATGCTTTTCTCCATT[C/T]CTGAACCTGTTTATTCCCAAAAGGTTAAAACTCTG
1,640	3	3005	86.46	89865623	F1Dsnp	PHR	T	C	3	29,863,198	+	AGGTAAACAACTGCAGGACAGCTTCAATCCCCTTC[C/T]TCTCCACAAATATACGACAAGTGTCACCATTCTGA
1,641	3	3005	86.46	89865624	F1Dsnp	PHR	A	G	3	29,865,167	+	AGCCTCAACCACATCGGCATCAGTGCAAGCAAGCA[A/G]AGATGAGAGATGCTGCTGCATTAACACATGAGCCG
1,642	3	3005	86.46	89865625	F1Dsnp	PHR	A	G	3	29,924,501	+	TTCTGGACGGTCATGGCGGCGAGTCATTCCTGTTT[A/G]GCTTTGTTGCCGAGCTGCACTAAAAGATTGTTCGA
1,643	3	3005	86.46	208_276133	GBS				3	29,942,394		ATGCTTTTATTTTACTCCGATCTAAATCTCTATAGATAAACCCGGCCAGAAAAGAGGTTAGACA
1,644	3	3005	86.46	TP9810	GBS				3	29,942,478	29,942,415	TGCAGTTTTATATAGTAATGGTGCTTGATGATCTAATCCATTATGAACTCGATCGTCTTAGATA
1,645	3	3005	86.46	89865626	F1Dsnp	PHR	A	G	3	30,032,310	+	TGTGGATCAATACTTCAAGACCTTTCACCTAAAGG[A/G]CTCCATGGTGCGCACACTGTTTCATTTTTCTAAGA
1,646	3	3005	86.46	89809661	F1Dsnp	PHR	T	C	3	30,039,361	+	AAGAAGCCGGTGGCATGAATGACATTCTTTATAAG[C/T]TATATACTATCACGGTAAGTAAACACTATCAAGCA
1,647	3	3005	86.46	208_181136	GBS				3	30,050,564		TCCACTGTTGCATTTTCTTTTTTGGATGCATRCGGGGAATTTGTTCAAGCCAAGTAAAACACAA
1,648	3	3005	86.46	89865627	F1Dsnp	PHR	T	C	3	30,070,412	+	GGGACTGAGACTCCGGTCATGTCCCCAACAAAGGA[C/T]ATAGAAATGCAATCTGATGAAGCTTTTGGTTGTGA
1,649	3	3005	86.46	89865628	F1Dsnp	PHR	T	C	3	30,131,042	+	TGAATCTTCTGCTACAGGAGTTACTTATGCAGCCA[C/T]GCTCGACACGGGAAACTTTGTACTGGCAGACCTCA
1,650	3	3005	86.46	89809662	F1Dsnp	PHR	A	C	3	30,131,257	+	ATGGAAATCTCTTGCTTTCTACAACATATTTCCCA[A/C]TGGATTCTGAAAACTTTGCTTATTGGTCCACCCAA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,651	3	3005	86.46	89865629	F1Dsnp	PHR	T	G	3	30,159,481	+	TACTATACTACTTACTATGCAAGTTATACACCTCA[G/T]AACAATTCTTTGAATGCAAGCTACGTGACAGACGC
1,652	3	3005	86.46	208_94257	GBS				3	30,163,358		CTGCACAGTTTTGACATTGATTTGGTTACTTGGAATTTTAGAACAACCTGGCAAAGGAAAATAT
1,653	3	3005	86.46	TP2420	GBS				3	30,188,176	30,188,236	TGCAGATGTGGCTATTGATGAGTATCATCGCTATAAGGTACAAAGTTACACACACGTTCTCAAT
1,654	3	3005	86.46	208_66084	GBS				3	30,190,121		CCAAACCACCGTATAAACAAGCAGTTATTTTAACTATGGACTTGCTACAGTAACTAATTAGCTA
1,655	3	3005	86.46	89865630	F1Dsnp	PHR	A	C	3	30,195,705	+	TAATGATCCCAAATTAACACTTGAGGAAGCCCTTG[A/C]TGACAACCAAAGAATTGACTACCACTTCCGCCATC
1,656	3	3005	86.46	TP545	GBS				3	30,197,618	30,197,680	TGCAGAAGAGCAGCTTCGGGTTTTTTCATGAACATTTCCCAAGCCTCATCGTCGGGGTCCTCCG
1,657	3	3005	86.46	89865631	F1Dsnp	PHR	T	C	3	30,227,899	+	GGGTATCATGTTCTGGATGAGTCGACACACTACAG[C/T]AGTGACCTTAGGCCTACAGCAAAGCAGTTGTGGAA
1,658	3	3005	86.46	89865632	F1Dsnp	PHR	A	G	3	30,239,838	+	GAGCTTTTGATGGAAATTCACGAGTCCAATCACTC[A/G]GTTATCTGGTTATTCCAACTTCTAGCTCTTCTTTA
1,659	3	3005	86.46	89883941	snp	PHR	A	G	3	30,263,809	+	CAGTTCAGCTGTCTTGATAGCTTGTGGTTTGACAG[A/G]GCAGTTTTCAGTTGCAGGCTTATATATTCTCATGT
1,660	3	3005	86.46	91_603715	GBS				3	30,268,130		AACAAAAGCCATGGATGAGGTTAAGGAGGCGATAAGAGATGATGAGATCACTGCCGTTGGTGTC
1,661	3	3005	86.46	89826807	snp	PHR	A	C	3	30,279,285	+	TCCGACCCGGATGACCCAATTCTTAAACAGAGAAG[A/C]CTCACTCCCTACTCCCTAGTAAAGCTTCAACCTTT
1,662	3	3005	86.46	89865635	F1Dsnp	PHR	A	G	3	30,354,667	+	TGTGGTCACTGATGTTAGGCCAGTTATGCAGGTTG[A/G]TCATAACTCTCCACCCAACACAACTAACCAAGTTG
1,663	3	3005	86.46	91_409406	GBS				3	30,387,716		TCTGCAGTTGGTGCAGACTGTGGGGAATGAGAACAGGCTTGGAGCTAGGCTATTTATTTGGGAG
1,664	3	3005	86.46	89809668	F1Dsnp	PHR	T	C	3	30,405,641	+	TCATCAGACGAAGATTCTGATACTTCACTTAATTT[C/T]CTTTTGCTGGTTGCAGGATTTCTGTCATTGGTGGA
1,665	3	3005	86.46	89865638	F1Dsnp	PHR	T	C	3	30,447,946	+	TACCCTGTTTTCTCTCCGGAAACTGAAAAACACAT[C/T]GTACTTCCAGCGACGAGCTTTTGATGATGGTTCAA
1,666	3	3005	86.46	89809687	F1Dsnp	PHR	A	G	3	31,279,578	+	ACTTTTTTATCATGTCGAACCTACTGATGTGCGGT[A/G]TCAAAAGGGGACTTTTGGTGATGCTTTCACTGAGC
1,667	3	3005	86.46	89809688	F1Dsnp	PHR	T	C	3	31,279,638	+	TTTCACTGAGCTTGAAAACTCTGGTCGGCACAATT[C/T]AGAGAAGGTGCAGCAGTGGAGAAATGCTTTACACA
1,668	3	3005	86.46	89809689	F1Dsnp	PHR	T	C	3	31,279,711	+	GTGGCCGGTTTCTCTGGCTGTAATGCAAAGGATCA[C/T]AAGTAAGCATCATGAGACTATCTCACTTACCATTT
1,669	3	3005	86.46	89865657	F1Dsnp	PHR	T	C	3	31,289,367	+	AGGCACATTGGCAGAGGCGAGCAGGTGTTGTACTG[C/T]GAATAGCAGTGGTAGTGCAAGTGTCGGAATTAAGG
1,670	3	3012	88.94	89809677	F1Dsnp	PHR	A	G	3	31,101,889	+	GGAAACTGGAGCTTTTAGGGAAGGTGTACAATGAT[A/G]TTTTGGACTCTGGGACTTACCAATTTGCACTTTAC
1,671	3	3012	88.94	89809678	F1Dsnp	PHR	T	C	3	31,122,726	+	CATTCCTCCATATTTTTGGCTGCTTTTCCAATTCT[C/T]CTGCGGAAGTATGTTAAGGTGAGTTCAATGATGCA
1,672	3	3012	88.94	89809679	F1Dsnp	PHR	A	G	3	31,126,437	+	GGAAAATCTCAGGCAAAGAAATCAAGGAAGAGAAA[A/G]AGCGCCAAGTGAAGATACAAAATGCCGTTAGTTAT
1,673	3	3012	88.94	89809680	F1Dsnp	PHR	A	G	3	31,142,123	+	TATGTATTTTACCAGCTTCAAAAATGGCAGCCCTC[A/G]ACTTAACCCTCAGGCTTGGATTACCAACCTCCACT
1,674	3	3012	88.94	89865651	F1Dsnp	PHR	T	G	3	31,148,100	+	TTATGAGTGAGATTGCGCAGAACTCTTGGATGGCT[G/T]CTAGTGTCGACAATCCAAATGTTAGCACATTGCAA
1,675	3	3012	88.94	89809681	F1Dsnp	PHR	T	G	3	31,148,933	+	TGGTTAATTCAACGGTTAGAGATGATCAGCGCAGC[G/T]GTTCTTGCCTCTGCAGCACTTTGCATGGTTTTGCT
1,676	3	3012	88.94	TP6332	GBS				3	31,149,080	31,149,143	TGCAGGATTTGTTGGGATGGCACTTTCTTATGGTCTATCATTAAACGTGACCTTGATCAAATCA
1,677	3	3012	88.94	89809682	F1Dsnp	PHR	T	G	3	31,149,099	+	TGATTATATATGTTACTGCAGGATTTGTTGGGATG[G/T]CACTTTCTTATGGTCTATCATTAAACGTGACCTTG
1,678	3	3012	88.94	89865653	F1Dsnp	PHR	T	G	3	31,152,914	+	TTTGCAGCCTTGGTGATGATACTTTTTAGTGTTAT[G/T]TTGAATGCTCCACTTGCTAAGCTACAACATAAGTT
1,679	3	3012	88.94	89884112	snp	PHR	A	C	3	31,153,256	+	TTCACTTTCATCTCCACTCTGAGACTTGTTCAGGA[A/C]CCCATTCGAACAATACCTGATGTTTTTGCGGTTGT
1,680	3	3012	88.94	89865654	F1Dsnp	PHR	A	C	3	31,186,038	+	ACAAGCACATAGTGAGGAAGGTGGTAAGGGTACTC[A/C]AAACCAAATTAGGGTACATGGAAATGGACAAGTAC
1,681	3	3012	88.94	89809683	F1Dsnp	PHR	T	C	3	31,186,203	+	TCCTTGTATTTCTGAGACAGCAGAAGAAAATGGGG[C/T]TGACGATGTTGAGCTAGTTTTCTATGATAAGGTCA
1,682	3	3012	88.94	89809684	F1Dsnp	PHR	T	G	3	31,186,498	+	TTAGTACAGGAGGAGGGAAAACTGGAACTAAATCT[G/T]GGGGGATATAGCAGCTACAAATTGCAAGAAAATAA
1,683	3	3012	88.94	89809685	F1Dsnp	PHR	T	C	3	31,188,940	+	ATCAGGAAGTAGAACCTGTCCATATGACCTTCATT[C/T]AAGTTATTTGGAATCCAACCTGGGTCTGAACCTCT
1,684	3	3012	88.94	89865655	F1Dsnp	PHR	A	G	3	31,189,258	+	TCCGTGACACCAGCTGCAACCATTGCGAACAATCC[A/G]ATGATTAGTCCAATTCCCATTCTCTGAAGCTCTGA
1,685	3	3012	88.94	89865656	F1Dsnp	PHR	T	C	3	31,199,956	+	TTACAGCAATAATTAGGGTGTGTATCAGAAAAAGG[C/T]GGAGGAGGGAGAATTTTCCATAAGTTATGAAAAGG
1,686	3	3012	88.94	89809686	F1Dsnp	PHR	T	C	3	31,203,600	+	GGAGGTATGAGCTCTGCAAAAGCTGCACTTGAGAG[C/T]GACACTCGGGTGCGTTTTTCTTACATGCACTTTTA
1,687	3	3011	91.41	89865590	F1Dsnp	PHR	A	G	3	27,901,945	+	CTCATCTTTGCCGGATATTTTCCTTTGTATGCCTC[A/G]TATTGAATTGGCTCTGTCCGACCATGACATTGACC
1,688	3	3011	91.41	TP1685	GBS				3	27,905,489	27,905,434	TGCAGAGGAAAGACAAGCGACTTCAATACAGGATTGCAGCCACTGGTGCCTACCCGAGATCGGA
1,689	3	3011	91.41	89865591	F1Dsnp	PHR	A	C	3	27,905,611	+	CTTCATCTTCTCCAATACCGACTCGAAGATCTTCA[A/C]GTATGATGGATATTCTCCTCCGTATTCAGTTTCTG
1,690	3	3011	91.41	89809627	F1Dsnp	PHR	T	G	3	27,905,636	+	AAGATCTTCACGTATGATGGATATTCTCCTCCGTA[G/T]TCAGTTTCTGTAGTTGGCTTCGTCTCACCGTCGCA
1,691	3	3011	91.41	89865592	F1Dsnp	PHR	A	G	3	27,908,380	+	TGACCATTCTGAAATCCCTTCTGATCAATCCCCAC[A/G]TTTCCTTTCAAACTTCCAATCTCATCAGTCTGTGG
1,692	3	3011	91.41	69_589410	GBS				3	31,027,961		GGCCCTTTCCGGTGAGCAAGTTCTGAAAGTAGTGGTTGTCGAATAGATCTCTCGAGTTCCGATC
1,693	3	3011	91.41	TP400	GBS				3	31,028,074	31,028,011	TGCAGAACCAATGCCCTACGACGAGCGACGGATTCAATACCGCGCCTCTTGATCGAAACTCGAG
1,694	3	3011	91.41	89865650	F1Dsnp	PHR	T	C	3	31,034,835	+	TTGTACAAGTGCAGAAAGTCTGGCTCCCGCACTTA[C/T]GATGTTACAATGGACGATGCAGCCATCATTGGCGG
1,695	3	3020	96.52	69_395094	GBS				3	28,048,996		ACCACATCTCTCACAGGCATTTCCTCAAACAGCTTCCGCGCAATCCCAACCTCACCGCAATCAG
1,696	3	3020	96.52	89809629	F1Dsnp	PHR	T	C	3	28,118,061	+	GAGTTAGTAATGCTAAAGATGTGGTGAAGAGGGGT[C/T]ATCAAGTTTATGTGAAGGTGGTTTCGATTTCAGGT
1,697	3	3020	96.52	89865593	F1Dsnp	PHR	T	G	3	28,132,698	+	GCGAACACAAATCCAACGTTGTTGATCACATAGCC[G/T]GATAACCCCAACACAGCTCTATGCCCAATCACCGG
1,698	3	3020	96.52	89865594	F1Dsnp	PHR	T	C	3	28,410,798	+	TTCAACAGTCTGGGGATGCTGTTCGAATTCACAGC[C/T]TTCATTTACTTGAGGATGAAGTTTCCTGATGTGGA
1,699	3	186	98.98	89865595	F1Dsnp	PHR	A	G	3	28,448,998	+	AGATGGAAAGAATGGCCTATGAAGTTGTCGTGGAG[A/G]ATGGAAGATTATTCTACAAGCAATCAGGGGAGCTC
1,700	3	186	98.98	89809631	F1Dsnp	PHR	T	C	3	28,463,093	+	CTCTTCACCGACTCCGAGAACGCTACTTTCAAGAA[C/T]GACAATTCTGTCCTCAAGACCGGCGAGGATTTCAT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,701	3	186	98.98	89809632	F1Dsnp	PHR	T	C	3	28,463,399	+	GTGCTGTGGAGGTTTCGGAACAAGAAGGAGAAGTC[C/T]TGGAGGAAGTACAGGGATTTCAGGAGGTTTCAGTT
1,702	3	186	98.98	89786425	snp	PHR	A	G	3	28,492,359	+	CAACCTACTTATAACAACAATAACAATCTCATGAC[A/G]ACTCAGTCGTGTTGGTGCAGGCTTGAACATAGCTG
1,703	3	186	98.98	89865639	F1Dsnp	PHR	A	G	3	30,609,692	+	ATCACTATGAGGAGCACGGGTGATCAGAGACGTGA[A/G]ATGGAGAAAAGATCAACAATGCATGCTATAGATCA
1,704	3	186	98.98	89865640	F1Dsnp	PHR	T	C	3	30,612,838	+	ATATTTGTTGTAGTCCTTCTTGCCATTTCAAGGAC[C/T]GTGAAGGGTTCTGGTAATGGGTGGACAAATGCTCA
1,705	3	186	98.98	89865641	F1Dsnp	PHR	T	G	3	30,612,875	+	TGAAGGGTTCTGGTAATGGGTGGACAAATGCTCAC[G/T]CCACTTTCTATGGAGGCAGTGATGCTTCAGGGACA
1,706	3	186	98.98	89865643	F1Dsnp	PHR	T	C	3	30,682,118	+	AGCTAATTTTGCTTGTTCAACTTCCTGTTTTCGTA[C/T]TGCAACTCCCTCTTGGTAAGTAGCAATCTTCTTTT
1,707	3	186	98.98	89809672	F1Dsnp	PHR	T	C	3	30,686,734	+	CGCACAATCAATGGTTGTCTCAGAACATTTGTCAA[C/T]GGCCTTGAAGAAACTGGTTTAACTCCAGCTTTGGG
1,708	3	186	98.98	89865645	F1Dsnp	PHR	T	C	3	30,745,749	+	TCCCCCAATAATTAAGATTGCCGATATCCTCCCCC[C/T]AATGCACCAACACCCCTTGAGTGTGAAGGTCATTT
1,709	4	4001	0.00	89809058	F1Dsnp	PHR	T	G	1	14,666	+	TTTTTCACCTTGCATCTTTATCCATCAACAAGGTT[G/T]TACGGCCCCATTAACGAATTGCTGTCAGAAAATCA
1,710	4	4001	0.00	89809479	F1Dsnp	PHR	A	G	2	5,710,149	+	ATACGGTTGTATTGAGAGAAGGGTATAAGAGGGGT[A/G]CTATTATTGAGAATCATCCGCTGATGGATATAAGA
1,711	4	4001	0.00	89810079	F1Dsnp	PHR	T	G	4	509,274	+	CACAGTTGCAAGGTCCACAAATTCCTTTTACACTT[G/T]GTCTACGAACACGATCCGTCCGTCCGTTTACAATT
1,712	4	4001	0.00	249_250985	GBS				4	753,406		AAGACGAAGACTGAATCCCGGTGTTTTGAAGGTACATGCAGAAGGATGTATAAGAACTGCGGAA
1,713	4	4001	0.00	89804712	del	PHR	-	CGA	4	840,351	+	TCTAGAGCCTTCCAGTCATTCTTCCAGTCAGTGTC[-/CGA]CAACAACGGTTTCAAACTAGACCAAAGAACCCTCA
1,714	4	4001	0.00	89810093	F1Dsnp	PHR	A	G	4	844,397	+	AATACTCTCTAACCATTCGATTGTTACAACGGTTC[A/G]GATTGACTTTCATAGCCTATTACTGCTAGACGATG
1,715	4	4001	0.00	89866057	F1Dsnp	PHR	A	G	4	845,472	+	TGTTGAGCCACCAAGGGAGGGAGACAAGCATGCGC[A/G]GCTTCTGGTATCCAATGTTGTGTACTATGGTCAAT
1,716	4	4001	0.00	89866059	F1Dsnp	PHR	A	C	4	868,536	+	ACTACTGCCCCTGGCTTGCCTTATGTTGATGAAGC[A/C]ATAACCAAATCTGGAAACTGGCTGATTGGAGGTGA
1,717	4	4001	0.00	89810095	F1Dsnp	PHR	A	G	4	871,903	+	ATCTGGTTGAGTGTGAGAGTACCTGTTTTGTCTGT[A/G]CAAATTATAGTGGCACATCCCATAGTCTCGCAAGC
1,718	4	4001	0.00	89866061	F1Dsnp	PHR	T	C	4	871,911	+	GAGTGTGAGAGTACCTGTTTTGTCTGTACAAATTA[C/T]AGTGGCACATCCCATAGTCTCGCAAGCTGAGAGCC
1,719	4	4001	0.00	89810096	F1Dsnp	PHR	T	G	4	872,026	+	GCAAGAGTTAGAGTCACAGCCAATGGAAACCCTTC[G/T]GGAATTGCAATCACAACAATAATGACAGCAACTGC
1,720	4	4001	0.00	89810097	F1Dsnp	PHR	T	C	4	872,740	+	AGTCCATCTTGCTTGATGCCAAAGCCAAGCGAAAG[C/T]GCAGCGCAGCCTAAAAGGATGACAATGGTGAGGTC
1,721	4	4001	0.00	89810102	F1Dsnp	PHR	T	C	4	930,783	+	TCTATTCTTGTTTTTACAATGAACCACATCGACCA[C/T]CCCAGTGTCACCAACACCATCACAAGTTCTCTTTG
1,722	4	4001	0.00	89809533	F1Dsnp	PHR	T	G	4	1,294,722	1,294,790	ACTCACTACTCCACACATCATTAAGTTTGAAATCA[G/T]GAAAACTACCCAAATAGAAATACCACCTGAAAACA
1,723	4	4001	0.00	89809903	F1Dsnp	PHR	T	C	4	1,485,756	+	GGGTTCATGAAGTTAGGGAGCATCTTCCTCATCTT[C/T]TTGGCCTCCTCTTTGGCGCTGCTGTTGTCCTCTAC
1,724	4	4001	0.00	79_73563	GBS				4	1,502,303		CAATACCAAACTGTATCTGATAATTCCTTGTYCATATCTGAAGGTTCCTTCATTTCCGGATGAT
1,725	4	4001	0.00	89804402	del	PHR	-	AGAA	4	1,510,990	+	CCAATCCATTGCTCAAGTCTAACCAATTTAATGAG[-/AGAA]AAAAAAGTACTGATAGTACTAATAAAAACAGTTAT
1,726	4	4001	0.00	89865867	F1Dsnp	PHR	T	C	4	1,593,541	+	TTGCCCCTATCATATAACATTTCTTTCCACTCTTC[C/T]CTTCTAGCGCAAAGCTCTGTGTTAAATTCACCACC
1,727	4	4001	0.00	89865873	F1Dsnp	PHR	T	C	4	1,643,213	+	GGTAGGATGGGTGCTGTAAATGGAATGCACCCTAA[C/T]GGTAGGGTGGATGAGTCTTGTATGCAATCTCGTGA
1,728	4	4001	0.00	89865874	F1Dsnp	PHR	T	C	4	1,647,181	+	TAAAAATGGCCAGGAAGATGCTAATTGATGGTGAG[C/T]TGAGCAAACCAAATGAAGAGGAGGCCCACTATGAC
1,729	4	4001	0.00	89809955	F1Dsnp	PHR	A	G	4	1,888,084	+	ATGTTTGGCAATTGTGGTCTTTCCTATTCCACCAG[A/G]CCCCCATATACCAACCACACGAAGAACATTTTCCT
1,730	4	4001	0.00	89809965	F1Dsnp	PHR	A	G	4	1,960,507	+	ATGCTCTCAGCAATGAACTTGCGCACCAAATCCTT[A/G]AGATCACAAGATGAGGCCTGGGAGACCATGATTTC
1,731	4	4001	0.00	89865903	F1Dsnp	PHR	T	C	4	1,965,160	+	CTAACACGATCGCGGAGACTGTGGAGTTGCCGATG[C/T]TTTGAGGCAATGAACACTTGAACTTGTTGTTGTTG
1,732	4	4001	0.00	89865907	F1Dsnp	PHR	A	C	4	1,989,215	+	ATTGGCGGCACGCCTCCCAAGCTCGCGTAGCTGAT[A/C]CCCTGAGGAACTGCCAGACTAGAAATGGTGATTCC
1,733	4	4001	0.00	89887916	snp	PHR	A	C	4	2,393,752	+	GTAATGTTAATGTAGAAGAAGATCATCAGCATCAG[A/C]GTTCTGATACCGATAACAGTACTACAATGAGTGCC
1,734	4	4001	0.00	89810023	F1Dsnp	PHR	A	G	4	2,458,738	+	GTTAACTAAGCCATCTGCTTCACCATGCTAGGCAT[A/G]GCACAAAATACGGTGAGCAAGGTGACCTCAACTGT
1,735	4	4001	0.00	89810027	F1Dsnp	PHR	T	C	4	2,489,223	+	TCATTCTTTCGATCTGAAAGCTCAATAACCTTTGC[C/T]GTCAACATTTCTGTTGACATCATCATGCCCTTGAG
1,736	4	4001	0.00	89865974	F1Dsnp	PHR	A	G	4	2,531,823	+	TGGGTGAGAGCAGTGGATGAGTTCTTTAGTGTTCT[A/G]AATTGTAGTGAGTTTAAGCATAAGCAAAAGGATTT
1,737	4	4001	0.00	89810033	F1Dsnp	PHR	A	G	4	2,540,932	+	GTTTTTTCTTGGCTTCTCTCATAAGTTTTGGAGTC[A/G]CCTCGTAAAGAATAAACCTAACAACTTCAAGAACT
1,738	4	4001	0.00	TP6893	GBS				4	2,553,695	2,553,758	TGCAGGGATTGCATAATGATCAATCACGACGGACTTCCATGTCCTTGTGACAAGGAGGAAGAAA
1,739	4	4001	0.00	89866022	F1Dsnp	PHR	T	C	4	2,700,581	+	AGTACATTGATCGCTTCTATAGCACCCAAAACACC[C/T]ACAACTCCGTCGTACTTTCCAGAGTATGGAATAGC
1,740	4	4001	0.00	89831429	snp	PHR	A	G	4	2,811,433	+	GATGTCGTTTGAACAAGGTGGTGGCTTTATCTCAA[A/G]CTAGTTAATTAGCATCAATCCATTTGGAAAATTTT
1,741	4	4001	0.00	131_460750	GBS				4	3,115,088		CGAACGTCGCCGTTTCGTCAACCTCAACCACAGAGAGCGAAGATGAAGTAAGTCACAGATCTGC
1,742	4	4001	0.00	89866028	F1Dsnp	PHR	A	G	4	3,126,976	+	TGATCAGCAAAATGTGGCCTCCCAATCATCGGCAC[A/G]CCATAAGTAACACTCTCCAAAACTGATTTCCAACC
1,743	4	4001	0.00	89810069	F1Dsnp	PHR	T	C	4	3,142,493	+	CGGGCTAACTCCGGTTCAGCTTGCACTTGGATTTG[C/T]ACGGGATCGTCCATTTGTGACTAGTTCTATCATTG
1,744	4	4001	0.00	89866029	F1Dsnp	PHR	A	G	4	3,143,745	+	ACAATGAGGCCGCTCTTTAGGTTACTAACTTCTGT[A/G]ATACTGCACTCTACAACATCATGATAATTTCCTTG
1,745	4	4001	0.00	TP5423	GBS				4	3,167,321	3,167,258	TGCAGCTGGCTTTGATCTTCGACTCTGAGGACCATCGCCGACAAAGGTTAGGTTAAATTCGAAG
1,746	4	4001	0.00	89866030	F1Dsnp	PHR	T	C	4	3,503,695	+	TACCTCTCCTATCCAGTTGAAGCTCATGATAGACC[C/T]GCTGCATCAAAAGGTTTTGTTTGCTGAAGTGGGCA
1,747	4	4001	0.00	89810073	F1Dsnp	PHR	T	G	4	3,559,605	+	ATAATGGGGATACCCTTCCTAAGTTTATCGACAAC[G/T]CCACAGATGATGAGGATGAGGTTATAAGAAATGGA
1,748	4	4001	0.00	89810074	F1Dsnp	PHR	T	G	4	3,572,018	+	CCATACCGTCCTGCCATCGATGGTATGCTTCTCCT[G/T]AAGAACCCTATCAAGAACAGCAGGATCCACAAAGA
1,749	4	4001	0.00	89810075	F1Dsnp	PHR	A	G	4	3,619,680	+	CAGTATTCCCCATACATTTTAAAGACAAACCAGAT[A/G]TCATAATCGCAACAACCTTCTTTCAGGTCTGTGGC
1,750	4	4001	0.00	89866031	F1Dsnp	PHR	A	G	4	3,671,714	+	TTGCAGAACAGGCATCTATAGTTTTGCGGTCTCTC[A/G]GCTTCATCTGATTCAAACTTCTACTATAATTCAGT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,751	4	4001	0.00	TP3571	GBS				4	3,719,418	3,719,481	TGCAGCATCAAATCCTTTCACTTATAACATGCACTAGGCTTATTTGCAGAATTTTAAGTAAACT
1,752	4	4001	0.00	89866032	F1Dsnp	PHR	A	G	4	3,934,599	+	ATACCCAACATTCATGCTGGGATACAGTCCATCTG[A/G]CATTTCAGGTCTTCTTTGATATTCCATGTGCCATG
1,753	4	4001	0.00	89866033	F1Dsnp	PHR	A	G	4	4,323,821	+	CCTCCAATCTCTGATGTGAATTTCTGGGAAGAATG[A/G]GAAACCTTTGAATTTGAGCGGTCCTCTAAAGGATA
1,754	4	4001	0.00	89791042	snp	PHR	T	G	4	4,451,798	+	TTGGCATGTAATCATAGACTATAAGCCTTTGATCT[G/T]CCCCAGCATAATAGCCCCTAAGACCCAACAAGTTC
1,755	4	4001	0.00	89810077	F1Dsnp	PHR	T	G	4	4,763,317	+	GATGGAAAATTAAGGACATGCTTGATTCCTATTGC[G/T]GGCTTTCTGAACCATTCAGTATGTCATCCATTCTC
1,756	4	4001	0.00	TP3593	GBS				4	4,909,481	4,909,418	TGCAGCATCATGATAAGAGCTGTCCAACCTTGGATCGGGAACCATTACAACAGACCTGCATATC
1,757	4	4001	0.00	89810078	F1Dsnp	PHR	A	G	4	4,964,941	+	TGGACATCCTTGGCCATGCCCTTAGCATCACCACA[A/G]ACGTATATATAACCTCCCTGAGATATCATGTTCCA
1,758	4	4001	0.00	89866036	F1Dsnp	PHR	T	C	4	5,315,613	+	TTCCGTTTGAGCAAGTGAGCACTAAGAACAGAGCA[C/T]ACAAAATCTCTAAATTCAATTCTGAGAAGCAAAAA
1,759	4	4001	0.00	89866037	F1Dsnp	PHR	A	G	4	5,454,613	+	AAGCTGTGGAGTTCAAGTCAGGGCTGAATTCTCAG[A/G]TTCCTGAATTTCAAGTGTTCTTTCAAGATCATACC
1,760	4	4001	0.00	89866038	F1Dsnp	PHR	A	G	4	5,481,789	+	TCTCTTGGTGTCAACTTAGATAATATCTTGAGAGC[A/G]ATAACCTCATCACTCAATTGCAATATCCCACAAAC
1,761	4	4001	0.00	TP2488	GBS				4	5,563,511	5,563,574	TGCAGATTCACTTGACAGAACCTGAGGGTGACATACTTATCTTCTTGACTGGTGAGGAGGAGAT
1,762	4	4001	0.00	89810082	F1Dsnp	PHR	T	C	4	5,878,190	+	GATCAGAAAGATATTTCCCGTGCACGGGTTTGGTT[C/T]TTTGAAGGAAAGAGAAAGATCATGCTCTACACAGA
1,763	4	4001	0.00	89888958	snp	PHR	T	C	4	6,207,551	+	ATGGCTCGAGAGAGCCATTCTATTAATGGTGTGAG[C/T]GAGCCAGTTTTATATCTGCAGTCCAACATCACCAA
1,764	4	4001	0.00	89810083	F1Dsnp	PHR	A	G	4	6,225,316	+	CCAAGGCATATTGTACAAGGTAATTGTTATAAGCT[A/G]TTCCTTCAGGCTGAGAAATGAGAGCAAAATCAGAA
1,765	4	4001	0.00	89810084	F1Dsnp	PHR	A	G	4	6,275,438	+	CTCCAAGTGCGCCTACAGAAGAAGAACATACGGTCTAA[A/G]GCAGAAGAAGATCACAATGGATCACTCAGGTTATT
1,766	4	4001	0.00	89810085	F1Dsnp	PHR	T	C	4	6,450,059	+	TAGTAGATCAAAGCTTGTTCAACAGCAAGGAGATT[C/T]GAATTCAAATTGGCAGGTTGAAACACTAAAGGGCA
1,767	4	4001	0.00	89866044	F1Dsnp	PHR	T	C	4	7,257,240	+	TTTGGCCATGTCAACCACATCACTCCAACTGTCAC[C/T]GATGAGGCGATGACGATTTCTACTTCTCCTCTTCC
1,768	4	4001	0.00	952_13068	GBS				4	7,422,108		CACTTCTACTCACCGGTCGATAGTTCCGTGCTCTATATAGTTCTTCCCATATCCACGAATTCCT
1,769	4	4001	0.00	89866045	F1Dsnp	PHR	A	C	4	7,473,024	+	GTTACCGAGCCAAGTAAATACCGGGAACTGAGCCA[A/C]AGCAATGAAGAGCAGGAGATAATGGTGCTTGCTTG
1,770	4	4001	0.00	89889135	snp	Other	T	C	4	7,551,797	+	CAAGTAGTTACAGAGATCTGACAACTCATCAAGTG[C/T]CGTACGTGTTGGTTTATCTACATTAAATTACTGCA
1,771	4	4001	0.00	89866046	F1Dsnp	PHR	T	C	4	7,551,798	+	AAGTAGTTACAGAGATCTGACAACTCATCAAGTGC[C/T]GTACGTGTTGGTTTATCTACATTAAATTACTGCAA
1,772	4	4001	0.00	89866047	F1Dsnp	PHR	A	G	4	7,559,196	+	CAACTAATAAAGCAGGAGATGAGGATGCTCACCTG[A/G]TAGTACCGTACAACATGTTGATGTTGCAAACGAGA
1,773	4	4001	0.00	89866048	F1Dsnp	PHR	T	C	4	7,621,741	+	CATTTACGCTCAGCTGGATTGCAATCGCTAGCTTT[C/T]ATGGTATATTACCTTTTCTTCTCTTGGCTCTAAGC
1,774	4	4001	0.00	89866049	F1Dsnp	PHR	T	G	4	7,628,638	+	TATATATTTCTTTTCTCTTCAGGATGAATTGTCTA[G/T]CATCAAGAAGCAACTCTTACTAGGTTTTTCACCGG
1,775	4	4001	0.00	89866050	F1Dsnp	PHR	A	G	4	7,629,305	+	CATAGTTTCAAGCATCAACAGGAAACCAAGGCGTT[A/G]GTGCTTTCCAGTGAAAGTGAAAACAAATCCCATGC
1,776	4	4001	0.00	89866051	F1Dsnp	PHR	T	C	4	7,681,739	+	GCATAAGGTTAGTGGTTTGTCTTGAGAATGTCCGT[C/T]CTGCCAAAGACTCTTTCCACTTTGCTATGTTTCCC
1,777	4	4001	0.00	89810090	F1Dsnp	PHR	T	G	4	7,764,336	+	TGCATTCGATGAGCATACTAGAGTGGTGGATTACA[G/T]TGACAATTCTATTACAGGTAAAATACCATCTGTTT
1,778	4	4001	0.00	89866055	F1Dsnp	PHR	A	C	4	8,071,828	+	CTGACTGCAATGAATGGGATAATGATGCAAAGGCT[A/C]TGTGCTTCAATTGCCAGTCATGCAAGGCTGGACTG
1,779	4	4001	0.00	89866056	F1Dsnp	PHR	A	G	4	8,071,921	+	GGAAAAAGACGGCTGTTGTCAATATTGTCTTCCTT[A/G]TCTTCCTCATCGTTGTGTATTCCGTAGGGTGCTGT
1,780	4	4001	0.00	89810092	F1Dsnp	PHR	T	C	4	8,434,225	+	CGAAGCTTGAAGCTGGGCCCGGCAAACCTAATGAA[C/T]TTGTCGCCGGACGCCTCCGATCGTTTATTGGAGAG
1,781	4	4001	0.00	89810094	F1Dsnp	PHR	T	C	4	8,632,227	+	CAATTTGAGGAAGGAATTATCTCTTCATCTATCTT[C/T]TTGTGTCCAGGTATAACAAATTTTGAATTTCTGCT
1,782	4	4001	0.00	89866058	F1Dsnp	PHR	T	C	4	8,676,987	+	TAGACACCCAAGTGCATTTCATCTAAAGAATCCGG[C/T]TTTCTCCCTCTACCATGAACTACAGGTTCCAATTC
1,783	4	4001	0.00	89866060	F1Dsnp	PHR	T	C	4	8,686,090	+	CATTACATTCTAGCTGGGCATTTGCATATTCATTT[C/T]TGACGGCCTCAAGTTCCACCTATTAGAGGCAAGAA
1,784	4	4001	0.00	271_39709	GBS				4	9,644,462		CACTTTCCTCTCCGGACTGTATTTTACTTGCATCACTTGCTTCAGTAGCTCTACAGAACCTGAG
1,785	4	4001	0.00	89810103	F1Dsnp	PHR	A	G	4	9,792,069	+	TATTAACGACCCTAACTTCTTCAAACTACTCGACC[A/G]CAATGGCGATGGCGGGTTGGATTTTGGAGAAGTTA
1,786	4	4001	0.00	89866064	F1Dsnp	PHR	A	G	4	9,814,498	+	TGTCTAGGTATCATATCTACTCACTTGCATGGGAT[A/G]TTTAGCTTGCCTCTTAATACAAAGAATACGGTGCA
1,787	4	4001	0.00	89866065	F1Dsnp	PHR	T	G	4	9,814,738	+	GTGATCGGAGGAAAGATTGACACAAAACTAGAAGA[G/T]TTCTGTTCTACAGGTTTTAATAATTTTGATATGTC
1,788	4	4001	0.00	89866066	F1Dsnp	PHR	T	C	4	9,856,733	+	GGTAAAATCACCTGAGTGCCTTCCTCCCATAGCCG[C/T]GTTTCCTGTACAATTTCTTTGTCTTGGCCCTGACT
1,789	4	4001	0.00	89810104	F1Dsnp	PHR	T	C	4	9,863,722	+	CTCTCAAAAAGATTGAAGGATCTGCATTCAGCTAA[C/T]GATGCTAACAGCTTGAAAGGTGAACATGTCTTTCT
1,790	4	4001	0.00	89810105	F1Dsnp	PHR	T	C	4	9,870,019	+	ATTCGGTAAATAGAACCTAGCAGGGATGAGCTCAA[C/T]TAGCTTGTCCATGAATTGAGAATGCTGATGAATAA
1,791	4	4001	0.00	TP7940	GBS				4	9,884,005	9,884,051	TGCAGTAGAAATTAACACCGAAAGCCATGGTTTTGGGGGGAACTGGGGTCCCAATAATTAGGAA
1,792	4	4001	0.00	89810106	F1Dsnp	PHR	T	C	4	9,898,353	+	AAATGGATGCAGATCCCTTTCCGGACTCCCAAGTA[C/T]TTCTTCAACTTGAGGTACGCCGCCACTCTGACAAT
1,793	4	4001	0.00	TP8415	GBS				4	9,899,415	9,899,352	TGCAGTCGATTGCATACTTCAACAGCTTTTCATTATTTTCTACCATGTCATCGGTTTCCCAAGG
1,794	4	4001	0.00	TP6459	GBS				4	9,915,254	9,915,193	TGCAGGCATCGTTTTGATGAAATATAATGCTCGATCGAGCTCTCCTGATCGACCTAACAGATCC
1,795	4	4001	0.00	89866067	F1Dsnp	PHR	T	C	4	9,917,783	+	ACTGTTGTGGAAAGAAGCATTAGCTGGCCAATTAC[C/T]CGAGACATGCCAATGACTGAAGGATCAAGATTTAG
1,796	4	4001	0.00	89866068	F1Dsnp	PHR	T	C	4	9,924,913	+	CAGGCTGAACATATATGCAATAATGGAGCTGGATC[C/T]GGTTTGTAAGGTCGAAATTCCCTGCTCAGAGCTGG
1,797	4	4001	0.00	TP8461	GBS				4	9,968,716	9,968,779	TGCAGTCGTACAGAACGCGAGAGAATAACCACGCATCATCTGCGTCACATATCTATACAATACA
1,798	4	4001	0.00	89810107	F1Dsnp	PHR	A	G	4	9,968,913	+	CGCTAATCTAATTTCTAAACAGAACGATCGTGGTG[A/G]TGTAGTAGGATCCGGATTGGTGATTTTGATATGTA
1,799	4	4001	0.00	324_140574	GBS				4	9,968,944		TATCAAAATCACCAATCCGGATCCTACTACAYCACCACGATCGTTCTGTTTAGAAATTAGATTA
1,800	4	4001	0.00	TP4908	GBS				4	9,975,824	9,975,887	TGCAGCTAGGGAGTTGGAAAGCTCCGATTGGATTCTGCTGACAACAGGTTGAGGCTCACTTTCA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,801	4	4001	0.00	89865797	F1Dsnp	PHR	T	C	4	10,452,950	+	TTGTAGATGGTCCTGGCATGAGTTTGCCTCTTGTT[C/T]GTACTAATATGGTGGATATCCATCACCCGTCTACC
1,802	4	4001	0.00	89788173	snp	PHR	T	C	4	11,017,550	+	ACAATATCCGATTAAGCGAAGCAAATTCCTGTGTA[C/T]TGCTAGGCTTATCATTTCCAATTCTGTCCTGAATT
1,803	4	4001	0.00	89809839	F1Dsnp	PHR	A	G	4	11,369,193	+	GATGACGAAACTGACCTTCGGATCTTGTTGCCCTT[A/G]CCGACCTGGTACATGCCCCAGGAGAAGGTACCGAA
1,804	4	4001	0.00	89865798	F1Dsnp	PHR	T	G	4	11,444,111	+	AGCTAAATCAATTTTTATTTTGTTGTATGTGCAGA[G/T]TGAAATTGTGCAAGAAAGGAGATCCTTCAGGTGAG
1,805	4	4001	0.00	89865802	F1Dsnp	CRBT	A	G	4	11,853,529	+	CTGGTACTGCAAAGCGGCTTTTTGACGAATGTGTG[A/G]ATAAGAACTTGGTTCTTTACAATACAGTTTTGTCA
1,806	4	4001	0.00	89865803	F1Dsnp	PHR	A	G	4	11,854,206	+	ATGTTCGCTAAATGTGGAGATCCTCAAAGTGCAAT[A/G]AAGGTGTTCAATACCATGGCCAGAAGAGATGTTTC
1,807	4	4001	0.00	89865804	F1Dsnp	PHR	T	C	4	11,948,840	+	GGGTGGACTCGGAGAGGGTCAGGGCGTGGTGGGTT[C/T]TCATGGAGTCGAGTATTTTCCACATGGACTCGTAT
1,808	4	4001	0.00	89865805	F1Dsnp	PHR	T	C	4	11,957,374	+	TTCTAAACTCCATCCCTGTGTCTTTGTCCATGACT[C/T]GCCTAATACATGCACTTATTTCTTCTTTCAGCACA
1,809	4	4001	0.00	89809845	F1Dsnp	PHR	A	G	4	11,964,097	+	CTGCTGAAGAAGATGCAGTTTACTTTCTTCAAGTT[A/G]GAGTATTGATTCATGGCAAGCTTAAGGAAAGCCGG
1,810	4	4001	0.00	89865806	F1Dsnp	PHR	A	C	4	11,984,665	+	AGTTTGATCCTTGAGGCTCGCTAATTGTTTCATGT[A/C]CATCCCAGTCAGAAATCACAATTCCCTGTAGCAGA
1,811	4	4001	0.00	89865807	F1Dsnp	PHR	A	G	4	11,989,391	+	CCCATAAGGTCAAGGTAATACTGGTAATGGGAAAC[A/G]ATGTTGTTCATGGCGTCAATGTCACCCTGGCCACA
1,812	4	4001	0.00	89865808	F1Dsnp	PHR	A	G	4	11,998,049	+	AGGGATTTATATCATTTTACAATTGAAAACCAATT[A/G]GAGGTTGGGAGAACACTCACCCATTCCATAGCCAA
1,813	4	4001	0.00	89865809	F1Dsnp	PHR	T	C	4	12,072,649	+	GTTAGCCAGGGGCAGTTTGAAGAGTCTTAGTGCTG[C/T]TGTTGTTCCCAAAGGTTATATGGAATTTTGAGATG
1,814	4	4001	0.00	89865810	F1Dsnp	CRBT	A	C	4	12,074,436	+	AAGGAGCAGGTGGAACCTGTTTTTGAAAAGCATGG[A/C]CTAACCTGCAGAATGGATGAGGTATCCTTTGATAA
1,815	4	4001	0.00	89809846	F1Dsnp	PHR	T	C	4	12,076,688	+	GATCTCTCTCTGAAGCGTCAAGAGCAAAGCCGTGA[C/T]TCTCAGCTCCACACCCGCCGCTTAACCTCAGCACT
1,816	4	4001	0.00	89809847	F1Dsnp	PHR	A	C	4	12,159,201	+	AAGATACAGCAAACCAGACATTCTCACTTCCTGAC[A/C]GAGCTGGGCAAGGCAGATACCAAATCATACAAGTA
1,817	4	4001	0.00	TP2697	GBS				4	12,162,100	12,162,163	TGCAGCAAAATTAACCCTTTGAGTTCACACTTTTCCATTTAGATGCAGTTTAGACCGATAACTC
1,818	4	4001	0.00	89865811	F1Dsnp	PHR	T	C	4	12,194,757	+	ACCACCCACATACATCTACAAGTCACCACCACCAC[C/T]ATCACCTAAACCTTACGTGTACAAGTCTCCACCAC
1,819	4	4001	0.00	TP7547	GBS				4	12,237,731	12,237,793	TGCAGGTTCAATCACAAAGAACATGATTTATATATTTCTTGTTGTAAAAATTTAGAATGTATCG
1,820	4	4001	0.00	89809848	F1Dsnp	PHR	A	G	4	12,262,027	+	AGCAACCTCATCTTCCACATGCTCTTACTATACTC[A/G]TCATCCAAATCGGGAATTTAAAGCATTCATCTTGG
1,821	4	4001	0.00	89809849	F1Dsnp	PHR	T	C	4	12,287,290	+	CAACTTGTTGAAGATGAATGTGAAGGTACTGATGC[C/T]GTTGTACGAATAGGTGAATTGACTTATTAATTGTT
1,822	4	4001	0.00	89809913	F1Dsnp	PHR	T	C	4	16,355,215	+	TGCCACTGAGTACCATTTGCAAGAAGATCACGAGC[C/T]TCAAAGATGCCCTTCCAACACTGAGATGGAGATGT
1,823	4	4001	0.00	89865962	F1Dsnp	PHR	T	C	4	24,021,199	+	AGAAGTAGCCCAGCTTTCTCCTTTCAGTGCTGTTG[C/T]GGATACTCCTGCAATATCCAAAGTGTTTCTACTAT
1,824	4	4001	0.00	89865963	F1Dsnp	PHR	T	C	4	24,022,372	+	TTCATCTGGGTTCTCAACTGCATGCTTATTCAACC[C/T]TCCATCATCATTCTCATTCACCCTGAAGAATATTC
1,825	4	4001	0.00	89866223	F1Dsnp	PHR	T	C	5	25,272,100	+	CAAACACCAGAACACCATGACCCTTTGCTTCAAAG[C/T]GGAGATCGAGCTGTAACTCTTTATGAGGCTCCCAA
1,826	4	4001	0.00	89810253	F1Dsnp	PHR	T	C	5	25,280,724	+	TGGGACTGCAACACTGGTCAATGCAGCAAGGTGAT[C/T]AATCTTGGTGCTGAAGCAGGCTGCTTGATCAGTAA
1,827	4	4001	0.00	89810255	F1Dsnp	PHR	A	G	5	25,445,138	+	TAATAATTGAAGTTGAAGCTGATTATCAGAGAGAT[A/G]TTGTAATTGTGGGTTCATTTGATCAGGCAGTGGAG
1,828	4	4001	0.00	TP8110	GBS				5	25,989,164	25,989,101	TGCAGTATCTAAAAACTCCTGCCAAGAAGCTATCTGTCCAAACTTGATTTACACCGCCGTAAAC
1,829	4	4001	0.00	176_373635	GBS				5	26,056,052		AATTAAGTGAAAGGAAAGCAAAGGAACGGCAAAAACGGCCACGAAGCGATTGATACCTAAGCAC
1,830	4	4001	0.00	89810256	F1Dsnp	PHR	T	C	5	26,209,501	+	CATTCCGTGGCTATTATGATCACTTCTCTCGTTTT[C/T]ATGTCTTGTTTCTTGATGGAGAGGGAAAAGAGGAA
1,831	4	4001	0.00	89894227	snp	PHR	A	G	6	10,305,708	+	CCTCAACAAGTGGTAGTTGAAATTCTAGTGAGGTT[A/G]CCCGTGAAATCTTTGATAAAATGCATCACTGTGTG
1,832	4	4001	0.00	478_24570*	GBS				6	11,442,711		TAAGCCTAATCCTAGAAGTTGTGGTGATTCTRCTTTGCAGCCTCCCATTACTCGAAAACCTCCT
1,833	4	4001	0.00	89894479	snp	PHR	T	G	6	11,701,316	+	CGGGGTCGTGTTTCTAGTGCATAGGGGAGGCCTCC[G/T]GGTCTCGTTCTAGTGACAGCTTCGAGTTCGGTGGG
1,834	4	4001	0.00	TP2491	GBS				6	26,135,710	26,135,647	TGCAGATTCATAAGCCATACCAGCTAGTCTGTGCGCTACTCTATTACAAGAACAAGAAGCAAAA
1,835	4	4001	0.00	TP2331	GBS				6	26,155,176	26,155,113	TGCAGATGCAGGAACTCAGTTGAAACTGAAATGACTCTTCATAATTAGCAGCAACAATTTGGTT
1,836	4	4001	0.00	739_11696	GBS				6	34,142,005		TGACAGCGTTGCCCTGCAGGTCTGTTGGATTTTTTTTTTTTAAATAGGTTCTTTTTTTCTGCAT
1,837	4	4001	0.00	33_166149	GBS				NGH			GATGTTAATACTTTCTCCAGATTCTTCCCGGTGCTCGACAGTTGCACAGCCAATTTTTTCAGAT
1,838	4	4001	0.00	821_1088	GBS				NGH			TTTATCAAAAAAAAAACTGCGCCACAAGTATATATAGTGATTTGGTCTAAGTTGATTGCATTTC
1,839	4	4001	0.00	271_272435	GBS				NGH			CGCAAAGAGCTAGGTATCATGCATTAAACCAYGGTGCAACTTCAGAGTGCAAAGAATATTGACA
1,840	4	4001	0.00	595_83381	GBS				NGH			AGGACAATGTGCTTGGGCTTGGGCCCGAGGACAATGTGCTTGGGCTCGGCAAGGGAGCCTGCAG
1,841	4	4001	0.00	TP7369	GBS				NGH			TGCAGGTCTGTTGGATTATTTTTTTTTAAATAGGTTCTTTTTTTCTGCATTCTCTGTGTGGTAA
1,842	4	4002	2.44	89779410	snp	PHR	T	C	1	19,699,961	+	CGATGATGTTACTGTCAATTCCCTTCCAACTCCAT[C/T]ATCTAGCTTCCTGAAGTCATTTGATAATGACTATC
1,843	4	4002	2.44	TP5694	GBS				3	2,929,906	2,929,948	TGCAGCTTGTCTGGCAGCGGCCCCGCCGCGGGCTCCATTCGCCGAGATCGGAAGAGCGGTTCAG
1,844	4	4002	2.44	TP3786	GBS				3	7,520,541	7,520,478	TGCAGCCAAGGTGTTCGACGAAATGCCTCAACCAAATGTCGTGTCGTTTACCTCGCTCATCTCC
1,845	4	4002	2.44	89865799	F1Dsnp	PHR	A	C	4	11,509,397	+	GTACAGAAGGCAGAGATGGAAGTTTTTGTTCAACT[A/C]CACACCACCACAAGACCTTGATAGAGCTCCATGGA
1,846	4	4002	2.44	89809840	F1Dsnp	PHR	T	C	4	11,516,160	+	TCGAAATACGTGGAGGAAGCTCTCTACGTTTGGCT[C/T]TTCAAAGACGGCGGCTCCGAGGTCAGCGTCCGCCA
1,847	4	4002	2.44	89865800	F1Dsnp	PHR	T	G	4	11,533,825	+	AGAGGGTGGAGGAAAGCTCACCGTAATAACACTAG[G/T]ATTGATGTCTGTAATGGTGATAACAGTGACGATGA
1,848	4	4002	2.44	89809841	F1Dsnp	PHR	A	G	4	11,593,674	+	GAAGAAAATCATGGTAGAGATATGGTTCTTGACGA[A/G]TACGACATGGTATGTTTTGCCTCCTCTCTTGGTGC
1,849	4	4002	2.44	89809842	F1Dsnp	PHR	A	G	4	11,604,504	+	AGTCTCGAAAAGGACATCACCATATGTTCCTTAGC[A/G]TATCTGCTATTGTGGCGATTTCAGCTGCTACTCTG
1,850	4	4002	2.44	89865801	F1Dsnp	PHR	A	G	4	11,605,517	+	GCCTTGGTGTGCACTTCTCAGATACCATCTTGTAG[A/G]CCAACCATGGCAGAAGTGGTGCAAATTCTTCAGAT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,851	4	4002	2.44	89809843	F1Dsnp	PHR	A	G	4	11,617,696	+	GCAGCTAACTTGGGTGCTGAATCAAATGCAAAGAA[A/G]GCAAATTTGTCTGCTGCAAAGAAGGAAAGAATTAA
1,852	4	4002	2.44	89809844	F1Dsnp	PHR	A	G	4	11,623,462	+	CCAGAAAACAAGTATACAACCATGTAGAGCTTCAC[A/G]AGAGTGCCGTTTGACACCTTATTCATCATCGAACG
1,853	4	4002	2.44	TP2540	GBS				4	11,638,703	11,638,638	TGCAGATTCTTGGTGAACAGAAAGCACGAACATATCTGATTCTTGAGGAGTAAAAAGGGAATCT
1,854	4	4002	2.44	TP6192	GBS				4	14,930,070	14,930,113	TGCAGGAGGGATTTTAGCAGTAGCTAGCAAGGTCTGGATCTTTTTACATGAGAAGTTGCTAACT
1,855	4	4002	2.44	111_194565	GBS				4	15,944,535		ACTCATCCCGGCACAGAAGTATGGAGGTGCAACTGCACATGATATAAAGCCCTGTCCGCTGCTC
1,856	4	4002	2.44	89865868	F1Dsnp	PHR	A	G	4	15,946,911	+	TGAGCCTTACTTTTCCCTCTGACCTTTACCACAGC[A/G]GCCATATGACTGCTGCCCTTTTGAAACTCATTCAA
1,857	4	4002	2.44	TP5789	GBS				4	16,020,835	16,020,898	TGCAGGAAAACGGTCCGAGATGCAGAAAAGATAAGGAAGTCACTCCATCGCTTCGCCTTTTGAG
1,858	4	4002	2.44	89809912	F1Dsnp	PHR	A	C	4	16,081,745	+	GAATCACAGATCAAAAGCCATGTGAAGATATTCCC[A/C]AAAGTGCAACATGGGTGGACCGTAAGGTACAACGC
1,859	4	4002	2.44	89865870	F1Dsnp	PHR	A	G	4	16,124,466	+	TGGCAGAGTAGTAGATGCTGAGAAATTGATAAGAA[A/G]CATGCCCATGAAGGCTGATGTTGTGATATGGGGCA
1,860	4	4002	2.44	89865871	F1Dsnp	PHR	A	G	4	16,203,388	+	AAGGCCAATGTTGTTGCCACATTGTTTATGGCTAC[A/G]TTCTCACAAAGTTTAGCCTCACACAGCACTTTGAG
1,861	4	4002	2.44	89865872	F1Dsnp	PHR	A	G	4	16,420,439	+	GTCGGATTGACGTCGCTGGCTGAGAAGTGTAGGTT[A/G]CTGAAATCATTGGATTTGCAGGTGAGTTTTTACTC
1,862	4	4002	2.44	89809915	F1Dsnp	PHR	T	C	4	16,615,108	+	TGTTAATGGCTGTGACATCTTCAACTCTAACATCC[C/T]GAATTCCACCAGACATTTCGCTACCTAGAGCAACC
1,863	4	4002	2.44	89809916	F1Dsnp	PHR	A	G	4	16,615,374	+	GGTGCAAGGATAGTGATGCCTTGTATAGTAATGTT[A/G]CTGCAATATAATACCAGAATGTTAGCACAAAGTGG
1,864	4	4002	2.44	89809917	F1Dsnp	PHR	A	G	4	16,615,762	+	ACATCGGTAAGATTTGTTCCGAAGATGAGACTGCT[A/G]AACCTTCCACCAGGGGCATCTCTCCCTTGCCCGTA
1,865	4	4002	2.44	TP8825	GBS				4	16,618,271	16,618,213	TGCAGTGCCTACAACCACAAACCTTGCTAACGCCATATTGGGCTGCCCCGCCACCAATGGCAGA
1,866	4	4002	2.44	89865876	F1Dsnp	PHR	T	G	4	16,753,779	+	GACAACAGGCCCATATTCTAAATCAGCTCCTACAA[G/T]ATCTGCATCCTTAAAATTAGAATTGCTCATTTCGA
1,867	4	4002	2.44	89809920	F1Dsnp	PHR	A	G	4	16,769,144	+	GTATTGTTAACTCGCTCTATTCGTTTTACTGGGAC[A/G]TAGCTCGAGATTGGGACTTGAGGTATGCCAGCGTA
1,868	4	4002	2.44	89865879	F1Dsnp	PHR	T	C	4	16,776,259	+	TTGATGCTACAATCTGTCGAACCATTAAACATCGC[C/T]TCACGGGTCACAACCTGCATTGAAAAGCACAAGAG
1,869	4	4002	2.44	89809922	F1Dsnp	PHR	T	C	4	16,784,600	+	TCCTGATCGACTCAATAACCTGGAAAGCATCTTTA[C/T]TTTTATTAATATCAGTAGGATGTTGTCTGTAACCA
1,870	4	4002	2.44	89865881	F1Dsnp	PHR	A	G	4	16,790,414	+	ACCGCCAGTACCATGGTCATTACCTTTGTCATCAC[A/G]TAAACAATCATTAATACCTTCATCCTCTGATCTTG
1,871	4	4002	2.44	89809924	F1Dsnp	PHR	T	C	4	16,910,548	+	AACACAACATTCCTACAGTCTGGCAAGATACTGAC[C/T]GACCATGGTGGGAGATTATATTTTTGACCAAGGAA
1,872	4	4002	2.44	89865882	F1Dsnp	PHR	A	C	4	16,911,074	+	GGTGAATCAGCAGCAACAAGAGCAGGCTCACAAAG[A/C]TTTATAGCAGCATGTAGATCCTTCAGATGTCCCCA
1,873	4	4002	2.44	TP109	GBS				4	17,199,894	17,199,831	TGCAGAAACAAAGAAAAAGCTATGAACTAAAGAGGATAGAGAAATTTAATGAAAACGGAAACAT
1,874	4	4002	2.44	121_179286	GBS				4	17,201,314		GTTGTTGGATTCTGCAAACATCTTACAGCCATTGGTGTGGTTCTTTTCTTTGCCTTTTGCTACT
1,875	4	4002	2.44	TP6471	GBS				4	17,201,368	17,201,403	TGCAGGCATGTTTGATTGTTTCAACGAGTGGTTTTAATGTTTTATATAATTTTTGACCCAGTTT
1,876	4	4002	2.44	89865884	F1Dsnp	PHR	T	C	4	17,218,339	+	GGTTCATCTGCAATTAAGATCCGTCCAATTTGAAA[C/T]GAACAACTTGAAGTCCTGCAAGAAATTAGAAGGTA
1,877	4	4002	2.44	89865885	F1Dsnp	PHR	A	G	4	17,223,949	+	TTTCCTCACAGTAGTATAAAATTGTTCAATTCCGC[A/G]TGTAAAAGCAAAATACTCAGAAGCTCGTTCATAGC
1,878	4	4002	2.44	89809929	F1Dsnp	PHR	T	G	4	17,237,238	+	ATTAGACTGCTTCTCATTGCAGCTTCCTCAAGCTC[G/T]ACCGGTTCAACGTTTTCACCTATTTTTCAAACAAA
1,879	4	4002	2.44	89809930	F1Dsnp	PHR	T	C	4	17,239,868	+	AAAAATTTATCAACATGTGATGGCAAACTACCTCC[C/T]CCACTGATGCCAGCCTGCAGGAAGCCAAAAAAGTT
1,880	4	4002	2.44	121_99798	GBS				4	17,247,367		CGCAGAAATAAAAGAGGGAGGCCATTTGGATTAACAAAATATGAAACCCTCTAAAGCAAAGAAG
1,881	4	4002	2.44	89809931	F1Dsnp	PHR	T	C	4	17,267,526	+	TCCAGAGATTCTGAATCCCAGATCCAGAAAACGAC[C/T]TGGGCAGCGGCCCGGTGAGATTGTTGTAGGACAAT
1,882	4	4002	2.44	89865886	F1Dsnp	PHR	A	C	4	17,278,545	+	GTTGAGCTGGAGCTTGGTGTTTTGCAAGGTTGTCT[A/C]ACTGTAAATGCTTGTTACAAGAATACAATCAGTGT
1,883	4	4002	2.44	89809933	F1Dsnp	PHR	A	G	4	17,278,858	+	TTCCGAGCTTTGTTTCACTCAAACATGCCATTGCC[A/G]GTTAGAGTTCAGAGGTAGTGTATAACTTTTTATTT
1,884	4	4002	2.44	89809934	F1Dsnp	PHR	T	C	4	17,340,861	+	TCTTCCCTAAACTTGAATTTTCTACAGTGCTTGCA[C/T]GAACCAAGGGTCAAGTTTGCAAATCACAGTGAGGA
1,885	4	4002	2.44	89809936	F1Dsnp	PHR	T	C	4	17,403,427	+	GACCTTCCATTATAACTTGCTGTAGCCAATAGAAG[C/T]TGAGGATTTGACGAATCAGAATCAAGCAATGCCCA
1,886	4	4002	2.44	89865890	F1Dsnp	PHR	A	G	4	17,455,748	+	GATGATAAAGCTGTCAAGGTTAGTGTTCCTGTAAC[A/G]ACAACCGTGAACTCAATTTTGAATCCTGAATCGCC
1,887	4	4002	2.44	631_48096	GBS				4	17,489,157		GGGATTCTATATGTTGAACGCTGCAGGAATTGTTCAATTGTCTCTGGTTTTGAATTTTTGGAAG
1,888	4	4002	2.44	TP5951	GBS				4	17,489,178	17,489,241	TGCAGGAATTATTCAATTGTCTCTGGTTTTGAATTTTTGGAAGATGTCTCCAGCGTCTTCGAAA
1,889	4	4002	2.44	631_49232	GBS				4	17,490,293		CAGTTCCAGCTGAGAGAAGGTGGTCAAGTGCCGGATCAAATCCTTCAGTTTCCTATTCTTTGGC
1,890	4	4002	2.44	89809938	F1Dsnp	PHR	T	C	4	17,493,629	+	TAAGCTCTGATGGAAGACGACTTTGATTTCCCAAC[C/T]GGCCCCAACCCTGAAGACGTCGACATGGACATCCC
1,891	4	4002	2.44	89809939	F1Dsnp	PHR	A	G	4	17,550,131	+	ATGGACTATATTTGTAATAATTGCAAGAACAGAAT[A/G]GACCAAGAGGGTAAAGAGGCTGATGAGCTTTCTAA
1,892	4	4002	2.44	89865891	F1Dsnp	PHR	T	G	4	17,551,168	+	CAGGAACTAGAAACAGAGAAGAAATGTGCCGAAGA[G/T]CTCAAGGAAGCAATGCAATTAGCAATGGAGGGGCA
1,893	4	4002	2.44	89809940	F1Dsnp	PHR	T	C	4	17,563,701	+	TAGTTGGCGGTGAAGAGTTTAGTGGGGTACTATAG[C/T]ATGAATTGTTAGTACTGTTATTGTAAGACAATGAA
1,894	4	4002	2.44	89809941	F1Dsnp	PHR	T	C	4	17,623,408	+	TCACTTGTGCCCAGGAGCGTGCAGTTAATTATCTT[C/T]TGACCAATGTTGATAAGGTCTCTGAATGGGGTGAA
1,895	4	4002	2.44	89809942	F1Dsnp	PHR	T	C	4	17,624,043	+	AATGTTGCTTCAGCCACTGATGTGATTGTGTTTGT[C/T]CGGGAGATAATCGAAACCAATCCTAAACTTAGGGT
1,896	4	4002	2.44	89809943	F1Dsnp	PHR	A	G	4	17,624,318	+	TCAGCAAGTGAACTCCATGACTGTGTCTTCTAAAA[A/G]ACCAGCTATTCTTTCTGATGGGACTTATGCTACAC
1,897	4	4002	2.44	89809944	F1Dsnp	PHR	T	C	4	17,625,680	+	ACTGTTATTGTCCTCAATGATATTCATATTGACAT[C/T]ATGGATTACATTTCTCCTGCTGTTTGTAGTGATGG
1,898	4	4002	2.44	89865892	F1Dsnp	PHR	T	C	4	17,658,682	+	GCCACATCGGTTTTGTTGAATGCCAGCACAAGGGG[C/T]AGCCGTGTCTTGTATAGGATACTACAAGCATAAAG
1,899	4	4002	2.44	89809945	F1Dsnp	PHR	A	G	4	17,678,621	+	TGCGCATAGTTCAAAGTTTGGTTCCCTAATCCATT[A/G]AGTTCCTCCTCTTCTCTATCATTATATTCCAAGAC
1,900	4	4002	2.44	89809946	F1Dsnp	PHR	A	G	4	17,678,771	+	GGGATGGACATCTGCTTTGTCTGTTGCTTGTTACC[A/G]CGCTTCACAAGAACTTTGACTTGGACCTCCTTGCT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,901	4	4002	2.44	89809947	F1Dsnp	PHR	A	G	4	17,704,345	+	CACTAAACTGATATTTGCTACAGAGATGGCGGGTT[A/G]TGACGTGGTTGCCAGAACGATCATGATGTTTCTGT
1,902	4	4002	2.44	89809948	F1Dsnp	PHR	A	G	4	17,704,398	+	CGATCATGATGTTTCTGTTTTCATCATCAACAGCG[A/G]CTCATGCAAACAACGTCGAGGTTGCCAAGATCTTC
1,903	4	4002	2.44	89865893	F1Dsnp	PHR	A	G	4	17,748,930	+	AACTATGGAATCACCCCCGGAGAAGACCATTATGC[A/G]TGCATGGTCGATCTTCTAGGAAGAGCTGGACGTAT
1,904	4	4002	2.44	89809949	F1Dsnp	PHR	A	C	4	17,782,510	+	TTGTGATTTTGCATCAGCAAGTAGTAAAACTCCAC[A/C]GGCAGATACCCCCTAGATGAAAATACAATTTGTGA
1,905	4	4002	2.44	423_83976	GBS				4	18,573,129		CATATGAGTAGTTTGAAATAATGACTCCCTTGCAAAAGTCCAACCCAGAAATTAACTTCTTCCT
1,906	4	4002	2.44	89809952	F1Dsnp	PHR	T	C	4	18,595,034	+	TCATGTTTAGTCCGCCTGGTTCGTTTCAATCCACC[C/T]AGCATTCAGCAAGTAATTGATATTCTTCCTTTAAA
1,907	4	4002	2.44	89809954	F1Dsnp	PHR	A	G	4	18,703,440	+	CTAGAGGATGTATTATAGAACCCAGATGTCAGCTC[A/G]GATGGGTGAGACCTTGTTTTGTACCAAGAGTACAT
1,908	4	4002	2.44	89809958	F1Dsnp	PHR	T	C	4	19,161,274	+	AATTGGATTTAGTTTGGCTCCAATTATGATGGAAT[C/T]AGACTTATTGAATATGGTGAATGGTACGAAATTGG
1,909	4	4002	2.44	89865904	F1Dsnp	PHR	T	C	4	19,810,640	+	TCAAACTCTTGCAGTCCAACAATGCAAACTTGTTG[C/T]CGTCCATCTTCTCTCATACAAAGTTTCCTTTAACA
1,910	4	4002	2.44	89865905	F1Dsnp	PHR	A	C	4	19,881,007	+	TCACGAGTCTGTCAGGATCCTATCCCTAACGAAGT[A/C]ATTCAAGTAAATAACTCTATGATTCTTTCAAGGAG
1,911	4	4002	2.44	197_39240	GBS				4	19,881,528		TAAAGAAGAAAGGTCTGCAGTTATCTGATTTGGCAAGTGCTCTAAAAAGAAATGTTCATGAGGC
1,912	4	4002	2.44	89865906	F1Dsnp	PHR	A	G	4	19,881,559	+	GACATAAAGAAGAAAGGTCTGCAGTTATCTGATTT[A/G]GCAAGTGCTCTAAAAAGAAATGTTCATGAGGCAGC
1,913	4	4002	2.44	TP572	GBS				4	19,887,243	19,887,306	TGCAGAAGATGTTGGATACAAATTCTGGGGTTAAGGGAATCATTTCTTAAATAAAGTTTGGTAG
1,914	4	4002	2.44	TP7997	GBS				4	19,940,783	19,940,744	TGCAGTAGCTAGCTACATAGTACGTCCATCAAACTCATCACCAACACCGACTTCTACCTATCGG
1,915	4	4002	2.44	89865908	F1Dsnp	PHR	A	G	4	19,963,894	+	AGGCAAATGTCAAAGAAGTCATGTATCATGGACTT[A/G]TGAAGCTTGTTTTGATGGACCCATCTAGTGGAGGG
1,916	4	4002	2.44	89865914	F1Dsnp	PHR	T	C	4	20,155,854	+	CCTTTACCAAGATGATCTTTGTCAGCCCCAAGGTC[C/T]GTGATATAAGGCTGCAAAGAGGAAAGTAGCAATCA
1,917	4	4002	2.44	89865915	F1Dsnp	PHR	A	G	4	20,165,568	+	TCTGATGAGGCTGCAGTATCCCATTTCCTTGATCA[A/G]CATACCTTCCAACACAACACAAAAACCCCATTTTA
1,918	4	4002	2.44	89809969	F1Dsnp	PHR	T	G	4	20,284,830	+	TTGATTTTCTCACAGATTGATGCCCACAGTGGTGG[G/T]GTGAATGACTTGGCATTCTCTCATCCAAACAAGCA
1,919	4	4002	2.44	TP5845	GBS				4	20,356,795	20,356,851	TGCAGGAACAAATATATCCTGGAGTTCTTAAAAAATCTAGTTTACAAAGTAGAACCGAGATCGG
1,920	4	4002	2.44	89865945	F1Dsnp	PHR	A	G	4	22,423,752	+	GCATCTGGACCTTTGAGTTGACAGCAACTGCCAAA[A/G]ACCTCCCTACCAACATTTTTCCAATCAACGGCTCC
1,921	4	4002	2.44	89810003	F1Dsnp	PHR	T	C	4	22,521,330	+	ATTAATTGCAGCAACTCCACATTGTATCTGGGAAG[C/T]TATCTCTCTAGCGCGACGCTGGCTGCCGGAAAAAA
1,922	4	4002	2.44	89865946	F1Dsnp	PHR	T	C	4	22,583,734	+	ATGCAGTGGCTGTGCTGTAGTATCTAGATTTATGG[C/T]AGCTGACACCTCAAAGGAAGAGAATGTTCCTAAAT
1,923	4	4002	2.44	89865947	F1Dsnp	PHR	T	C	4	22,584,269	+	ATTATCTGGAGTCTTGACAATCGCTTTGTTCTTGC[C/T]GCTATCATGGGTGATTTGTTCATTTCTCCTTTTGA
1,924	4	4002	2.44	89810004	F1Dsnp	PHR	A	C	4	22,586,655	+	GCACTGGTTATTGTGAAAACACTAGGCATGATACC[A/C]TATCCGGAACCCTACCAGAGTGCGTACCAGAAGAG
1,925	4	4002	2.44	89865948	F1Dsnp	PHR	A	G	4	22,586,679	+	GGCATGATACCATATCCGGAACCCTACCAGAGTGC[A/G]TACCAGAAGAGACGATTAGGAGCCCTGGGTTCTGA
1,926	4	4002	2.44	89887719	snp	PHR	T	C	4	22,587,180	+	TCTGGAAGGTGTATTAAAAGGAGGAACTTGGATGA[C/T]CGTGATGATCACTCATTCAGAAGTAATAGAAAAAG
1,927	4	4002	2.44	89865949	F1Dsnp	PHR	T	G	4	22,587,880	+	GAACATCAAAGCGGCTGAGAGTGGGAGAAGCCACA[G/T]CACTGGATGCACTTGCCAGTACCAGTCTAGCTGTT
1,928	4	4002	2.44	TP1268	GBS				4	22,594,989	22,595,048	TGCAGACTCTCAATAGTTTCCAGGGTTGAGACCCGCAAGAACACATTTTTGAAGGGCTTTTCCC
1,929	4	4002	2.44	1105_4501	GBS				4	22,595,110		AATATTAACATTTCCGGGGAATACCCTTGAARTTGCAACAATTGTCAAATAAGGGCCTGGGAAA
1,930	4	4002	2.44	89810005	F1Dsnp	PHR	A	G	4	22,626,642	+	AGGTTATATCGATTGCCATTACCAACAAAAGCATC[A/G]ACAATTGGCTTGAGAAGGTTGTTCCTCACAATATG
1,931	4	4002	2.44	TP6275	GBS				4	22,626,700	22,626,637	TGCAGGATGAACATCTGATAAATCATATTGTGAGGAACAACCTTCTCAAGCCAATTGTCGATGC
1,932	4	4002	2.44	89810006	F1Dsnp	PHR	T	C	4	22,627,112	+	CAATTCGCATATGTTTGACAGTACTTCAGGCTTCG[C/T]GACAGTCTGAGTTTCAATTCTTTCGCCAGAGCATG
1,933	4	4002	2.44	89865950	F1Dsnp	PHR	T	C	4	22,641,560	+	AGCTTATGCCTGGTTTTGATCCCGAGATTGGGAAG[C/T]TAGCCCAGAGGGTTCTAATTAATCCACGAAGGATT
1,934	4	4002	2.44	89830563	snp	PHR	A	G	4	22,657,384	+	GAAACAAAGAACAAAGCATACCTTCCATGATATGC[A/G]GCCCAATGAAGGGCTGTCCATCCACGTCTATCACG
1,935	4	4002	2.44	89865951	F1Dsnp	PHR	T	C	4	22,657,933	+	AGGCTAATGAAAAGGTTCACTAATCCGGCCACATG[C/T]GGTGGTATGAAACATCGATATACCCCAACCTGAAC
1,936	4	4002	2.44	89865952	F1Dsnp	PHR	T	C	4	22,684,864	+	AATATGAGAAGTTCTTGGAAACTGGTGACCCTGAG[C/T]ATGCTTGGCAACCACCAAAGGATGAGTGGCAAAGT
1,937	4	4002	2.44	89865953	F1Dsnp	PHR	T	G	4	22,686,456	+	GATATAATGAAGTTCTGCCGGGAAAAGATGCCGGC[G/T]TATTGGGTTCCCAAATCTGTGGTGTTCGGACCATT
1,938	4	4002	2.44	109_91976	GBS				4	22,699,096		GCTCTTGTTGGTGTCCCGGCATGACCAGGTCGGTCCTGTCCCGAAATTCTGCTTCAATAGATTG
1,939	4	4002	2.44	109_23884	GBS				4	22,756,186		CCAATAGAAGTTCCTCTTGAAGTTTTCCAAAGGCATAAGGAGTAAGAACAGAGGCAGCATGTGA
1,940	4	4002	2.44	89865954	F1Dsnp	PHR	A	G	4	22,824,867	+	TCGACGCTTATGCCACGAATATGTATATCAGATGC[A/G]TTCTTCTGGGTAATTATTGGGTGGGACCTGGAATT
1,941	4	4004	4.88	89866063	F1Dsnp	PHR	T	G	4	9,218,815	+	CATCTTGGGGAGCTATCACTTGCAGGTGCTTCTAT[G/T]GCCACTTCTTTTGCATCTGTGACTGGTTTGAGCGT
1,942	4	4004	4.88	89809970	F1Dsnp	PHR	T	C	4	20,410,535	+	TCTAGGTCTTTGGCCACTTCTGCACGAAGGATCTT[C/T]GTTGAATCTACACCTAATGAGTTGCCTACTTCTTT
1,943	4	4004	4.88	89809971	F1Dsnp	PHR	T	G	4	20,510,978	+	TTAATTGGACTAGGAGGTGGTGGAATTAGAGGAGC[G/T]ATTCCTGCTTTAGGTGCTGATCAGTTCAACTACAA
1,944	4	4004	4.88	89809972	F1Dsnp	PHR	A	C	4	20,543,154	+	TGGTCAAGTCATTTGGTCACAAATCTACTGTCATT[A/C]GGTATGTCATCTCACTCCACTAAGTTTTAGAAATT
1,945	4	4004	4.88	89809973	F1Dsnp	PHR	A	G	4	20,607,260	+	TTAAAATCTGATGCCATCAGCTGATTCTGTAATTT[A/G]GGGACTATGTCATAAGAGATGATGTTAAATAGGCC
1,946	4	4004	4.88	89865919	F1Dsnp	PHR	A	G	4	20,646,384	+	TTTCTGTTAATTGTCTCAAACATTTTATAAGCTGC[A/G]GCTTGTCCAGAAGCAAATGCACTGATACAAGGAGA
1,947	4	4004	4.88	89809974	F1Dsnp	PHR	T	C	4	20,704,411	+	TTCCCAATAGCGCCAATCGTACCAACCGACATTAA[C/T]AAGTAATCCAAGGAATCAGCAAATGAGAAGAGCTT
1,948	4	4004	4.88	89809975	F1Dsnp	PHR	A	G	4	20,719,907	+	CCCTTATCTGTCCTACTTGCACCAACCAAATGAAG[A/G]TCGTTCCTTTCCAGCTGCGTTGCTACCATTAGAGC
1,949	4	4004	4.88	89865920	F1Dsnp	PHR	A	G	4	20,723,985	+	TTCCCATGATGAAAAGCATCAAAAAGCTGCACAAC[A/G]GTGGGAAAACACCATCACTGGAGTGGACCAACGAT
1,950	4	4004	4.88	89809976	F1Dsnp	PHR	A	G	4	20,759,655	+	GAAGTGACATATTGTGATAAGGCTCCACAGGATGT[A/G]TACATGAGTATGAAAGCAAACATGGAAGGATGTCG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
1,951	4	4004	4.88	89809977	F1Dsnp	PHR	T	C	4	20,760,060	+	TATCTTAGAATGAAGGAGAATATGAAATGGCATCG[C/T]ACTGGGAGGAGACAGAGACAGCCTGATGGAAAGGA
1,952	4	4004	4.88	89830212	snp	PHR	T	C	4	20,802,817	+	GTGGATCCAAATATTGAGACCAGGCCATCGACAAG[C/T]GCCCTTAAACGAGCCCTCTTGACTGCATTGAGGTG
1,953	4	4004	4.88	89865921	F1Dsnp	PHR	T	G	4	20,865,022	+	TGCAGAAGGAAAATCTTTTGGTGAACCTAAGGCTA[G/T]TGTAGAACCTAAGAAGGGTGAGGATGATCTTGTTC
1,954	4	4004	4.88	89809978	F1Dsnp	PHR	T	C	4	20,882,406	+	GGTCAGCCAGGAGCCTCTGCTTTTTAATGACACTA[C/T]AAGAGCCAACATTGCATATGGTAAGGATGGGAGTG
1,955	4	4004	4.88	89809979	F1Dsnp	PHR	T	C	4	20,882,643	+	GCAGGGTTATGATACAATAGTAGGTGAACGAGGGG[C/T]TCAACTTTCTGGTGGACAGAAGCAAAGGGTAGCTA
1,956	4	4004	4.88	89809980	F1Dsnp	PHR	T	C	4	20,900,601	+	AGAGGTCAACACTGGGGAAATTGTTGGCAGGATGT[C/T]GGGCGACACTGCGCTCATTCAGGAAGCGATGGGCG
1,957	4	4004	4.88	89865924	F1Dsnp	PHR	T	C	4	20,902,775	+	ACAATCCGGAAATAATAGTCCCCTCTCACCAGGTG[C/T]GCCTAATTTATTTGGTGTTCTTGAAATAGAACCAA
1,958	4	4004	4.88	89809981	F1Dsnp	PHR	A	C	4	20,908,271	+	ATATCTCCTTCAATAGTACCTCCGGTTTTCCTTCC[A/C]GAAAGAACATCCATTAGAGTTGTTTTCCCAGCCCC
1,959	4	4004	4.88	89809982	F1Dsnp	PHR	A	G	4	20,911,589	+	TTATCCAGTTTTCCAGCAAGTGCCAATAAGAAGGT[A/G]GTTTTACCACACCCTGGGGGACCAAGAAGGAGAGT
1,960	4	4004	4.88	89865927	F1Dsnp	PHR	T	C	4	20,984,770	+	AAAGAGAAAGAAGAATTACATGTTGATGAAATGGT[C/T]AAGGTAGAGAAGCCAGAGAAAATTAGACGGCCTAG
1,961	4	4004	4.88	89865929	F1Dsnp	PHR	A	C	4	21,099,857	+	TGAAGGCCAAGCTTATCGGTGATTTCATCAGCATT[A/C]ATGGCATTTGGAAGATCTTGCTTGTTTGCAAAGAC
1,962	4	4004	4.88	89809983	F1Dsnp	PHR	T	C	4	21,106,038	+	AAGCCCCACCATCCATCTTCTTCAAATAGTGTCTT[C/T]GCTGTCTTCAATACCGTTGGTCTTCCAGCACCATA
1,963	4	4004	4.88	89809984	F1Dsnp	PHR	A	G	4	21,113,056	+	CAGGAGGAGGTTTTGAAATTTGGCAGAGCTTCCAG[A/G]GTATCCTGCACGGTGGGTGCTCTTTGCTTGATTTC
1,964	4	4004	4.88	89809986	F1Dsnp	PHR	A	G	4	21,196,501	+	GGGTCCTGTTTCAACCTTACGTTTTGGAGGCCACG[A/G]GCACCTTCAAATTATGTTATCTTGGGAGATTGCGT
1,965	4	4004	4.88	89865936	F1Dsnp	PHR	T	G	4	21,711,522	+	CATGGCGGGCCTGAAGCAGCTACTTATATCAAGAG[G/T]AATGCCATGAGACTATTTTTTGAAGATGCTGATTT
1,966	4	4004	4.88	89865938	F1Dsnp	PHR	T	C	4	21,912,800	+	GTGGTCTTAGCTGGCTATCACCGCACTTTTGGTCA[C/T]AGGCCGGATGGGACTTTTAAGTGTATGATATATGA
1,967	4	4004	4.88	89809992	F1Dsnp	PHR	T	C	4	21,933,983	+	CCTACTGATTCCCCTGAAGAAACATCTGGAATGCA[C/T]GATCAACAAGGCTTCTTCAATGGTGAACATGTGCA
1,968	4	4004	4.88	89865939	F1Dsnp	PHR	T	C	4	21,934,626	+	ATTTTTCTGTATATTATTTTGTAGGTTTTACTTGA[C/T]TCCTTGAAGCGAAAAGCATATGATGATGAATTAAG
1,969	4	4004	4.88	89809994	F1Dsnp	PHR	T	C	4	21,959,293	+	CAAGCAACTTATGTGCACCATCCACCCTATCATTC[C/T]TACACAATGCCTTCAACAAAATATTATAAGTAAAC
1,970	4	4004	4.88	89865940	F1Dsnp	PHR	A	G	4	22,058,293	+	GATAATTCACATCCTAATGTAAGCCTGTCATTAGT[A/G]GAAATCACTGGAAGAACAAGACTTTCTGATGGAAT
1,971	4	4004	4.88	TP5854	GBS				4	22,133,222	22,133,173	TGCAGGAACAGAAACAGAGATGTTTTGTCAAGAAAGAAAGGTCATGGTTTTTGGTGAGAGGATT
1,972	4	4004	4.88	89865942	F1Dsnp	PHR	A	G	4	22,173,808	+	TCAACTTCCTTTTCCGAAGCTTGTTTGTTTAGTGA[A/G]CCCACAAACAGTTTGTACTCAACTGCACCTACCAT
1,973	4	4004	4.88	89865943	F1Dsnp	PHR	A	G	4	22,178,053	+	GTTCTCTTGTCTTTGATCAGCGCAACCTCTACCAC[A/G]TCTCCATGTTCTTCAAACAAAGGGCGAATCTACAT
1,974	4	4004	4.88	89887641	snp	PHR	A	C	4	22,189,089	+	TTTGCCAGATCTCGAGGAATAGATTTGGGTGCACC[A/C]GTGGGACTTGATGTTCTTATTGATGGAACAGTTCC
1,975	4	4004	4.88	89865944	F1Dsnp	PHR	T	C	4	22,197,467	+	AGTGATAGCTCTGTTGCAAGTGTCAAAAAACAGGC[C/T]AAGACACTGCTAGCGAAGGTGTATGGTGGTTTTTC
1,976	4	4004	4.88	89809999	F1Dsnp	PHR	T	G	4	22,198,607	+	ATTTTTACACCTTGCAGTATGGTAGAGCAGGTTGC[G/T]GGTTCAGATCAGCATGAGAAGTTGAAAAGATGGGC
1,977	4	4004	4.88	89810007	F1Dsnp	PHR	T	G	4	22,948,875	+	TTACCCTATCATCTTTTAAGATTACCACCAACTTT[G/T]TTGCAAGTCCTTCCTCTGCAGCTTTGGTCACATAT
1,978	4	4004	4.88	89810008	F1Dsnp	PHR	A	G	4	23,037,067	+	AAATTTCAAAAATGAAGTCTGAATTAGACTCGAAA[A/G]GGGAGGTGGACTTCTTTGTCTGCACTCTTGGGAAA
1,979	4	4004	4.88	89865964	F1Dsnp	PHR	T	C	4	24,265,058	+	GATGGGCATGGTGGAAGTAAAGCTGCAGCGTTTGC[C/T]GCTGAGAATTTGCATAGCAATATAATTGAAATGAT
1,980	4	4004	4.88	89810021	F1Dsnp	PHR	T	G	4	24,278,459	+	AAATCAAGGGGTGGATTAGAAGATGAGGATGATGA[G/T]AGTGCAGGTGGGTCATCTGGATTTTCCTTACTGGT
1,981	4	4004	4.88	89810022	F1Dsnp	PHR	A	G	4	24,473,131	+	ACGTTTTGGGTGTTCTGCAAGTGAATTCCATCAGT[A/G]TTTGGGCTATTCTCTGGTGAAGATATGGTAATGTT
1,982	4	4004	4.88	89865965	F1Dsnp	PHR	A	G	4	24,473,945	+	CATTCTTTTACCTTAGAATCGTCGGAGACACCATC[A/G]CCCTTGGCTCCAAAAGACAAGACAGAAAAGGAACC
1,983	4	4004	4.88	10_646328	GBS				4	24,475,808		CCGGGGGGCCACGAGTGGGTCACTGGTCGGTRCCATTATGCAGCTGCATCATCTTCACAACTCG
1,984	4	4004	4.88	10_723374	GBS				4	24,547,714		CCCAAAGCAAGTCATTGATTTCAAGGGATTAAATACAACTTAATTGCATACCCAGATACACATG
1,985	4	4004	4.88	89810024	F1Dsnp	PHR	A	G	4	24,623,671	+	GTGATTCCAGAGCTTATCATCATTGGAAACACATT[A/G]TTTTGCGTCTGTAAGAATCTATTGAGGCATTGGAG
1,986	4	4004	4.88	89865966	F1Dsnp	PHR	A	G	4	24,631,966	+	TTGGCTACACTTTTAGTAACGCGAGAGATGTCATT[A/G]ATTACGTCACAACCATGGCTCCTCTTGTTTGTCTA
1,987	4	4004	4.88	89865967	F1Dsnp	PHR	T	C	4	24,654,612	+	TCGCATGGGAGTATGGTTGGTGCTGGGCCTACTCT[C/T]TCTTCTTGTGTCCACGCTTCTGTAAAGCAAGTTGT
1,988	4	4004	4.88	89810025	F1Dsnp	PHR	T	C	4	24,656,928	+	TCAAGATGATCAAATATACTCATCTCTTTATCATC[C/T]GGCAGTAGCTCTTGACTCGGATATAAAAAATTGTA
1,989	4	4004	4.88	TP5341	GBS				4	24,732,700	24,732,637	TGCAGCTGCTACCATTGGCAAAGTTGACATCGACCAAACGGATAAGATTCTCATCATAAGAAAT
1,990	4	4004	4.88	89810026	F1Dsnp	PHR	A	G	4	24,775,207	+	TATGTCAGGCCAATACCAAACGTCGTGCTTAGACC[A/G]GTGAGGACTGAGACGATGGAGAAAGTCACTGAGAA
1,991	4	4004	4.88	89865969	F1Dsnp	PHR	T	G	4	24,777,031	+	CTTGTTGTCGACGCTCAGCTTTTGGTACTTTCTCC[G/T]CCTCCAGTACCTCTTCACGTTGGTGTAGTACGAAC
1,992	4	4004	4.88	TP158	GBS				4	24,814,543	24,814,601	TGCAGAAACGATTCAGAATCCACCTAATTTCGACGAAACTTACAAACCGAACAATCTCAAAACG
1,993	4	4004	4.88	10_1022387	GBS				4	24,885,245		CTTCGCAAAGTGACCAAGAAGATGAGGTTGCCGATGTTATCTGCAGTGCTTTCGATCATCTTAA
1,994	4	4004	4.88	TP2464	GBS				4	24,885,435	24,885,390	TGCAGATTAGTCATCATTCATCAAAAATGGATATCTTTGATTTGGCCAAGAACATCTTGAAGAT
1,995	4	4004	4.88	89865970	F1Dsnp	PHR	A	G	4	24,888,552	+	CCAAGGCCCTCATTATGGTGCTTCTCCCACCCTCC[A/G]GTATCAGCTTTGGAATGTGACCAATAGTACAGGTT
1,996	4	4004	4.88	89807588	ins	PHR	-	TTGC	4	24,930,035	+	ATATCTTGCAAGAAGAAGGCTAAGAACCTAGCAAA[-/TTGC]ACCTGATTTGCTAAATTTGTGTTGTCAAACTAATA
1,997	4	4004	4.88	TP3077	GBS				4	24,936,445	24,936,473	TGCAGCACCAGATTAGGATTCCAACAAAAGGAAACCCATACACGTGTCAGCTTTACACCATACA
1,998	4	4004	4.88	10_1116666	GBS				4	24,950,954		GCATAAGGAGAAACCAATCATCCAACAGAACWATTTTCTTTCTAAAAAAGAAAATCCGGAATTT
1,999	4	4004	4.88	89830919	snp	Other	T	C	4	25,006,982	+	GTCAAGGTTTTATTTGAGTTCTTTGCTGCAAATTT[C/T]ATTTGAACAAATGTTGGCAAGTAATGCTCGTCTGC
2,000	4	4004	4.88	89810035	F1Dsnp	PHR	T	C	4	25,550,235	+	ACCAAGATAAGGTCTGCTGCTTCAAGAAATTCTAA[C/T]TGGTGAGTAGCATAGATGACGGTTTTTAGAGACAA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,001	4	4004	4.88	63_7046	GBS				NGH			CTTGTTGGTGTCCAATTCGTTGAAATTCTCCTGAGGAGGTCTGCAGATATATAAAATTTAACGA
2,002	4	4004	4.88	TP1151	GBS				NGH			TGCAGACCTCCTCAGGAGAATTTCAACGAATTGGACACCAACAAGAAGCACGACCTCCCTATGG
2,003	4	4004	4.88	TP1626	GBS				NGH			TGCAGAGCGCGCGCTGTGTTTGGACGAGATCGAAGCGGAGCAACTGGCGCGGGTGATTCTAGGT
2,004	4	4004	4.88	TP1474	GBS				NGH			TGCAGAGAGCACACCACGTTCCGTCGCCGCCGCCGTCGCCGAGATCGGAAGAGCGGTTCAGCAG
2,005	4	4004	4.88	TP5210	GBS				NGH			TGCAGCTCTTTTTTCAGGAGAGAGAGAGACAGAGAGAGAGAGTCTCGACTCTGCAAATAAAATC
2,006	4	4004	4.88	408_115553	GBS				scf^{v}	407,799	407,739	TTCTATGAATGATCAATGAAGTATGATCAGTCGATTATATGCCGGCTTTGCATTTCTGAATCAA
2,007	4	4004	4.88	408_76134	GBS				scf^{v}	458,402	458,340	TGTTTGATGACTGGAGCCCGGAACCGACTATMTCTGTTAATGACTTGGTACGAGTGGACTCTCC
2,008	4	4004	4.88	TP5079	GBS				scf^{v}	999,007	999,068	TGCAGCTCCCTATAAGTTAAAATAAACGCATCTTGTTCTTGCTGCTTACTATAACATCAAAAGT
2,009	4	4004	4.88	261_80205	GBS				scf^{v}	999,026	999,089	AAATAAACGCATCTTGTTCTTGCTGCTTACTATAACATCAAAAGTAGTTACCTACTGATGCATA
2,010	4	4004	4.88	261_80223	GBS				scf^{v}	999,054	999,117	CTTGCTGCTTACTATAACATCAAAAGTAGTTACCTACTGATGCATAACATCAACTCAAAAGGCC
2,011	4	4004	4.88	TP3728	GBS				scf^{v}	1,844,752	1,844,815	TGCAGCATTTATATGGAAAAACAGCAAATTTCTTTTAAAACATGATGCTCCTAAAATGTTAACA
2,012	4	4004	4.88	242_111394	GBS				scf^{v}	1,844,802	1,844,739	GGAGCATCATGTTTTAAAAGAAATTTGCTGTYTTTCCATATAAATGCTGCAGGTATTGAAGTCG
2,013	4	4004	4.88	TP8619	GBS				scf^{v}	1,956,816	1,956,753	TGCAGTGAAGGCTATAATAGCTCCAACGGTGACAGACAGATAAAAGAAGTTGAAAAACCTATCC
2,014	4	4007	7.32	TP6348	GBS				3	18,115,835	18,115,776	TGCAGGCAAAGTCTTCATCTTGTTGAACGAAAGGTCCAGATACTCCAACCTCTTCAAGCAGCAA
2,015	4	4007	7.32	89865972	F1Dsnp	PHR	A	G	4	25,047,900	+	TCTTTTAAAGCTTTCGGTCTCCAGATACTCTCATT[A/G]CCCACATCCATGATTTGAATACCCTTTTCCTCCAT
2,016	4	4007	7.32	TP1342	GBS				4	25,049,790	25,049,727	TGCAGACTTTGCATTGTGGAAGGTCTGAAACCGTCACAAGTTACCTTGCTGTTAGTGTTCTTGT
2,017	4	4007	7.32	89865973	F1Dsnp	PHR	A	G	4	25,075,580	+	AACAGCCCTTGGAGGGATAGGCCAATTGAAGAGTC[A/G]CTGAAACTTTTTGAGGATATGAGGCGAGGCCTGAT
2,018	4	4007	7.32	89810028	F1Dsnp	PHR	A	G	4	25,179,421	+	CAACAGCGCATTCCATAGAGCAAAATTTGGTTCAG[A/G]AATTTGATCGAACACCTGGTGGGCATAAGCCATTC
2,019	4	4007	7.32	89810029	F1Dsnp	PHR	A	G	4	25,181,464	+	CTTTCAAGATTGCAGATGATGTGATGCCTCCAGCT[A/G]TAGTGCTGAAGCTATTAGCCTTCATGTCTGAAGTT
2,020	4	4007	7.32	TP1981	GBS				4	25,185,740	25,185,803	TGCAGATAAGGTGACTGATCCCTTGGTGAGCCAGTTTCTTTATGAGAAGGCATCAAGCAAAGAC
2,021	4	4007	7.32	89810030	F1Dsnp	PHR	A	G	4	25,185,799	+	AGTGAGCCAGTTTCTTTATGAGAAGGCATCAAGCA[A/G]AGACAAAAGTCTAAAACTCTACCCTGATGGCTTTC
2,022	4	4007	7.32	10_1283306	GBS				4	25,185,834		CATTGCATTCTTGAAGGTGAACCTGATGATAGAATTTTTTCAGCCCTTGAAGATATTATCACTT
2,023	4	4007	7.32	10_1347761	GBS				4	25,240,643		AAATGACAAAATGAAATAGGTACTGAACTTAATGCAAGTGAAAATCTCCGAGTGTAACTTATAT
2,024	4	4007	7.32	89810031	F1Dsnp	PHR	A	G	4	25,243,224	+	AAAACCGAAAAGGGATTCGAAGATAGCAAACGAAG[A/G]GTGCCCAGTTGCCCAGATCCTCTCCACAACTAGTA
2,025	4	4007	7.32	89810032	F1Dsnp	PHR	T	C	4	25,322,012	+	GCTGTAAATAAATATTACCTAGGTTTGTCCTTGTT[C/T]GGAAATATATCAATGGTGCTGATGAGCTGGCATGG
2,026	4	4007	7.32	89865975	F1Dsnp	PHR	A	G	4	25,406,736	+	CCCTCTTTTGCTCAGCCAACTGTTCTTGCAGCTTC[A/G]TATTTGCTTCCTTCATCTGACTAAGCTCCTCACTG
2,027	4	4007	7.32	89865976	F1Dsnp	PHR	A	G	4	25,411,057	+	ATGGTCAGGAGAGGATCTGCATAACTTGGTGGTCA[A/G]AAATTTCAAGGAAGTTGCTACTTCATTAGAAGGTA
2,028	4	4007	7.32	TP121	GBS				4	25,412,076	25,412,014	TGCAGAAACAGACCTCAGGTCAAGCACAGTTTCACTCAAGGACTTGAGTCCCAATTTCATATCA
2,029	4	4007	7.32	89810034	F1Dsnp	PHR	T	C	4	25,423,179	+	ATGTTAGGTTTTCTTGCTAGCTATATCAAGCTTTA[C/T]CCGCCGATGAAGAGTTATGAATATGGATTTCGGGT
2,030	4	4007	7.32	15_101401	GBS				4	25,529,425		CCTTGTTGTCTAAGCAATCGAAAACGGAGAGCAGTAGTGTAAAAGTCACCATTATTTTCAAGAT
2,031	4	4007	7.32	15_101413	GBS				4	25,591,472		AGCAATCGAAAACGGAGAGCAGTAGTGTAAAAGTCACCATTATTTTCAAGATCTTTACGTCCGT
2,032	4	4007	7.32	89865977	F1Dsnp	PHR	A	G	4	25,615,142	+	CGGCGGAGGGGTTTTAAGGAGAAGAGAAGAGAGGC[A/G]GAGAGGTTTGAATTTCCCACCAATTAGCGGTGAGA
2,033	4	4007	7.32	89865978	F1Dsnp	PHR	T	C	4	25,618,481	+	GAGTTGCCAAAACCAGATGGTAACAAAATCGCCAG[C/T]ATTATACCTTACATTCCCAAAAGATGGGAAAGAGA
2,034	4	4007	7.32	15_129680	GBS				4	25,622,498		GCAAAGATGTCAACTAAATAGAAGAAGTACARAGTACATAGCTGACTCGAGCCAATAGAGAAAA
2,035	4	4007	7.32	89810036	F1Dsnp	PHR	T	C	4	25,680,888	+	GCTCTTGCTTCAGCTCTTTGGCTGCAGAGGAAGAT[C/T]GTCAGAACATTGAATGAGAGCATGAATGAGCTTAA
2,036	4	4007	7.32	TP2676	GBS				4	25,681,519	25,681,576	TGCAGCAAAACTCAGATATGTAAACTGGAGCTGCTACTCAGAACCGTACAATCCACCGAGATCG
2,037	4	4007	7.32	89865979	F1Dsnp	PHR	A	G	4	25,689,621	+	ATCTCTTGATCTGTTGGATCAAATTTCACACCCTT[A/G]GGTAATCCTGGCCACTCTTGAGAAACCTGGAAACA
2,038	4	4007	7.32	89865980	F1Dsnp	PHR	A	G	4	25,693,138	+	TGATGCCGAGTCGAGATTGGCCTCGATGGGGATTG[A/G]TAAGGACACGTCGGAGTATCCTGATCAGGCCACCA
2,039	4	4007	7.32	15_238515	GBS				4	25,726,792		TTGGAATCATCGGAGAATGCAAGAGCTAGAGCTAGAGACATGTATTATTTTGGAGAACCTAGCT
2,040	4	4007	7.32	89810038	F1Dsnp	PHR	A	C	4	25,758,767	+	GGCGAAAAGTCATACTCTAAATGGGCTTTCCAGTC[A/C]ATCAGATCCTGTCGGGATATAAACCTGCAGCACCA
2,041	4	4007	7.32	89865981	F1Dsnp	PHR	T	C	4	25,786,215	+	GAAGATGGTGGTTTGAATCGAAAATCCTACATCAC[C/T]ACTTCTTTGGGATTCTCAAGTCGTGGTGGCATTGA
2,042	4	4007	7.32	89810040	F1Dsnp	PHR	T	C	4	25,927,851	+	GCACACATAGGGCAGGGTTCAAGTGTTACATAAAG[C/T]GTACACTCCTAAGATATATAGGAAAACAAGATTCA
2,043	4	4007	7.32	89865982	F1Dsnp	PHR	T	C	4	25,928,412	+	GAAGCCTCCCTTATGCATATCATTTCAGCATGGGC[C/T]GTTGAATCTCGTAATTCTTCCACTCTAGTAAACAA
2,044	4	4007	7.32	89865983	F1Dsnp	PHR	T	C	4	25,941,016	+	TATGTGTCAATAGAGATTGTTAAAGTTCTTCAGAG[C/T]GTGTTCATCAATCAAGATATTCACATGTACTATGA
2,045	4	4007	7.32	89810041	F1Dsnp	PHR	A	G	4	25,942,182	+	AAGAGATTATATTCATTGAATTTTCTGGTTTGCAG[A/G]TTGTACACTCTTCTGAATGTGTTAGAGTTCAACAG
2,046	4	4007	7.32	89865984	F1Dsnp	PHR	A	G	4	25,942,920	+	ATTATGATAAATTTGGAGTCTCCAGAAATTAAGGT[A/G]CTGGAAAAGGAAGGAGATAAGGATGCCATCACCAA
2,047	4	4007	7.32	89865985	F1Dsnp	PHR	T	C	4	25,944,849	+	ATGATACAATGGATTAGGTACGAGGGACAGTCAAA[C/T]GATCCCGAGTTTTGTGATATGGTTCGGCAGAGATC
2,048	4	4007	7.32	89810042	F1Dsnp	PHR	T	C	4	25,985,124	+	CATCAAGCAACCTTCTCATTGTATTTCCAGAATCA[C/T]CACCCCAAGTAAGCACATCTTGTCTTCCACCAGCT
2,049	4	4007	7.32	89865986	F1Dsnp	PHR	A	C	4	25,985,332	+	TGTAGGACAATTCGGATAACACCATCAAAACAAGC[A/C]TCATATACTGCTTTCACCACATCGCTGGGAGCATT
2,050	4	4007	7.32	89865987	F1Dsnp	PHR	T	G	4	26,053,578	+	TTCTGCGCCGATCCAATCCACAGCATTCCGTTGTG[G/T]TCTTCAACTTCACTAACAGACTGAAGCAAGGCTGC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,051	4	4007	7.32	89865988	F1Dsnp	PHR	T	C	4	26,053,646	+	TGCAGCACTATCTTTTCCATCCAACACCTCCAAAA[C/T]GTTTCCATCCTCATCAAACTTTGCTCCTACAGGAT
2,052	4	4007	7.32	89810043	F1Dsnp	PHR	A	G	4	26,063,666	+	TACTCGTACAAGCTCATCATCAAAACTTGTGGGAC[A/G]ACGAAGTTGCTCCTGGCAATCCCACCTATCCTGAA
2,053	4	4007	7.32	89831116	snp	PHR	A	C	4	26,073,047	+	AATTGAAACAGTATAGTGGGAAACCATCAGATTTG[A/C]GCCGCTGGAATGGAGCAAGACTGCTTTGGGACAAC
2,054	4	4007	7.32	TP2295	GBS				4	26,091,857	26,091,796	TGCAGATGAGGAACATCTTTCATCGTACACTTCGATGTATTACATTGATAGTGAAAAGATTTTT
2,055	4	4007	7.32	89865989	F1Dsnp	PHR	T	C	4	26,148,762	+	GAAATGTGGAGAGTCTTGCAGAAGTTCTGTCTGCT[C/T]TAAGTGTTGGGAGGCAGCTGTAAGTGCTCTGACTA
2,056	4	4007	7.32	89865990	F1Dsnp	PHR	T	G	4	26,163,152	+	ATTCAAACTAGGAGCTACAGCTGCTGGGTAGATCA[G/T]AATCAGTGGAAGCCTCAAAGATCAAATTACTTGCC
2,057	4	4007	7.32	15_617666	GBS				4	26,169,208		TCAATACTTTCATAGAACTCTCCAAGTCTTGTGCCCCGGATTCATTAGATGACACTTCTTGGTC
2,058	4	4007	7.32	89888329	snp	PHR	A	G	4	26,203,688	+	CTAACAATATTAACCTCATTAATCAAAAGCCTAGC[A/G]TGCAATGTATTTGGATTAATGGCTGGATCTTTCTC
2,059	4	4007	7.32	89865991	F1Dsnp	PHR	T	C	4	26,204,371	+	CTTCCAAGGGCAGCATAGTGTTGTAAACCATTACA[C/T]GAACCATCCTTGCAACAGAAAAGGAGAAACTAAGA
2,060	4	4007	7.32	89865992	F1Dsnp	PHR	A	G	4	26,225,987	+	CATGGATCGCTCTCTGCCCTCACTTCTGATGGTTC[A/G]ATTACTTGTGTTTCAGAGGCTTCAACAGTGCTTGC
2,061	4	4007	7.32	89810044	F1Dsnp	PHR	T	C	4	26,226,824	+	TGATCACCAAGTTGTTGCTTTATCCAATCACAGAG[C/T]AGAGTGTATTCTTGTTTAGTTTCCCTGTCCTTGAC
2,062	4	4007	7.32	89865993	F1Dsnp	PHR	A	G	4	26,227,371	+	CACTTTTCAGACTGTCTGTTGCCAAGTAATAGATG[A/G]CCTTCTGGGTCTCAGGCATGTTATCAACATATTCA
2,063	4	4007	7.32	89810046	F1Dsnp	PHR	T	C	4	26,232,110	+	AAACCTCAAGCATCGAAATTTTCGAAAGCTGCTGG[C/T]TTCATACAATCAACATTGCACAATCCAACTGATCT
2,064	4	4007	7.32	89865994	F1Dsnp	PHR	A	G	4	26,233,049	+	AATGTTTTCTTAACAGGGTACATTACTCGAAGACC[A/G]GAAAGTATTGGACTGTGAAGAACCACAGCTCTCAG
2,065	4	4007	7.32	89865995	F1Dsnp	PHR	T	C	4	26,254,626	+	AGATAGCATCATACAGAAAAAATATTTCGCTTCAG[C/T]TATTAGAGACCTTTTGCATAACCTATTTATTACAG
2,066	4	4007	7.32	89810047	F1Dsnp	PHR	A	G	4	26,254,897	+	TTGATGAGGACATTATATGTCACAGGAGTAGGCTC[A/G]AGATTATGCTTTAACATCTCATCGTGCAACTGAAA
2,067	4	4007	7.32	89865996	F1Dsnp	PHR	T	C	4	26,255,965	+	GTGTCAGGGTGTAGCCCGTGCCTCTCCATGTCTTG[C/T]GTAAACTCCAAAGCTTCTTCCAAAGAACCTGCTAC
2,068	4	4007	7.32	89810048	F1Dsnp	PHR	T	C	4	26,263,276	+	TGTATATATACAGATAAAGTTTATGTTGCATTTCA[C/T]GATGAATGCTGGGGAGTTCCAGTATATGATGACAA
2,069	4	4007	7.32	89810049	F1Dsnp	PHR	A	C	4	26,266,261	+	CTTAGAAGGGCAGGACATTTTTGAGATGTTGATGA[A/C]GTTAGCCTCATTTCTTGTCAAAAATACTTACAGAC
2,070	4	4007	7.32	89865997	F1Dsnp	PHR	A	G	4	26,267,202	+	GTTCTCAGAAGGGGTTGCTAAAGCTACTAACAATA[A/G]CATGGTCGCATACTTACCTTTCGGAATGGGACCTA
2,071	4	4007	7.32	89810050	F1Dsnp	PHR	A	C	4	26,294,114	+	ATATCACTTTCCAGTGATACTAGGTAATCCAGTGC[A/C]GCCATTTGGTTTGAATGGTTTCGGAAGGGCTCAAG
2,072	4	4007	7.32	15_737153	GBS				4	26,302,381		TTGCCGGTGAATCTCTGAACGACTTCTCCTCGAGAGAAATCCAAGCAAAGGCTTGCACTAGGAA
2,073	4	4007	7.32	89865998	F1Dsnp	PHR	A	C	4	26,304,214	+	TCCCTCCTTTCACAGCAGTATTCACCAGAAAAATC[A/C]TTCCATGTTTGTGATTCACTTATATGGACATTTCT
2,074	4	4007	7.32	89865999	F1Dsnp	PHR	A	G	4	26,318,429	+	GCTGATTCTAATCCCCGGGAATTCTGATTAATCTC[A/G]TTGTGATCAAAAGATTTAAAATCAGGCTTGTGGCT
2,075	4	4007	7.32	89866000	F1Dsnp	PHR	A	G	4	26,373,108	+	TCTCGTAATTGTCAGTCGGGTCCAGAGGATCAAGC[A/G]AGTGGATCTGGATCTCATGGTGATACTGTTGATGC
2,076	4	4007	7.32	89866001	F1Dsnp	PHR	A	C	4	26,386,986	+	AATGAACATAACCAGGGGAAAGGGTGAAGGAGTAG[A/C]GTTGTAGAATCATTGACAAAGCAATCTTTGCTTCA
2,077	4	4007	7.32	89866002	F1Dsnp	PHR	T	C	4	26,387,244	+	TAGCCGGAACAATGAGGTTTCCTAGTCTAACTTCC[C/T]TTTTCACTATCCTCACAAGGTTCAGAGCAGGAGGA
2,078	4	4007	7.32	TP256	GBS				4	26,398,096	26,398,033	TGCAGAAAGTTTCCATGCAGTTTGAAATCCTGATGTGTTTTCTATATCTTTAATTTCATGCAGA
2,079	4	4007	7.32	89831213	snp	PHR	T	C	4	26,419,651	+	AAACTGGCTTAACACCATACCATTGAAGAAAATTC[C/T]TCCCTGCATGTGTTAGCAATGACCACTAATTACAC
2,080	4	4007	7.32	89866004	F1Dsnp	PHR	A	G	4	26,427,712	+	GTTGTAGAATCATTGAAAGAGCAATCTTGGCTTCA[A/G]TGGTGCCAAAGTGAAGTCCCACACAATTCCTAGGT
2,081	4	4007	7.32	89866005	F1Dsnp	PHR	T	C	4	26,446,670	+	GTGCATGCTGGAGATTTCCTGGGTGTTCCCATGGA[C/T]GAGTCTATAACAAGGGCCTTTGATTCCTTGAGAAG
2,082	4	4007	7.32	89810051	F1Dsnp	PHR	T	C	4	26,449,705	+	TACGTCTGTATTGTCCCTCCAGGTCCCAAAATCAT[C/T]CAATTTCAGTTCTATCCACCCTCACTGGGAAGCAC
2,083	4	4007	7.32	89866006	F1Dsnp	PHR	T	C	4	26,462,457	+	CTCAGTCAATGTGCATTCAGAAGAAAAAGCTCATA[C/T]ATTGAAGTTGAAACGAATTGACGAAACCCCAGATG
2,084	4	4007	7.32	89866007	F1Dsnp	PHR	A	G	4	26,484,183	+	AGATATTGACATATCCACGTAGAGTTTCAATTACA[A/G]TCACCAGCACACTAGACCTGAAAATTGTAAATTTG
2,085	4	4007	7.32	89810052	F1Dsnp	PHR	A	G	4	26,484,551	+	GGCAGGTCCATAATTGTGAGAAAATTAAGTGGATC[A/G]ATCTGATTTATACATTCATGTATAAGTAAAAGGGG
2,086	4	4007	7.32	89866008	F1Dsnp	PHR	T	C	4	26,487,064	+	CAAGCAAGCATATAAATGAATGAGATACCTCCAAT[C/T]GTTCTAGTTGCTCCCTCTCTTCTTGTGCTATCTCT
2,087	4	4007	7.32	89810053	F1Dsnp	PHR	A	C	4	26,492,369	+	GAGGCAGAAACTTGGCAACTTTGTGCCTATCCTCC[A/C]CATTTGTCCTCAGATAGAAATGAGACTACCTTGAT
2,088	4	4007	7.32	89866009	F1Dsnp	PHR	A	G	4	26,523,269	+	AAGAACCCTGAAGAACAAATGAGGAATTGTTGCCA[A/G]ACCGGCCTATCGGAGAGTGATATCCAAAATAGAAA
2,089	4	4007	7.32	89866010	F1Dsnp	PHR	A	G	4	26,530,108	+	TTTTTTTTTTTTTTGTAGGGGAAAGATCGATATCC[A/G]TATCCGATAGGGTATGGAGCTGTTCGAGCTCACAA
2,090	4	4007	7.32	89866011	F1Dsnp	PHR	T	C	4	26,531,429	+	CGCCTGACTGATGTTGAACTTTATGCTCCTGATAC[C/T]TTAGATTTTACACAAGGTAATCAGTACTATCTACT
2,091	4	4007	7.32	15_982953	GBS				scf^{x}	46,413	46,476	CAAGCCAAAGTAATTTTGAAGAGAAATATAAYTTGGCTGACGTACATCTTGTGGTAGGCTAAAG
2,092	4	4023	15.03	TP5699	GBS				scf^{x}	712,514	712,455	TGCAGCTTGTGCTTTCCAAGTTTCCATTTTTGTTTTAGACTGATGAATTGTCCAAGTCCGAGAT
2,093	4	4023	15.03	TP3485	GBS				scf^{x}	864,220	864,158	TGCAGCAGTAGCTCTTGTTAACCTTTCCCAAAGGTCGGCTGTGGCAGCAAAGATGGTTGACATG
2,094	4	4023	15.03	0_2468585	GBS				scf^{x}	864,230	864,167	TATCGGAACCTGCAGCAGTAGCTCTTGTTAAYCTTTCCCAAAGGTCGGCTGTGGCAGCAAAGAT
2,095	4	4023	15.03	TP8459	GBS				scf^{w}	842,211	842,245	TGCAGTCGTAACACTACCCAAACAAGAGCAGAACCGAGATCGGAAGAGCGGTTCAGCAGGAATG
2,096	4	4012	17.47	0_2316501	GBS				scf^{x}	1,016,342	1,016,279	GTGCCGYTTAGTCCAGTTAATTGACTGAGGTKCTGCTTCCATATCAAAGCRCCGGTAAATGCAT
2,097	4	4012	17.47	0_2316476	GBS				scf^{x}	1,016,366	1,016,304	CACTGTCACATTCACTACGACTCCTGTGCCGYTTAGTCCAGTTAATTGACTGAGGTKCTGCTTC
2,098	4	4012	17.47	0_2265539	GBS				scf^{x}	1,060,730	1,060,667	TGTTGGGGCATTGTTGTTGGTTGTATAGAGGGTTGGGACTGGTTGTGATTGTGATGATTTGGTG
2,099	4	4019	22.50	TP7921	GBS				scf^{x}	1,664,434	1,664,485	TGCAGTACTTGATGGTGATTTGATTTATAACCAATATACTTGAACCTTCACCGACTTCCTTAAT
2,100	4	4019	22.50	0_1627440	GBS				scf^{x}	1,664,537	1,664,475	CATCTACAGTAACATATGCACAAGTAAGCTCAGACTTATTGAAAGGAAGCATTAAGGAAGTCGG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,101	4	4019	22.50	0_1627428	GBS				scf[x]	1,664,549	1,664,484	CGCAACTAATCCCATCTACAGTAACATATGCACAAGTAAGCTCAGACTTATTGAAAGGAAGCAT
2,102	4	4021	27.55	89866474	F1Dsnp	PHR	A	G	6	2,555,802	+	CTTTGCCTTCTCAAATTGACCCGATTCACAATATC[A/G]ACACACCACAGCAAGTTGTTGTTCAACTCCAGGGC
2,103	4	4021	27.55	TP820	GBS				scf[x]	1,435,643	1,435,702	TGCAGAATCTATTACTTATAATCAATCTCGAAGATGTCCACTTTCTACCACAACATCCTCATGG
2,104	4	4021	27.55	0_1457393	GBS				scf[x]	1,846,145	1,846,082	TCGTGTTGGGTTGGAGGTTCTGTCACTTCAACGGCGTGTGCGCACCACAGGCCGGTAAGACATG
2,105	4	4011	35.40	TP967	GBS				scf[x]	2,317,368	2,317,410	TGCAGACAAGGACAGTAGTACACATGTATGAGTTAGAAAAAACTACCAAGGAATAAAGGACCAC
2,106	4	4008	40.48	89866012	F1Dsnp	PHR	T	C	4	26,637,025	+	CGTCCCTTCTGCAATACCATCTTAGTACTAACGAC[C/T]TTTACAGTGAGAGTGTGACCAGAGGTGCCTGGGCG
2,107	4	4008	40.48	89866013	F1Dsnp	PHR	T	C	4	26,661,050	+	GAAATGCATGAAGTTGTTACCATGTTAGAGGCTAT[C/T]GACAACTCGAAACATCCCCACGGTTGCTTCTGCTT
2,108	4	4008	40.48	89831263	snp	PHR	A	G	4	26,682,024	+	AACAAAGGAAAAAATAGCAATCTGGCAATTGTGCC[A/G]CCAATTGCAACCTTGGAGTTCTCAAGGAGATATAC
2,109	4	4008	40.48	89810055	F1Dsnp	PHR	A	G	4	26,692,119	+	TGTATGAGTTCAGTTTTGGCCTCTTCACGCAAAAG[A/G]CGCTACACAAGTCCAAGCGTGCCGCGGCTAACTGA
2,110	4	4008	40.48	89810056	F1Dsnp	PHR	T	C	4	26,692,767	+	CTCTGGTTTGATCCAACAACACAGCACCATCAGTA[C/T]ACCATCATCTGGAACAACTATCACGCAGTGTAAGA
2,111	4	4008	40.48	89866014	F1Dsnp	PHR	A	C	4	26,693,187	+	TGTGAAGTTGACTAACCAACAAGTTAGTGCTATGG[A/C]TTGGGCAAGAGGGAAGCTAATGTTTTACTCTTATT
2,112	4	4008	40.48	0_903428	GBS				4	26,702,920		GAAATGGAAGAGAAAAGGGTATTTACGGCCTYCAGAATTACTTGCAAGTCAAGGCTGTGGTCAC
2,113	4	4008	40.48	89810057	F1Dsnp	PHR	A	G	4	26,709,137	+	TGTCTGCGTAAGGAACAGAATCGGAGATGAGACTT[A/G]TGAGGAGGCAAGAGCTATTGCCCACCAGCTGTTTG
2,114	4	4008	40.48	0_890013	GBS				4	26,719,028		TGACGTCACACTCGGTTGGCGGGAGTTCGGTKATGGGAGCGAAGTTGCCGGCGAGGACGTGTTT
2,115	4	4008	40.48	0_873666	GBS				4	26,737,575		CTTCCTAGCGACAGTCACAGTCACTGATTCTACTTCAACAATATATAAGGCCGGAGCTGGGAGG
2,116	4	4008	40.48	TP4881	GBS				4	26,737,684	26,737,623	TGCAGCTAGAACAGCTCAGTTCCCACTCCAACATACTCATATCTATTACCTCATGGCTTCTAGA
2,117	4	4008	40.48	89866015	F1Dsnp	PHR	T	C	4	26,763,611	+	TCAGAGTTGTTTCCCTTTCTCCAAATTTCAGGAAG[C/T]TGTCTGTAGACCATATTGTCTCGGCTTATAAAAGA
2,118	4	4008	40.48	89810058	F1Dsnp	PHR	T	C	4	26,766,776	+	TTCAGAGATTTTAAATGGGTACTTCTCAAATTTGG[C/T]GTCTGTGTTTATGAAATGGCTGTGGTCACTGAAAG
2,119	4	4008	40.48	TP1504	GBS				4	26,805,336	26,805,279	TGCAGAGAGTTTGGGTATCTGACACAAGAAGCGAGCTCGGTTCGTAGCATAGAGTTCTAGTGCA
2,120	4	4008	40.48	89857310	mSNP	NoCls	A	G	4	26,825,351	+	ATTGACTCAGCAAAAGACTCAGCTAAAAGCCCAAC[A/G]GTGATGTCCAACTCCTCTGACCTCATGACCCGAAC
2,121	4	4008	40.48	89866016	F1Dsnp	PHR	A	G	4	26,861,311	+	AAGCATGCAACACTTAAAAGTTGCATTGGCCACCC[A/G]TTTGCTTGCTGAAACATTAAACAAATTAAGCGTGT
2,122	4	4008	40.48	89866017	F1Dsnp	PHR	A	G	4	26,862,362	+	GGAGGAGTCCTCGCCGCAGAGTAGGTCGGATAAGC[A/G]GTCTGAGCATGAAAGTGACATGATCGCAGTCGTTG
2,123	4	4008	40.48	0_1098089	GBS				scf[x]	2,328,008	2,327,945	TGCCAATTTGTAAACACGAGATTGGTGGCAGTGTCGGGGTCCTTAACTCCCCGAATGTCTGCCA
2,124	4	225	45.54	89866018	F1Dsnp	PHR	T	G	4	26,880,616	+	GCTCTTGCTAATATAAGCCATTCGCCCATCTCACA[G/T]ATTTCTATCTTGTGGTTCAAGCCAAGGAAAGCCGA
2,125	4	225	45.54	89810059	F1Dsnp	PHR	A	G	4	26,887,585	+	AACTCGGTAAAGCAGATGAACCTCCTATTCAGCAC[A/G]TCATTCCCTGTCCAAGCTATCAGTCCAAATGCATA
2,126	4	225	45.54	89810060	F1Dsnp	PHR	T	C	4	26,922,470	+	TTCTTGATGCATATCAAGGCCATCATTAGACGATT[C/T]GAGGCGCAGCTGCCTAATGCTACTATGGATATTGA
2,127	4	225	45.54	89810061	F1Dsnp	PHR	A	G	4	26,929,207	+	TCCCTCCGAATGACTGCACTTGTTTTGATTTCTTC[A/G]TATGCTAGTTCTGGGTGTTCATGGATTTCCCTCCT
2,128	4	4010	47.98	89866019	F1Dsnp	PHR	T	C	4	26,981,288	+	CTGAAGATTTACAAACGCAATCTGTTCCGAGGCAA[C/T]GAGCATAATTGCTTAGCTTGATCCTCTCACCATCC
2,129	4	4010	47.98	89810062	F1Dsnp	PHR	A	G	4	26,982,639	+	ACTGTAGCTTCTTCAGAAAAAGTGAAAGGAAACTC[A/G]TTCAAGATATCTATCTGCTCCATTTGTTCTTCTAA
2,130	4	4010	47.98	89810063	F1Dsnp	PHR	T	C	4	26,993,864	+	TCGAGGGAGGTCTTCCACGTCTAACATGGATTTAG[C/T]GCCCGAAGGAAATGAGCAGATTCGAATGGGAAGTA
2,131	4	4010	47.98	TP8820	GBS				4	26,994,030	26,994,072	TGCAGTGCCGCTGCCGCCGCCTCCTCCGCCTGTGAAGAGCCCGAGATCGGAAGAGCGGTTCAGC
2,132	4	4018	50.42	TP9034	GBS				4	27,009,555	27,009,492	TGCAGTGTCAAGCTATTTTATCGGAAGTGAATAACAGAGAACGGAGGCTACAGTGGGGTCACTG
2,133	4	4018	50.42	0_616057	GBS				4	27,018,952		CCAGTCAACCATGGAAACCCTTTCTTACAAGTGCATTGCGCCTTCCGGTTATCCTGGAAAACAT
2,134	4	4018	50.42	89810065	F1Dsnp	PHR	A	G	4	27,069,388	+	GCCGGATTTGTCCAAATTCGAAAAGGATGATTTTG[A/G]AGGGAACGGTAAGCTTTGTGGGAAGCCGCTTGGGT
2,135	4	4018	50.42	89866024	F1Dsnp	PHR	A	G	4	27,070,067	+	GGACTTGCTTGGCTTCACCATGCTTGCCAGCCGCC[A/G]CAGATGCACCAGAACATTAGCTCGAATGTGATTCT
2,136	4	4018	50.42	89866025	F1Dsnp	PHR	A	G	4	27,111,045	+	CCAGCACCACGTGGAGATATTCCCCAACCACAGCG[A/G]TCATCAGGATCAGACCATAGGAGATCACACATTGG
2,137	4	4018	50.42	89810066	F1Dsnp	PHR	T	C	4	27,159,946	+	TTCTTCTATTTTGTGACTAGCTCCAGTCATACAAG[C/T]GTGGATCCATCTGGCAAGATGTTTGGACTTATGGA
2,138	4	4018	50.42	89866027	F1Dsnp	PHR	T	C	4	27,159,958	+	GTGACTAGCTCCAGTCATACAAGCGTGGATCCATC[C/T]GGCAAGATGTTTGGACTTATGGATATCAGCACGAT
2,139	4	4018	50.42	0_483846	GBS				4	27,189,686		CTTGTGGGGCGGGCAAGTCGAGCCATGAGGTTGCGAATTATATACAGAGGGTTATAGCGGCCAG
2,140	4	4018	50.42	89810067	F1Dsnp	PHR	T	G	4	27,204,165	+	TTTTGGATTTGTTTGATTGGGCATGCTTACGTAGG[G/T]ATCCAACTCTGGAAGCTCGTTGCATTGTTGTGCAC
2,141	4	4018	50.42	89810068	F1Dsnp	PHR	T	C	4	27,205,811	+	TTGCACAAAGAAATGGCAGGGAAGGGATTTATTCT[C/T]ACAGCTAGTTCCTACATTGCACTTATTAATGGTTT
2,142	4	4006	52.88	89809900	F1Dsnp	PHR	T	G	4	14,714,341	+	ACCTTTTGTACTAGGAGTATACCTGTGCTTAAGAA[G/T]AAGTATTGTTCCATTTGTAATAGTAGCTACGTACA
2,143	4	4006	52.88	TP5348	GBS				4	14,782,468	14,782,412	TGCAGCTGCTCATGAGACTAAGAGTAATATATATCTCTAGATTGGCCAGCTCCCTCAGTCCGAG
2,144	4	4006	52.88	89865861	F1Dsnp	PHR	A	G	4	14,809,887	+	GATCACATGGTAATTTGGAAAAGGGTATAGGTGTT[A/G]GATCAGGGCTTCAAGTTGTCTTCTACAATCTGGGT
2,145	4	4006	52.88	89865863	F1Dsnp	PHR	T	C	4	14,821,000	+	TTGCACCTCTGACATAGTCAATTGTGCAGCCGAAA[C/T]GTAAGAGCTGCCTTAATCCGTACGTTACTGAATAT
2,146	4	4006	52.88	89809902	F1Dsnp	PHR	A	G	4	14,825,230	+	TCCATTGCAGCATCCTTCAAAACCTCCTCAATCCC[A/G]CGTTCCTCACTGACCTACATACACACAAGTTTCTA
2,147	4	4006	52.88	0_300026	GBS				4	14,849,638		AGATGCAGATGAAGATAAAGACAAAAAGTAGAGTCAGAAGGATTGAAAATGCAAGGGGGAGACG
2,148	4	4006	52.88	0_387870	GBS				4	14,922,187		TAGTGTTCTCTGGAGCAGGGAAGGCGTTTTGTTATGGACACCCGAACGTCAACGCCGTGCTCGA
2,149	4	4006	52.88	89809905	F1Dsnp	PHR	T	G	4	14,930,211	+	GCTTCCCATACACCCTTAAAGTCCATAGGAAGAAG[G/T]TGATCTTTGTTAATAGGAAAGTCATAGCTGGGAGT
2,150	4	4006	52.88	89865864	F1Dsnp	PHR	A	G	4	14,934,966	+	GCCTGCAGTTCTGGTCGGACAACATGTCGCACGCT[A/G]CAAGTGTCTTGGTGCTCAATGAAACTCTCCACTCT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,151	4	4006	52.88	89809906	F1Dsnp	PHR	T	C	4	14,948,320	+	CAAGTGAAGGTTATAACTTTGCTAATCCAATTGAT[C/T]TGAGGACTCACTGGGCAAGACATGGTACGAACAAG
2,152	4	4013	53.70	89865845	F1Dsnp	PHR	A	G	4	14,296,888	+	ACGGTTGGTTTTAACTCTTTGGACAACTGCTGGTC[A/G]GATTCTAATTTTGCTGGACTGTGGTAGGCGTGCAC
2,153	4	4013	53.70	89809887	F1Dsnp	PHR	A	G	4	14,322,503	+	GAGGCTACTACGATGCCGGAGACAATCTCAAGCTG[A/G]GATTTCCGATGGCCTTCACAGTAACAATGCTTTCA
2,154	4	4013	53.70	89865846	F1Dsnp	PHR	A	G	4	14,322,551	+	CCTTCACAGTAACAATGCTTTCATGGAGCACAATC[A/G]AGTTCCACGGCAAGCTCAGGGAAAAATATGAGCTT
2,155	4	4013	53.70	89809889	F1Dsnp	PHR	T	C	4	14,333,314	+	AAAGACTTCTCTGTGTAGCACCTTTGTTAAAGCAG[C/T]GACTCTAGGATCATAGAGCCTGTGAAAATATAATA
2,156	4	4013	53.70	137_266372	GBS				4	14,342,469		GGAAAAACTAGATGCCCTAAATATCACACATCTACACCCTATAAATAAAACTAAAAAGCACTTC
2,157	4	4013	53.70	89809890	F1Dsnp	PHR	A	G	4	14,345,611	+	AGTTGCATTCAAACCTTCTCATCCTCTGAAGAACT[A/G]TCAGACTCATCCTCGCTGCTGCTCTCCTCTTTCTT
2,158	4	4013	53.70	89865848	F1Dsnp	PHR	A	G	4	14,362,370	+	GTAAAATGGAGGATATATACCAAGGCTCTTCGGCG[A/G]CAACAGCAGGGTTATTGAATATCTTGGCAGCAGCA
2,159	4	328	55.40	89865849	F1Dsnp	PHR	T	C	4	14,367,469	+	CAGATCACTGATGTTTTTCTTCTGCTCATTTCTTT[C/T]AGCGAGTTCCTTCAAACTAGTCCATGATTTTCTCC
2,160	4	328	55.40	89809891	F1Dsnp	PHR	T	C	4	14,373,847	+	GGCTGCGGATTTGTTAGCTTCCCAACATTTGGTCT[C/T]CAAGCTAAAGCACAGAGGTAAGTGCACACCCATAT
2,161	4	328	55.40	89865850	F1Dsnp	PHR	A	G	4	14,376,673	+	AGGAAGCTGGAGCATGGAGTTCATGTGGTGTCTGG[A/G]ACTCCTGGTAGAGTCTGTGACATGATAAAGAGGAG
2,162	4	328	55.40	89809892	F1Dsnp	PHR	A	G	4	14,382,723	+	CGTACATACTCAAGCTGACCAGAAAAATGTCTCGA[A/G]GGGGGTTCTTTATCCAACAAGCTAAGAAGAGGCCG
2,163	4	328	55.40	89886269	snp	PHR	T	C	4	14,384,662	+	ATATGTGAGTACCTGTAGGGGAAAAAGGTTTTCTC[C/T]GGGCAACTTTTCATCAAATACCTATAAACAAGATG
2,164	4	328	55.40	89865852	F1Dsnp	PHR	A	G	4	14,384,663	+	TATGTGAGTACCTGTAGGGGAAAAAGGTTTTCTCC[A/G]GGCAACTTTTCATCAAATACCTATAAACAAGATGT
2,165	4	328	55.40	89809893	F1Dsnp	PHR	A	G	4	14,388,451	+	AACTTATTTGGCTTAATGATGTTTGCAAGTGAGCC[A/G]TTCTCCACGTATCTACCATGAGAAAAATAAAGAGT
2,166	4	328	55.40	89865853	F1Dsnp	PHR	T	C	4	14,391,254	+	TGCGCAAAAGTGGTTGCCACGTCTATTGACTCCTT[C/T]AGACGAGATGCATCTGTTCCCTGAGATTCACAATT
2,167	4	328	55.40	89829131	snp	PHR	T	C	4	14,394,665	+	CATGAACTCTGAACCAGTGTAAATTGCTTTAATCA[C/T]GCTTTCATGGTCCTGAATTGGTAACATAAAGCCCA
2,168	4	328	55.40	89809894	F1Dsnp	PHR	A	G	4	14,401,126	+	ATGCTCTCAGCTCTTGGTATTGGAGATTCCAGTTC[A/G]TGGTTGGCAGTGTTATACTTTGCTGGATGCCCCAG
2,169	4	328	55.40	89809896	F1Dsnp	PHR	A	C	4	14,416,757	+	TGCTCAAAGCCTGGTTCAGCGTAGATCATTGTCTT[A/C]ACAGGACTCTTGTACAGTCTGTGAGGACAGAGCCA
2,170	4	328	55.40	89809897	F1Dsnp	PHR	T	C	4	14,417,440	+	AAGAATCACTATATGCCTGTGCAATCTCCTGCAGA[C/T]TTCCCTTTACCGGTTTGTATGTCAACCTCATGTAT
2,171	4	328	55.40	89809898	F1Dsnp	PHR	A	G	4	14,441,166	+	AAAAATTTCGAGCTAAAACATCACAGCAAGCTGAG[A/G]CTGGACGGGCTCTTCCAGGTGCTGGGCGTGCTGGA
2,172	4	328	55.40	89865855	F1Dsnp	PHR	A	G	4	14,479,346	+	ATAAAACCATATGAACAATTACCAATGGGTTCCAT[A/G]ATCCTGTGCTTCAGCATTTCCGAAAGGCGCGTAAC
2,173	4	328	55.40	89865856	F1Dsnp	PHR	A	G	4	14,487,750	+	TGGTCATTAGAGATGTAGCTGCACCTGTCCTTGCA[A/G]CAACAATATGGGAAGCAGTAAAGACTAGTAACTTG
2,174	4	328	55.40	89865857	F1Dsnp	PHR	T	C	4	14,518,944	+	GAGGCGTTTGCAAACGCACAAAAAAATTACAATGC[C/T]TTGCAGGACAAGATGGCAACAGCCATCGACGAATT
2,175	4	328	55.40	89865858	F1Dsnp	PHR	T	C	4	14,539,646	+	ATGTTCTCAGTTAGCATACATGCAACAACCCTTTA[C/T]TTGATTTATCCATTGATCAAGATGCACAATTAATA
2,176	4	328	55.40	89810251	F1Dsnp	PHR	T	C	5	25,082,095	+	ATCAGTAACAAACTTTCGCTGACCCTTGAATTCTC[C/T]ACATAACTTCGACCATCAGAAGTGTCACCAACTAA
2,177	4	4003	60.40	89865832	F1Dsnp	PHR	A	G	4	14,064,216	+	TTGAGTTCACCTTCCATGCCAGTGATGTCAACCTC[A/G]GGAACTCTGGGCACGTGGTACACCTTAAGAGGCAC
2,178	4	4003	60.40	89865833	F1Dsnp	PHR	A	G	4	14,074,490	+	CTTCTTCGAGGTTTCATGAAACAAGAAAGGCCACA[A/G]GAACCTTTTTTTAAGGGATAAGAATGTACGGTGAA
2,179	4	4003	60.40	89865835	F1Dsnp	CRBT	A	G	4	14,089,771	+	CCTGGGTTAGAATACTCGCATGAAAAATTTCATGG[A/G]TGGAAGCAAGCATTTTTGGGCTGTGTTACTTTGCC
2,180	4	4003	60.40	89809878	F1Dsnp	PHR	T	C	4	14,097,996	+	CAGCATTGCACTGTTTTCACAACGGCACCTCACAA[C/T]ACCAGCCGCTGGATCACAAGACAAGACAGCGAGGG
2,181	4	4003	60.40	89865837	F1Dsnp	PHR	A	C	4	14,125,148	+	TTGGAATTATCTTTTAGTGTTAAAATTCAGGATCT[A/C]TGTCTTTTTAATGATCACCTTGTTATATATGAGCG
2,182	4	4003	60.40	89865838	F1Dsnp	PHR	T	C	4	14,133,273	+	TGACCAATCTGGTCCAACTCAACTTAGCAAGAAAT[C/T]TGCTCACAGGTCCAATTCCACCCACTTTCCAAAAC
2,183	4	4003	60.40	89809881	F1Dsnp	PHR	T	C	4	14,133,599	+	CGACTTAACGGTCATATTCCAGCATCCATTTCAAA[C/T]TTGCAGAACCTTTGGTACCTCAACTTATCCAGAAA
2,184	4	4003	60.40	89809882	F1Dsnp	PHR	T	C	4	14,134,003	+	CATATCTTTGGTTGATTTACACTCAAATCACCTTG[C/T]TGGATCTATCTCGAGGATGTTGAATAACAGGGAAA
2,185	4	4003	60.40	89809883	F1Dsnp	PHR	A	G	4	14,134,404	+	TGTGTGGAGAGATCCCACAAGGGAGACCATTCAAC[A/G]TTTTTCCTGCAGCTGCTTATCTCCACAATTTGTGC
2,186	4	4003	60.40	TP5810	GBS				4	14,134,415	14,134,352	TGCAGGAAAGACGTTGAATGGTCTCCCTTGTGGGATCTCTCCACACAACTTATTTGCCCTGAAG
2,187	4	4003	60.40	89809884	F1Dsnp	PHR	T	C	4	14,134,455	+	CTTATCTCCACAATTTGTGCTTATGCGGCAAGCCT[C/T]TGCCACCTTGTAGAGGAAAGACTCAAAGCAACAAG
2,188	4	4003	60.40	89809885	F1Dsnp	PHR	A	G	4	14,162,413	+	TTGCTTTCATTTCAGGTCAGACATCCCAACATCTT[A/G]TCATTTCTCCACAGTACTGAAATCGAAACCATGGA
2,189	4	4003	60.40	89865839	F1Dsnp	PHR	T	C	4	14,174,664	+	TTTCAGCTGTTGGCACACCAGTGAATCTTGTTGGC[C/T]CTTCTCCACACATGGCATATGGTGTGAGAGCCCCT
2,190	4	4003	60.40	89865840	F1Dsnp	PHR	A	C	4	14,175,477	+	AAAGCCAGCCGGCAGACATCAGAAAACACTAGTAG[A/C]CTTTGGAGCGTGTCTGAGATTGCTCGAGCTGTCAA
2,191	4	4003	60.40	TP5	GBS				4	14,210,744	14,210,808	TGCAGAAAAAACAAATGTAAATTTATAAACGCTTCCAATTTACTGACAGAGTTCCAATAAAAGT
2,192	4	4003	60.40	TP3466	GBS				4	14,237,623	14,237,686	TGCAGCAGGTATTAGTAACAAACGATGGAAGCAAACAACACCTGTAGGTGTTAACATTCGAAGA
2,193	5	5030	0.00	206_7311	GBS				5	143,289		ATGTAGGATTGGAGGGCCTGCAGAATGTGCTSTGGGAATGGAAGGTCACTTCTATCACACCCTC
2,194	5	5030	0.00	206_7342	GBS				5	143,321		STGGGAATGGAAGGTCACTTCTATCACACCCTCTATCCAAAGACACCACAATTTTGGGAGAGAG
2,195	5	5030	0.00	89810160	F1Dsnp	PHR	T	C	5	143,351	+	TGCTGTGGGAATGGAAGGTCACTTCTATCACACCC[C/T]CTATCCAAAGACACCACAATTTTGGGAGAGAGCTG
2,196	5	5030	0.00	206_7398	GBS				5	143,376		GGAGAGAGCTGTTTAACAAAGCGAAGGAGATYGGGCAAAGCAGCCGGTTGATTTGAACTAGACC
2,197	5	5030	0.00	89866170	F1Dsnp	PHR	T	C	5	192,270	+	CGGTTTCGGTTTCGTATTGCCGATCATCTTGACGT[C/T]AACGCTCAGGATGTGCAGGTCAGTGACTTGTTCAT
2,198	5	5030	0.00	89810211	F1Dsnp	PHR	A	G	5	198,898	+	CCCTTGTACTCAACCTCATCCACCAATACCACCTA[A/G]ACATCATCCAGGCCATTCCAAAATTCCTCCCCACC
2,199	5	5031	2.44	89810285	F1Dsnp	PHR	T	C	5	302,043	+	CGTTCTGGCTGACATTTCCTCAAAGAACACGGGGA[C/T]GCAGCCGGCGAGAATGCTGTCGAATATGGACCGTC
2,200	5	5031	2.44	TP5900	GBS				5	320,666	320,729	TGCAGGAAGAGCTTTGACACAATCTGTTGATATTTGAAAGCACAAGTCTTTTCTTCAAAGATCT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,201	5	5031	2.44	89866263	F1Dsnp	PHR	A	C	5	343,887	+	CTGGTCATATGTGTATAGTATATACCTGGGAACAA[A/C]GCTCGGGAATAAACAACTTCATATCAGAAACAGAC
2,202	5	5031	2.44	89866266	F1Dsnp	PHR	A	G	5	360,215	+	TTTGGGATAGGATCAGCTGCCCAATTTGGTTCTGC[A/G]GACCTCAGGTCACTTCTTTGTTTTCCTTTTCTTTC
2,203	5	5031	2.44	89810303	F1Dsnp	PHR	A	G	5	386,209	+	CGTGGAGCCAAGCAGCTGTGTTTTCCTAATAACTC[A/G]GGTTACATGCGGGTTGGACAGTCCCCGGATGAAGC
2,204	5	5031	2.44	89835663	snp	PHR	T	G	5	414,657	+	CAAGGCATTGCACACACAGAGCTGGGTACTGTGTT[G/T]CTCTGCATGAAGCTTTGATGAACTTAGTGGAACTT
2,205	5	5031	2.44	89810306	F1Dsnp	PHR	T	C	5	418,276	+	TTCTCTAACAGCTCGACGGCGCTCTTTCTCTTCAA[C/T]AACTTGGCGCTCAAACGCCTCTCGAGCATCGGAGT
2,206	5	5031	2.44	89866274	F1Dsnp	PHR	T	G	5	420,875	+	ATCAAACGGGTGATGTCAAACGTGGAAATCCGTCT[G/T]GCAGTTCTCAGAATAATGTTCCTCGAGCAGGCTTG
2,207	5	5032	4.88	89866276	F1Dsnp	PHR	A	G	5	427,034	+	TCTCGGAGCTACTGTGCCTTCCTCTGCTAGCAACA[A/G]GGAAGATTCGAAACCGGTACAGTCTCTCTTTCTCG
2,208	5	5032	4.88	206_272089	GBS				5	446,544		TAGTTCCCATTGGTGCTGTTGGAACTGGAGCACCTTTGAGAGCATACATGCAAAGAAGCACAGC
2,209	5	5032	4.88	500_10455	GBS				5	538,346		CTGAGCCTGATTCTCAATAAACCCACTTGGCAACATACCTGGGAAAATTCTTGGATTCATACCA
2,210	5	5032	4.88	89866295	F1Dsnp	PHR	T	C	5	558,137	+	TCACATACAGGTTCCAGGCAAAAATGGTGGTCCAC[C/T]GGAGAAAAAAGAGGTTCTCTTAGAAGATCATGATC
2,211	5	5032	4.88	89810326	F1Dsnp	PHR	T	C	5	560,577	+	TTTCCTGCTGCCTACAGTGATTCAGTATTGAGGCA[C/T]GCATCTAGTGATTTCAAGAAGATGGGCCAACGCAT
2,212	5	5032	4.88	89810328	F1Dsnp	PHR	T	G	5	565,262	+	ACTAAGCCTCTTACACATTTCCTCCTTACATTTCC[G/T]AACCTCCCTCAAAGGTGAAAAATCTGTCACCAAAA
2,213	5	5032	4.88	89866300	F1Dsnp	PHR	A	G	5	596,578	+	TGCTCGTAAACTCGCTAAACTTGTTAGAAGAACTC[A/G]TAGACTTTGGAAGGTCATAGTCTGTATGCGATGAG
2,214	5	5032	4.88	89810340	F1Dsnp	PHR	A	C	5	648,272	+	AGGCAGCAAGGTCCACAAAGCTTGAGCAGCCTAAT[A/C]CAATCCCAAACACATTGGTCCAACCACCCTCCTTC
2,215	5	5032	4.88	89866306	F1Dsnp	PHR	A	G	5	648,570	+	GCAATGCGGTGATAACTAAGTCTGGTAGGAGATAG[A/G]AAAGGTAGGTCTTTGCAACTGTTGAGATATCTTCT
2,216	5	5032	4.88	89810341	F1Dsnp	PHR	A	G	5	648,638	+	TCTTGTTGGCCAAAATGAATGAGGATTTTGTCAAC[A/G]CTGAGCCACAAAAATGAAATAGGAAGAGTTGCAAG
2,217	5	5032	4.88	89810342	F1Dsnp	PHR	T	C	5	648,874	+	AAGCTCTCCTAGTCTTCCTAGAAAAGCTGTTGTGA[C/T]GGCTATCTTGGCAAACCATGTCAAGTTCATAGCCA
2,218	5	5032	4.88	89810343	F1Dsnp	PHR	A	C	5	648,957	+	CTATCCCTCTTTGTATTTTGAGCTCTGCAAGCATG[A/C]TGTTGAGGAAGTTGGTAGGCCATTTTTGGGTGTGA
2,219	5	5032	4.88	89866336	F1Dsnp	PHR	T	C	5	790,107	+	TTCTCATCAGTATCCAATGTTCCCAGGTCGCCAAG[C/T]GGCTGAAATAATCCAGCATACCACTTAGAGAATGT
2,220	5	5032	4.88	TP6218	GBS				5	800,111	800,174	TGCAGGAGTGAGCATCAAAACCTATATAAACTCAACCTCAACACCTACAGCGACAATCTTGTTC
2,221	5	5032	4.88	89810376	F1Dsnp	PHR	A	G	5	825,890	+	TCGGATCATGTGCACCAGGCGGCCAATTACATAAA[A/G]CATTTACAAAAGGACCTCGAGGAGCTGCGAGAAAA
2,222	5	5032	4.88	89866340	F1Dsnp	PHR	A	G	5	831,532	+	AGAGCTTCCTGGCTCTGCCTGAACAGTTTGTGCTG[A/G]ATATGCTCGAAGAAAGTCCGTGGTGGGAAGATCGC
2,223	5	5032	4.88	89866341	F1Dsnp	PHR	A	C	5	837,803	+	CCATACTGTAGCATAGACAAGAAGCAGAAGAAGTC[A/C]TTGGGAGAAATGGAACAAGACTTTCTTCAAGCACT
2,224	5	5032	4.88	89810377	F1Dsnp	PHR	T	C	5	845,222	+	CAGGTAAAGGAATTTCATCTAGGCATTGGTGTGTC[C/T]GTGAATCCATGTGCAGAGAGGGTGATGGTAGTTGC
2,225	5	683	15.80	89866343	F1Dsnp	PHR	T	C	5	877,137	+	ACGGATTTCTCTATGGATCAAGCTGGCTCTGATGC[C/T]CATGACATGATGGGATTTGGACTCCCTACTGAATC
2,226	5	5011	18.24	89810387	F1Dsnp	PHR	T	G	5	959,396	+	GACCCTAAGAGCATCAACACCAAGAACCTTGTATT[G/T]CTGATCAACAACTCTCCCAACTTGGCATCCTCCAT
2,227	5	5011	18.24	89810389	F1Dsnp	PHR	A	C	5	966,564	+	ATATAAAGAAATGTATTTGCCAAGTTTAAGAGAAG[A/C]GAATTAAAATGGTATCTCTGATCATCAGCTTGTTC
2,228	5	5011	18.24	7_1499002	GBS				5	966,595		AAGCTGATGATCAGAGATACCATTTTAATTCTCTTCTCTTAAACTTGGCAAATACATTTCTTTA
2,229	5	5011	18.24	89810395	F1Dsnp	PHR	A	G	5	997,610	+	CGAGATTTAAAGCCAAGATGTCCACTCTGGATCCA[A/G]CTACTGGAGGTCGCTTATTTTCTAACTATAGTAAA
2,230	5	5011	18.24	89866359	F1Dsnp	PHR	A	G	5	999,156	+	CTATCTTGATTACTACCATCATTTCCATCACCATC[A/G]CCCTACAAAATGAGAAGAAATTGCAGTCTTTATTA
2,231	5	5011	18.24	7_1460469	GBS				5	1,007,317		TAAGAACTTTCCGGGGTTAACGTCAAGAAATGATCTCACAAATAAAAAATATCCATTTGAAACT
2,232	5	5011	18.24	89810112	F1Dsnp	PHR	T	G	5	1,030,011	+	TGATGCTCTGCCACATGAAGTTTGGATTGTTCTTC[G/T]TCTTCGCCTTCTTTCTGATCGTGATGAGCTGCTTC
2,233	5	5011	18.24	89810113	F1Dsnp	PHR	T	C	5	1,056,710	+	TTGGCCAGTTTACAAATCTCCGGCGGGTCCAAGTA[C/T]CCCATAATCTCCGCCGCGCAGCTCTCCGGCAAGTC
2,234	5	5011	18.24	89791673	snp	PHR	A	G	5	1,063,764	+	TAATTCTCACATTCATACATCTTCAGCAGAAACTG[A/G]CTCTGAAGAAACTCCCTATCTGTGATCCCATTGCA
2,235	5	5033	20.68	89810115	F1Dsnp	PHR	A	G	5	1,070,171	+	GCCTCAAGCATCACTGCTTCATCATGCTCCTGTGA[A/G]GACATGCCTCCCCACTACGTTATAGAAAGATTAAA
2,236	5	5033	20.68	7_1387757	GBS				5	1,075,218		GCAGCCACAAAAACCAAACTGTATCCAAGAAYGTGTAGGTATCAACCATCTCACTACATATTGA
2,237	5	5033	20.68	89810131	F1Dsnp	PHR	A	G	5	1,186,413	+	CTACCCTATATTATGCAGAGAAATAGCTCAAGATC[A/G]AATGGTAGGATTGTTGGTGATTATGACAAAACTCA
2,238	5	5033	20.68	89866087	F1Dsnp	PHR	T	C	5	1,188,174	+	TGCTCATTTCAACTCTGTTCATCTTTTTGTACTCC[C/T]CTCTCATTTTCTTCACGAAATCATAAGATTGGTGA
2,239	5	5033	20.68	89810133	F1Dsnp	PHR	A	G	5	1,191,784	+	AAGACCAAGCTCAGCATGTTTGCAAGCACATGAAT[A/G]ACACCGGCATGCAACCAAATACAAGTGAGAAGCCT
2,240	5	426	25.73	89810136	F1Dsnp	PHR	T	C	5	1,209,237	+	TCAGGATTAAAGAGTAGAAAATGGGATAAACCAAA[C/T]GTGCAGTCACAGCCTCTTGATAAAAACTTACAGCT
2,241	5	426	25.73	89866088	F1Dsnp	PHR	T	C	5	1,212,291	+	AGTTATTGATTTTCTTATGTCAATATGTAGAAACC[C/T]TTTCTGGATGGAGTGTCATCTCTTTCTGAAGATGT
2,242	5	426	25.73	89866089	F1Dsnp	PHR	A	G	5	1,212,354	+	GAAGATGTTAAAATTGTGCTTCCAGCTGCTGATTT[A/G]TTGGATCATGTCCTAACTCAGCTATACAATACTGG
2,243	5	426	25.73	89866090	F1Dsnp	PHR	T	C	5	1,216,803	+	CACCTTATGTGGTGTTTAGGAAGGCTTTGCGTGGG[C/T]TTTGCTTGATGGTGGGCCTTCCCGTGCATTTTGTG
2,244	5	5001	28.20	7_1290016	GBS				5	1,246,608		TCACTCCTAGATCTTCAAATCTTACGTCTCCCGGCAAAGCAACAACCTTTTCTAATATGAAGGA
2,245	5	5001	28.20	89866096	F1Dsnp	PHR	T	G	5	1,265,931	+	TCTCACCTTCAGAAAGCTGCCGCCTGGTGACAGGG[G/T]GCTCCAATTTTTGCTTTTTAGTTGCAGATGACAGC
2,246	5	428	30.74	89866103	F1Dsnp	PHR	A	G	5	1,280,194	+	ACTCGACGTTGGAGCAAAACTGCTCGATCAAAGAC[A/G]GCAGCCCGTTTCTTGTATTTGGAAGAAAGATGTAC
2,247	5	5002	33.18	89810143	F1Dsnp	PHR	T	G	5	1,306,924	+	GCAGTTGTTACTGGAGCCAACAAAGGGATTGGACT[G/T]GAGATTAGCAAGCAATTAGCTGCTAAAGGAGTTGG
2,248	5	5002	33.18	TP8025	GBS				5	1,308,131	1,308,180	TGCAGTAGGTCCTGTGAAGCAGGCTTTGATAGCCGAAACTAGAATTTCCGAGATCGGAAGAGCG
2,249	5	5002	33.18	89810144	F1Dsnp	PHR	T	C	5	1,308,208	+	AATTTCCGGCCTCTTCTTCAACAGAAATGAAGAGT[C/T]GACCTTTGATTAGGTCAACGTGATCCCTGATGAAC
2,250	5	5002	33.18	89866110	F1Dsnp	PHR	T	C	5	1,336,790	+	GGAGGTTTCTTGAAGTTACTCTCCTTGAAGAGTTG[C/T]TCGAAATGAGGCTTGCAGTATAGAGCTCCCTCCCT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,251	5	5002	33.18	TP463	GBS				5	1,340,062	1,340,125	TGCAGAACTGATCAGTTGGATTCCAAGCTAGGCTAGGATTGATATGAGGAATTTCAGAGCATAC
2,252	5	5002	33.18	89807757	ins	PHR	-	ACA	5	1,376,243	+	AAACCAAAATACTATGATTTCTTCACAAGAAGTCT[-/ACA]ACAACCAATGCACCATTACTGGCCTATAAGGAATG
2,253	5	5002	33.18	89810155	F1Dsnp	PHR	A	G	5	1,379,173	+	GGTTATGCATGGTCTGTTAGTGAGAAGTACATTCT[A/G]GCATGTGATTCAGTAACATTGCTGGTGAAACCAAA
2,254	5	5002	33.18	89810157	F1Dsnp	PHR	T	C	5	1,419,958	+	ACAGCAATTCACCTTTCCCGGAAAACCTTTTCCCG[C/T]ATTCGTTTGAACTACATTTGGGCGTTGGGTTACAA
2,255	5	5002	33.18	89810158	F1Dsnp	PHR	T	C	5	1,419,994	+	ATTCGTTTGAACTACATTTGGGCGTTGGGTTACAA[C/T]GTGCTTGGAATCCCGATAGCTGCAGGAGTCCTTTT
2,256	5	5002	33.18	89866120	F1Dsnp	PHR	T	C	5	1,421,148	+	AAAAGCCTCTCAGCTTCAACAGCTGCTTGTGGACT[C/T]GCTGGAATTCCAAGCACAGGTGCAAGTACAGTATT
2,257	5	5002	33.18	89866133	F1Dsnp	PHR	T	G	5	1,528,927	+	GTCTTCATCTTCTTGTTTGTAGCCAAAACAAGAAG[G/T]CAGGCATGAACGTATTGTTGATATCATGATCATCA
2,258	5	5002	33.18	89866146	F1Dsnp	PHR	A	G	5	1,604,730	+	ATTTGATACTTCTCCTCGCGGGACTTGTACATATT[A/G]TTTTGCTACAAGCATCCAACAGAAGCACTTCAATA
2,259	5	5002	33.18	89810177	F1Dsnp	PHR	T	G	5	1,642,507	+	GGTAATAGACTTTTCAATGCAATCGGATGTTCTTA[G/T]ACCTTCCGAAGAATTAGTTTCTCCACGGTGGACAG
2,260	5	5002	33.18	89866149	F1Dsnp	PHR	A	G	5	1,652,064	+	CCTAATGCACCGTTCTTCATTTCACAAGGGAACCC[A/G]GATGTTCCAGTTGTGACCTTTGCCATGGAGAATAA
2,261	5	5002	33.18	89866152	F1Dsnp	PHR	A	C	5	1,686,041	+	GCAGTAACAATGCAGGGGTTATGGTAGGTAAATTC[A/C]AGCTATCTCAAGACAACATAGAACTCGATTTTGCA
2,262	5	5002	33.18	7_881892	GBS				5	1,736,846		TAAGAAAACAGAACCCTCGTGTATCAACGGCYGAGAGTCGTCCTCCTACAAAGGTAGTAGCTAG
2,263	5	5002	33.18	89810184	F1Dsnp	PHR	T	C	5	1,778,288	+	AGGACGCCCTGCTGACACATCATATGGAATAGGGG[C/T]AGGAGGTGGTCTGTAAGTGTCAGGTATTGATGTAT
2,264	5	5002	33.18	89810193	F1Dsnp	PHR	A	G	5	1,857,146	+	AACCGGTAAAAGAATCGACCATAACGCATTCGGAT[A/G]GCTTTCTCCACTCTCATCTTCTCCCTATCCTGAAA
2,265	5	5003	35.72	89866166	F1Dsnp	PHR	T	C	5	1,889,356	+	CAGCCATCTTCCACTTGCACAAGGGATGAGGGACA[C/T]GATGCTGGACATACTCGCTGAATGTCGTATTCATA
2,266	5	5003	35.72	89810201	F1Dsnp	PHR	A	G	5	1,889,571	+	TCCCGGGGTGAAAAAACTCCTCGAAAAATTTGGAC[A/G]GCAAAGCCCCATGAAACGGAAATGGTCCAGCTCCT
2,267	5	5003	35.72	89866167	F1Dsnp	PHR	T	G	5	1,898,460	+	ATGAGAAAAACTTGAAGCAACTAAGTCACTACATC[G/T]CAACTGATTGCTACATTGAGGAGTGCTCCTTTAGC
2,268	5	5003	35.72	89810205	F1Dsnp	PHR	T	C	5	1,920,676	+	ATCAGTCTGATATTTGGAACCAACCTCACTGATGT[C/T]GTAGTAACAGGTAACAAGCACGAAATATGCTTCAA
2,269	5	5003	35.72	89810210	F1Dsnp	PHR	T	C	5	1,962,470	+	GATGCGATGTAATCTTGACTTACAAAATCTAGTTG[C/T]TGGGTCGAGTCATTATAACCCATTTGAGCAAAAGG
2,270	5	5003	35.72	89866172	F1Dsnp	PHR	A	G	5	1,972,646	+	TGCCGAGGAACTTGGTGTGGGCGCAGTCGTTGATT[A/G]GCTTGCAAGACAAGATAGCAGAGGAGTGGAAGAAG
2,271	5	5003	35.72	TP4433	GBS				5	2,007,972	2,007,911	TGCAGCGAGGGCAGCAGCAGCCTCAGCTGCGGCCTCACTGCCTGGAGAACTCGAAGTGATCTGG
2,272	5	5003	35.72	89810213	F1Dsnp	PHR	T	C	5	2,015,590	+	AAGTGGCCATTAGCTTTTTGACTGCATAGGGGAAG[C/T]GGAATTGCTCGAGAAGCAGCACAGTGGAATAAAGT
2,273	5	5003	35.72	89866174	F1Dsnp	PHR	T	G	5	2,018,034	+	ATTGAATGAGACGCCGTCCCTCGAAGGACCCGCTC[G/T]CGAGCACCTGTCTTTACATCCCATATGTACAAAAT
2,274	5	5003	35.72	89866175	F1Dsnp	PHR	A	G	5	2,021,054	+	TGAGCAAAACCACTCAGAGAGGCTGACTAGTAGGC[A/G]TTTGAGGAAGCTGAGAGCTCATATCAGTTGGCAAT
2,275	5	5003	35.72	89810216	F1Dsnp	PHR	A	G	5	2,039,520	+	CCAGGGGAATACAATTTCTGTTGTGGGCAAGCCTG[A/G]GCTAGATCTGCTACTGGAGATGGTGGTCATCTTTG
2,276	5	5003	35.72	TP3896	GBS				5	2,086,934	2,086,871	TGCAGCCAGCTCAGTGGCAAGGCTGGAATCACTCGAGCTTACCTCAATGGTCACATTGAACCTC
2,277	5	5003	35.72	89866184	F1Dsnp	PHR	T	C	5	2,122,758	+	GAGAGATTTTTCTTTCCGATTCTATTAACAGATGG[C/T]TGAGAAGACCAACCAAGCTTATCCTTTGGCCCCTG
2,278	5	5003	35.72	89834245	snp	PHR	A	G	5	2,169,534	+	TCACGTATTTCTTCATTTGAGAGATCCAGTTTTAC[A/G]TTATGCTCACCTATCTGCTGGATGATCAGTGGTTG
2,279	5	5003	35.72	89891459	snp	PHR	T	C	5	2,177,602	+	TCATCTAGGTTTGCAATCAGTCTATCTATCTCTCT[C/T]TGTAGAGACTCGTCCCATTGAATAAGTTTGCTGTT
2,280	5	5003	35.72	89810226	F1Dsnp	PHR	T	C	5	2,194,883	+	CCAGCATGCTTTGCATTCACAAGTTCCAAGAGCTG[C/T]TCCCTCACACGAGGATCCTTGTACTTTGTATCCAG
2,281	5	5003	35.72	89866192	F1Dsnp	PHR	T	G	5	2,203,063	+	TGAAGGTCACATCGTGTTAAGGTGGAAAAACATGC[G/T]TAATCCATCTTTTTGTTTGATCACTTCCTCCAGTG
2,282	5	5003	35.72	7_496478	GBS				5	2,208,114		CACCCCACTTTCAGACAAAGACTCCCTCTTTCCCTTTCCCCCAATATCTCTCCTTTGACCCGCC
2,283	5	5003	35.72	7_496421	GBS				5	2,208,167		CATTTCTAGTCAACCGGCCATGCCGTCCACTATAGTCCAATATCAATCTTCCATTCCCACCCCA
2,284	5	5003	35.72	89866194	F1Dsnp	PHR	A	G	5	2,213,943	+	GGGTATCGGATGTCAATGGGAAATCCCATGAGGAC[A/G]GCCATGGATCGACTCTACTCCATAGCTATCGGAGG
2,285	5	372	38.21	89810230	F1Dsnp	PHR	A	G	5	2,255,608	+	GAGTGCAGATTGTTGTCAAGGGTGATGGGGTCATC[A/G]AAAACAGCAATGTTCCCGAAGTGGAATTGGGAAGC
2,286	5	372	38.21	89866197	F1Dsnp	PHR	A	G	5	2,293,577	+	TCGTTCACAGTGACAGACATTAATGAAACGACGAG[A/G]AAACTAATGGCATTAGGAGCTGAACTTGATGGTCC
2,287	5	372	38.21	89866198	F1Dsnp	PHR	T	C	5	2,315,921	+	TTGAATCTCACAGAGCCACTGAATAAGGTTGGCTC[C/T]TGTGGGATGATCCCCAAACGTGATCTTAAATCATG
2,288	5	372	38.21	89866199	F1Dsnp	PHR	A	G	5	2,315,963	+	ATGATCCCCAAACGTGATCTTAAATCATGAATACC[A/G]ATGGTACAAATGTCATAATCATCTACAATGACTTT
2,289	5	372	38.21	89810233	F1Dsnp	PHR	A	G	5	2,338,833	+	CAGGTTCAACCACCAAATTCAGGTTCCTTAATGTG[A/G]CCTTAGTTGCACCAGTGTCCCATGAAATTTCAGAG
2,290	5	372	38.21	89866202	F1Dsnp	PHR	T	C	5	2,343,585	+	GCCCGAATAATGATCCTTCATTGCTCATCAGCTTT[C/T]TTGGCGAATCATACTCTACCAGTTTACCTGTCAAT
2,291	5	372	38.21	89866204	F1Dsnp	PHR	T	C	5	2,379,461	+	TTGATTCCTTCCATTGGCTTTACAGGATGGTCAAC[C/T]AGAGGCATCTGAGGAGGCTTCGAAAAAGATGAAAT
2,292	5	5004	40.75	TP7830	GBS				1	4,112,982	4,113,043	TGCAGTACAAGGACACAACTGAAGCTGCTATTGCTGGGGTGAGAAGCATTGCTGATTCTTGCAT
2,293	5	5004	40.75	89810254	F1Dsnp	PHR	T	C	5	2,529,229	+	TTGGGTACTAAACCCTTGTACAGTGCTCCAAACCC[C/T]TCATGACGAACTGTTTTCCTGAATGTATCAACCAT
2,294	5	5004	40.75	89866226	F1Dsnp	PHR	T	C	5	2,591,438	+	CGTAGGGTTAGTAGTGACCTCATGGGTTCCTCAGG[C/T]CTTAATTTTGAGTCATGGTTCGATCAGCGGGTTTT
2,295	5	5004	40.75	7_95068	GBS				5	2,663,506		CTGTTCTCTGCCCAACTCAGTTCCTTGCAAGYTACTTCCATGTTCATAGCTTCTTCCTCTAAAA
2,296	5	5004	40.75	7_95031	GBS				5	2,663,543		TTTGCCTCTGCAGCTTCACATACTCAATACCTTTCTTCTGTTCTCTGCCCAACTCAGTTCCTTG
2,297	5	5004	40.75	89810268	F1Dsnp	PHR	T	C	5	2,671,628	+	AGAGTCAATAGATGGGCAATGTCCTTTGTGGATGC[C/T]TCGCTTTCAGACAAGCCTTCATCGATCAAGTGAAA
2,298	5	5004	40.75	7_60037	GBS				5	2,697,163		TGTTGTGACCAGAGGGGGGTAGATATTAGGAACCCCCAGCAATACACTGCAGCTATAAATAGGG
2,299	5	5004	40.75	7_59972	GBS				5	2,697,240		GGGCAACATAGTCATATCATTCACCATGCAACTTTGACCAAATTTCAAATCTCTAACAATTTTC
2,300	5	5005	45.94	89865813	F1Dsnp	PHR	T	C	4	13,296,601	+	TAATCAAACCTTCATCGATGCAAGTATGAATGAGA[C/T]GCTTAAAGGCTTGTGCTGCTGTATCGATGTCCTCT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,301	5	5005	45.94	89865815	F1Dsnp	PHR	T	C	4	13,368,576	+	CAAACCTTATAGGGGTTACGTAAAAACTGCCTTGC[C/T]AAAGATTCAACCTCCCTTGGCCATGTAGCACTCCA
2,302	5	5005	45.94	89865816	F1Dsnp	PHR	T	C	4	13,378,376	+	CCAAGTATATCTAAATATCAGTGGCACTCATTCAG[C/T]ATCATATCCAGTTCTAGTGTTGATGCCAATTCAAT
2,303	5	5005	45.94	89865817	F1Dsnp	PHR	T	C	4	13,384,886	+	TGGTTTCCTTTTCTACACCACCCTCGCATTTGGAC[C/T]AAATTCTTATGCTGCAGCCTCCCCATGCTTGAAAT
2,304	5	5005	45.94	89865819	F1Dsnp	PHR	T	C	4	13,435,587	+	CAGTCGAAGATGTCGGTCTTGATCCTAATACATGG[C/T]GCTCCACCTATATGGATGGAACTTTGTACTGTTAC
2,305	5	5005	45.94	3_981481	GBS				4	13,446,485		CATTTCCAAAACATGAGCTTTTTGTTTTCGGYTTTTTGCTACCACTCAAGTGATATAGATTCTA
2,306	5	5005	45.94	89809854	F1Dsnp	PHR	T	C	4	13,458,804	+	TTCAATGTGAGGCTTCTTATGATGATGTTGTAAGC[C/T]AGAGTATCGGGTTCTTCGAGATTGCGAAAAATGGA
2,307	5	5005	45.94	89809855	F1Dsnp	PHR	T	C	4	13,466,570	+	CTAGCGCATGCTGCTCTTTCAAATCCTTACAGTTG[C/T]GACCCTAGCAAGTTCTTATGCGCAATGACAGATAC
2,308	5	5005	45.94	89810273	F1Dsnp	PHR	A	G	5	2,730,670	+	GGAGACAACCCAAGAGCCACTAGCTACATGGTTGG[A/G]TATGGAAACAACTATCCTCAACAAGTTCACCACAG
2,309	5	5005	45.94	89810274	F1Dsnp	PHR	T	C	5	2,755,296	+	TTTCCATCTCTTCCTTAAGTTCCTCAAGGCGTGGC[C/T]TCATGAGCTGCAGAGAAAGTAACACCAACAACAAG
2,310	5	5005	45.94	3_42026	GBS				5	2,770,916		AAGTTGTTCAATACTATCACTTCCTATCAGCCTCAATGCAAACCAGATCAACCACAGTCCCACT
2,311	5	5005	45.94	89810277	F1Dsnp	PHR	A	C	5	2,770,947	+	CCGGAAGTTGTTCAATACTATCACTTCCTATCAGC[A/C]TCAATGCAAACCAGATCAACCACAGTCCCACTGAC
2,312	5	5005	45.94	3_101994	GBS				5	2,854,108		ACCAAATCATTACACAAGCACATAAATCGAAYGGTAACACAAGATTCTGATGTAATGAAACAGT
2,313	5	5005	45.94	3_102053	GBS				5	2,854,167		ACAGTAGAAGACTACAAAGACCAGCACAGTATAGATTCTAACCTTGACCGGCAGTTTTGGGGGC
2,314	5	5005	45.94	89866254	F1Dsnp	PHR	A	C	5	2,994,037	+	GATTTCGAAAAGGTTGTAAATGATCAAGCCAGTCT[A/C]GAAACCAAAGAGCTTGCTATTTTAGCAGTTAGTCT
2,315	5	5005	45.94	89866255	F1Dsnp	PHR	T	C	5	3,052,103	+	CAGCTTCAACACCTCTTTAGGTTACACGACTCGGG[C/T]CTAGACCAAGCAGTCATAGACTCTCTACCTGTGTT
2,316	5	5005	45.94	89810286	F1Dsnp	PHR	A	G	5	3,055,648	+	AGGTGTACAGATTTTTCTGAGATGAAGTCGATTGG[A/G]CATTCGACTGCCTTTTGCTGGGAGATTCAGGAGGA
2,317	5	5005	45.94	89810287	F1Dsnp	PHR	T	C	5	3,082,769	+	CATGCTGTAGAGCTTGCACACTTTGCTCTCTTCTT[C/T]AATCAGGTTCCTTTCAATAATTTTCTTAGAGCCGG
2,318	5	5005	45.94	89810288	F1Dsnp	PHR	T	C	5	3,095,101	+	AAACCGTCTATACTACTATCTTCATTTTATACTCC[C/T]CTGGATCAAAACGTGTAAGTGATGAGAATATATAT
2,319	5	5005	45.94	89866257	F1Dsnp	PHR	T	C	5	3,111,837	+	TCATTGTTGGTATTGCTGCCCAGTGAAGCAGAAGG[C/T]GAGAGTGATAGGATGAGAAAGAACAAGAAGATGAT
2,320	5	5005	45.94	89866258	F1Dsnp	PHR	T	C	5	3,115,480	+	TTTGCACCAGGAGAAGTCAGATTTGTCGATACCAA[C/T]AGTGTACCTACTTACAAGCAACCTGCATCAGCTGT
2,321	5	5005	45.94	TP3052	GBS				5	3,125,635	3,125,602	TGCAGCACAGTCTTCTGTTCCTCGGCTTGGATTGGAGAGAGAAGGTGAGGAGGCTTTTAGTAGC
2,322	5	5005	45.94	89866259	F1Dsnp	PHR	T	C	5	3,126,554	+	CCCCTATTTGAAATTTTTGTCGTTAAAAATGCAGA[C/T]GGGACATATGTTATGCAGGTGATGTGAAAATTTAC
2,323	5	5005	45.94	89810289	F1Dsnp	PHR	A	G	5	3,132,782	+	GACTGGCAATCGAATTGGGGGAAAGATGAGTTCAC[A/G]GAGATGGCCACTGCTTCAGTTAGCATGGCCTTCCT
2,324	5	5005	45.94	89810290	F1Dsnp	PHR	A	G	5	3,179,420	+	GGCACTATGACAGGAGTTCTTAGTGCAGCAAATGA[A/G]AAGGCTGTGGAGATGTTTATCGATGAAAAGTATGT
2,325	5	5005	45.94	89810291	F1Dsnp	PHR	A	G	5	3,191,711	+	GCAAAAGATGCCGCATACCGTCTTCATCAGCACTC[A/G]AGCTTTCCAAACTAGAAAACGCAACCAAAACGATG
2,326	5	5005	45.94	89866260	F1Dsnp	PHR	A	G	5	3,201,465	+	TTCCATGGTTTTTGCTCTAGTCCATTTGGATCGAT[A/G]TCTCTTGATCATCAAGGGAATAACAATGGGAATAA
2,327	5	5005	45.94	89866261	F1Dsnp	PHR	T	C	5	3,207,265	+	CTGCCACAACCGTTCTCAACAACCATTAATGGAAC[C/T]GATGATGAATTTTCTTTAGAACCATCTAAGTTGCT
2,328	5	5005	45.94	89810294	F1Dsnp	PHR	T	C	5	3,214,689	+	AACTATAATACCTTAATAACAGCATTTTCATTGAT[C/T]GGGGCATCAGGATTCCAAATACGAGCATCCATCCC
2,329	5	5005	45.94	89866262	F1Dsnp	PHR	T	C	5	3,275,932	+	TTCTTTGCATATAGAATAAGAATCACTAATAACTC[C/T]GACCGTCCTGTTCAACTTCTTAGAAGGCATTGGAT
2,330	5	5005	45.94	89810295	F1Dsnp	PHR	A	G	5	3,295,585	+	AAGGAGGGGCTCTCCACTGTCTAACTTACTTGGTC[A/G]TGTATAGAATCGAGATAAGATTTAGCCAACTGTGA
2,331	5	5005	45.94	89810296	F1Dsnp	PHR	T	C	5	3,298,035	+	CTCAGTTGACCACTTGATATCTCAGAAAGGGGGTC[C/T]AGTTTAACTTTTATCTTCCCCAAATTTTTATCACA
2,332	5	5005	45.94	89810297	F1Dsnp	PHR	A	G	5	3,387,026	+	GTGGATAAGATCCAGGCTTTTCTATAGCTTCCATG[A/G]ATGCAATGTTGTCATGCACACGATCATTAGAATGA
2,333	5	5005	45.94	3_707208	GBS				5	3,422,609		GGTCTGCCCTTCAACACCTCCCTCACAGCCTTGGTATCAGGACAAACCCCCTTAGCCATAATGA
2,334	5	5005	45.94	3_713730	GBS				5	3,424,026		TTGGTTCCACCCCAGAAACCGACATGTGCTTRAACACTCTGAGAGCATCCTTGGTCCTGTCCCC
2,335	5	5005	45.94	89810298	F1Dsnp	PHR	A	C	5	3,457,683	+	CTGGTACGCCTTCAAAGCATGTCCTATGGTGTTGC[A/C]AGCGCCATAGATATGGATGACTATGGTGAAGATAG
2,336	5	5005	45.94	TP3307	GBS				5	3,458,202	3,458,263	TGCAGCAGCAAGAGCCTTGATGACAACGCCATACGTGTAGGCATTTGGTTCCACCCCAGAAACC
2,337	5	5005	45.94	89866264	F1Dsnp	PHR	A	G	5	3,463,144	+	GAGGAATAATGTGACGAAATGGATTACACAGGCGG[A/G]GCTCCATTTCTGGGTAAGTGGTGTGAAGAAGAAGA
2,338	5	5005	45.94	89866265	F1Dsnp	PHR	T	C	5	3,465,390	+	TAGACGCCTACATGATGTTACAGAAGTTCAAGAAA[C/T]AGGCTTGCTCTTGGATGCAGACCAGCATCTTTGAG
2,339	5	5005	45.94	3_740314	GBS				5	3,485,216		AAAATAGCACATAACCAACTCACCACGCCGAACCAAAGATCATGAAGTTTCCTCCGGTAACTAT
2,340	5	5005	45.94	89810300	F1Dsnp	PHR	A	G	5	3,515,714	+	GCTCTTCTATCAGCAGCTCTATCCCTATATTGATA[A/G]CTTTCAAGCTGGAAATTTGAAAGCAGTCAAATTAA
2,341	5	5005	45.94	89810301	F1Dsnp	PHR	A	C	5	3,540,252	+	AAAAATGGCAAACTTCTTTAGCATTTTCACAATCA[A/C]AAATTTGCTTATTCTGTCTCTCGCCCTCAATCTAA
2,342	5	5006	48.43	3_1024375	GBS				4	13,492,552		CAACACCTCCTCATCCAGAACCTAAGCCAAAGAGACAGAAGCTTGATAATTCCATGCTTATTCC
2,343	5	5006	48.43	3_1024424	GBS				4	13,492,601		TTCCATGCTTATTCCAGAAGCTGAATTTCTTRCACAGCATCCGGGACTGGTATGCATCAATATT
2,344	5	5006	48.43	89809857	F1Dsnp	PHR	T	C	4	13,507,397	+	AACGGAACACTCCTGAAAGCTGGGGAAGACAAAAT[C/T]TCAGTAACATGGGGATTGAACCAGAGCCTCCCAGC
2,345	5	5006	48.43	89809858	F1Dsnp	PHR	T	C	4	13,517,079	+	CAGTATGACATCACCCATCTTAACAGGGCTGAGGC[C/T]TGAAGAAGAATTGGTTGATGTGCTTGTCATTGAAT
2,346	5	5006	48.43	89865820	F1Dsnp	PHR	A	G	4	13,517,117	+	AAGAAGAATTGGTTGATGTGCTTGTCATTGAATCT[A/G]ATGAAACTGGAAATACAATTTCAACATTGATCTTT
2,347	5	5006	48.43	89809859	F1Dsnp	PHR	A	C	4	13,541,418	+	TCATCATGGTTCTGCACGATTTGCTTGGTCATCTC[A/C]GCAGATGAAACTACTAGTGTTGGAACTTGGCCCAA
2,348	5	5006	48.43	89809860	F1Dsnp	PHR	A	G	4	13,541,456	+	AGATGAAACTACTAGTGTTGGAACTTGGCCCAAGC[A/G]CAGCAGCATTAGAGGGCCATACGTCTTTGAAAGAG
2,349	5	5006	48.43	89809861	F1Dsnp	PHR	A	C	4	13,641,221	+	TGAGCTGTGTCTACCTTTTTGTGTTCTGTAGAGGG[A/C]CGGACATCAAGAAGGGTTTTGTTAGATAGCTGAAT
2,350	5	5006	48.43	89809862	F1Dsnp	PHR	T	G	4	13,647,184	+	ATGTAATCTGAAACCTTCCTTGATGACGCACTTTA[G/T]GTACATGAGATGAGAAAGGTCACTTTCTTCAACCT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,351	5	5006	48.43	TP9544	GBS				6	20,353,999	20,353,952	TGCAGTTGGAGGGTGAAAATTTTAAACCTGAAGCCGAGTATCTCTCCGAGATCGGAAGAGCGGT
2,352	5	5007	50.89	89865822	F1Dsnp	PHR	T	C	4	13,676,740	+	GAGCCTGAGAATACGGGAAATTATATGCTACTTTC[C/T]AGTATCTACGCATCAAAAGAGCAATGGGATGAAGC
2,353	5	5007	50.89	89809863	F1Dsnp	PHR	A	G	4	13,679,457	+	GACTTGTGATTGAAACATACCATTGCCTACGATAT[A/G]AGCAGATTGGTGAGTATATTCACTGCTCACAGCTT
2,354	5	5007	50.89	89809864	F1Dsnp	PHR	A	G	4	13,681,673	+	AGAAGTGTCAAGAACTGGAAAACCCATGTAATGTA[A/G]AACAGTTCTCTCCCTGTAAGACAAAGAGAGACAAG
2,355	5	5007	50.89	89809865	F1Dsnp	PHR	A	G	4	13,686,419	+	GTGAGTGGAACATAACGAACTGCAGTTTCAGTCCG[A/G]ATACTTACAGAACCATCCATGTTCTTGTCCACAAC
2,356	5	5007	50.89	89865823	F1Dsnp	PHR	T	C	4	13,686,427	+	AACATAACGAACTGCAGTTTCAGTCCGGATACTTA[C/T]AGAACCATCCATGTTCTTGTCCACAACCTTTAAAT
2,357	5	5007	50.89	89865824	F1Dsnp	PHR	A	C	4	13,727,874	+	ACAGCGCGGAGGAGTACCACCAGCAATATCTGGAA[A/C]AAGGAGGAGATCATGGCAACAAACAATCCGCTGAA
2,358	5	5007	50.89	89809866	F1Dsnp	PHR	T	C	4	13,729,637	+	AATGGCAATAAACAATCTGCTCAAAAGGGTTGTAA[C/T]GATCCTATTAGATGCTATGGTTGAGTAACTAATGC
2,359	5	5007	50.89	89809869	F1Dsnp	PHR	T	C	4	13,896,911	+	TTGGACATCTTGGATGCTTCAAATGAGCTTGCTCT[C/T]TTTCTGGCCAGGGCTGTGATCGATGATGTGTTGGC
2,360	5	5007	50.89	89788544	snp	PHR	A	G	4	13,899,319	+	GAGCTTGAGGAGCTTCTTTCGAAACTAAAAGAATC[A/G]ATGCAGTCTGATGTACGACAGGCAGCTGTGTGGAA
2,361	5	5007	50.89	89865825	F1Dsnp	PHR	A	G	4	13,913,061	+	ATTCCAGCAGCTTTTGCAGCTGCAAGGCCTATGCC[A/G]CTGTCTTCTATCACAACACAACTGTTAGAAAAGAA
2,362	5	5007	50.89	89809870	F1Dsnp	PHR	T	C	4	13,933,596	+	ACACATTTTGAGAGGCAAGCTGTTTCACTGGAACT[C/T]AACTTGCTCCCAAGCGTGGTACTGGTGATGCACTT
2,363	5	5007	50.89	89865826	F1Dsnp	PHR	T	C	4	13,954,344	+	CAAATTCTTTAGCCAGCTTCTCCATATACATTTTC[C/T]TATAATACAAGAATTTAGGGAGTACCACAACAATT
2,364	5	5007	50.89	89809871	F1Dsnp	PHR	A	C	4	13,954,488	+	TCCAGGAGTGGTATATTCTAATTGCACGCCAGTTG[A/C]TTTGCATTGGAATGTTGGGGGACAAATCTTTTCTT
2,365	5	5007	50.89	TP2744	GBS				4	13,979,493	13,979,430	TGCAGCAAATATTCCTAAAAATCTTGAAGCAAGAAGAAGATTAGAATTTTTCACAAATTCGTTA
2,366	5	5007	50.89	3_1186039	GBS				NGH			TCAAAAGGGAGATCAGCTAGGTCTTGAACAACCTAGCACAACAATCAAATGAAGTACATACTGC
2,367	5	5034	53.35	89809872	F1Dsnp	PHR	A	G	4	13,975,887	+	CTCACACCAAGAATAGATGGGGGACGAAGACCATG[A/G]ATTTTGCGAAATTCCTCGAGAAGATTTCTCATTTT
2,368	5	5034	53.35	89809873	F1Dsnp	PHR	T	C	4	13,979,475	+	GTGAAAAATTCTAATCTTCTTCTTGCTTCAAGATT[C/T]TTAGGAATATTTGCTGCAGAATCCTTTACAGTAAG
2,369	5	5034	53.35	89865828	F1Dsnp	PHR	T	C	4	13,992,838	+	TGTTCCGCTTTCTGCATATCCTCCAGGCGATGTCG[C/T]TGCTTGTAGCGCTGGTAAAATTCCCAGAGGTGCTC
2,370	5	5034	53.35	89809874	F1Dsnp	PHR	T	C	4	13,996,842	+	CCATCTGTTATATATTCTACCGTAAGACTATTCTA[C/T]GAAACACGAGCTCAACAAGGTGGCAATATTGTTCA
2,371	5	5034	53.35	89865829	F1Dsnp	PHR	A	G	4	14,008,277	+	TCAAAAAGATAAGAACCTGTGGCAGTGATGGAACT[A/G]AAGTTTCTGTAGTGAATGAAACACATTCATATTGT
2,372	5	5034	53.35	89865830	F1Dsnp	PHR	T	C	4	14,014,064	+	GTCACCAAGTGGTGTGTTAGGAAAGACTGTCACAC[C/T]TGTGTCCCTAAACCATGAGATTAGTGTTATAAATA
2,373	5	5034	53.35	89865831	F1Dsnp	PHR	A	C	4	14,022,262	+	GTATTGTACAAGCACAAGATTATTGTTTTTGGCGG[A/C]TTTTATGACACTCTCAGAGAAGTGAGGTTGTTGGT
2,374	5	5034	53.35	89809875	F1Dsnp	PHR	T	G	4	14,031,816	+	CTGAAACTTAGAAACACATCGTATGTGTATGAACC[G/T]GTAGGAAAAGGAATAGAAGAGAAAGAGGAAGAAGC
2,375	5	5034	53.35	19_569783	GBS				5	4,000,184		GTTGGAAAAATCAAACCGACGTGCTATTACCAAAGGAAAGTAGAAGAAAAGCTAAAAGCCAGAA
2,376	5	5034	53.35	89810305	F1Dsnp	PHR	T	C	5	4,078,668	+	GTGTGATGTTTTTGTTGTTTTATGGGTTGCAGAAA[C/T]GGGGGGATGTGTATGCACGATGAGGCGGCTCCCCA
2,377	5	5034	53.35	89866270	F1Dsnp	PHR	T	C	5	4,085,864	+	CTATGGTGGAGAGAACAAAGCGAGGCGATCCAAGA[C/T]ACAGTCAAGCAGCTAGTCAGCTCTGGTCAACTGGA
2,378	5	5034	53.35	19_467845	GBS				5	4,116,090		TGGGAAGCAATCTGGAATCTCTGAATGTTGCRAACAAAACGAAAATTGTTTTCGTGGCGTGCTT
2,379	5	5034	53.35	89866271	F1Dsnp	PHR	T	C	5	4,136,588	+	AATAATGCAAGATCCTCATTTGAGCAAGCCCGCTT[C/T]AACCTGGTAAGATATGTTTCGCAAAGATATTTCGG
2,380	5	5034	53.35	89866272	F1Dsnp	PHR	A	G	5	4,181,788	+	TGTTGCATATTGAGGCGGAGGAGATAGCGCGGCGG[A/G]CATTGATAGTCGAATCGAGCGGATTGGTCCAGATT
2,381	5	5034	53.35	89866273	F1Dsnp	PHR	A	G	5	4,204,975	+	CTGAACTTCAAATTCTCCACAACACGGGCAGGAAA[A/G]TCTGAGAGTTCTTCCTCACCTTGGTGGAAAGGGTG
2,382	5	5034	53.35	89866275	F1Dsnp	PHR	T	C	5	4,259,666	+	TTCATGGGGTTTAGTGATAGTCCTGGCTATCTCCA[C/T]TGCTTCCAACATATCTCCACCATTGTGAACAGCAA
2,383	5	5034	53.35	19_304135	GBS				5	4,277,701		CTTAACTTGGAGATCATCATATGTGCCTAGCTATACACTACGTACCTTGTATATCTTCAGTTGA
2,384	5	5034	53.35	89810307	F1Dsnp	PHR	T	C	5	4,282,617	+	AAGAAATGTACTTTTCGGCTTCTTAATAGGGGATC[C/T]GCTAAAGCTCTTGATAAAGTTGTGGAGTTAGATGG
2,385	5	5034	53.35	89810308	F1Dsnp	PHR	T	C	5	4,287,008	+	TTGGAGGACCTCAAGGACATGGGGATAAATGCGGT[C/T]GGGTCCAGGAGGAAAATGTACTGTGCTATTCAGAA
2,386	5	5034	53.35	89810309	F1Dsnp	PHR	T	G	5	4,345,250	+	CAGGAGTCTTAATCAGTGCTTTCCAAATTGATATG[G/T]CCTCGCTGTTCATGATCATCTTGACATAGACCCAG
2,387	5	5034	53.35	89866277	F1Dsnp	PHR	T	G	5	4,497,958	+	TTGGAGTATGGCTACAAAAGTGACGGTCCAATTTT[G/T]CTTCCTTGCGATGTGGATCTGTTCTGCAATGTTTT
2,388	5	5034	53.35	89810310	F1Dsnp	PHR	A	G	5	4,497,987	+	AATTTTGCTTCCTTGCGATGTGGATCTGTTCTGCA[A/G]TGTTTTGGCACAGATGGAGAGCGATGATATTGATG
2,389	5	5034	53.35	89810311	F1Dsnp	PHR	A	G	5	4,502,882	+	TTGGAGTATGGATACAGAAATGATGGTCCGCTTTT[A/G]CTTCCTTGTGATGTGGATTTGTTCTACAATGTTTT
2,390	5	5034	53.35	89866278	F1Dsnp	PHR	T	C	5	4,522,444	+	GAACATGACCCGGGTTCAAAGCAGCTCCGACCCGA[C/T]GAACCAGAGCTCGACCTCTACACCATCCCAAGCCA
2,391	5	5034	53.35	TP3399	GBS				5	4,551,966	4,551,903	TGCAGCAGCTCAGCTTTGTCCAAAACCATGTTGGGTCTTATCCACACATTCCTGAACCTCTCAG
2,392	5	5034	53.35	89866279	F1Dsnp	PHR	T	C	5	4,617,160	+	TCCTCCACCTCTCTCGAGCCACCTCAATCCAGGAT[C/T]AAACACAACCCAGAAAATGACTTCTTGGAAGATGA
2,393	5	5034	53.35	3_1861836	GBS				5	4,633,090		AAGATCAGAAGTAATCAAGTGATGGGGGCAGATTGGGGACCGGTGGTTGTAGCGGCGGTGCTGT
2,394	5	5034	53.35	89810312	F1Dsnp	PHR	T	C	5	4,665,966	+	CTAGATTGGGTTGCTTGTGGTTTTCCTAAGACTAG[C/T]GGGGACCTTCGGATAGGGAAGCATGGAGTTTATAA
2,395	5	5034	53.35	89866280	F1Dsnp	PHR	T	G	5	4,715,084	+	CTGACACACCAGCGTCTCTGAAGGTTCACAAAGAT[G/T]TGGAAATGAAACAAGAAGCTCCACTACCCTGTAAG
2,396	5	5034	53.35	89810313	F1Dsnp	PHR	A	C	5	4,770,110	+	ACGCCGAAGGAGGTGCGGGAGGATATGCTGTTGATT[A/C]TTCTCCAGCTTTGATAATCGGCTGTCCAATTTGAC
2,397	5	5034	53.35	89810314	F1Dsnp	PHR	A	C	5	4,770,975	+	AGCTGTTGAATTTTGGAGAGGCTGTTGCCATTGGG[A/C]GAAGGTCTCCCGAAAAGCTGTTTCGGATTCTAGAT
2,398	5	5034	53.35	89810315	F1Dsnp	PHR	T	C	5	4,771,819	+	GAGGTTTGGGAGTCAGCTAGAGAGTGGAAGGCATG[C/T]TGGGAAATATATAAAGTACACTGCAGATGATTTGG
2,399	5	5034	53.35	89810316	F1Dsnp	PHR	T	C	5	4,775,770	+	ACCTTCTTTTTCCTCATCAGCTTAAATGCTTGGAG[C/T]ACTGGTTCATCCTCATACACCTGTAAATATAAACA
2,400	5	5034	53.35	3_1708216	GBS				5	4,887,946		GATGGAAATTCAAACAAGAGTCGGTCAACTAAGACACAATCAGATAAAGCCAAGGACAACATAG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,401	5	5034	53.35	89866283	F1Dsnp	PHR	A	G	5	4,914,721	+	ACAGTTGGCAGGGCGTATCGACACAAGGGGCACAA[A/G]TGACTTCTCTCCAGCCACTGAGAAATGCAATCTGC
2,402	5	5034	53.35	89810317	F1Dsnp	PHR	T	C	5	4,925,669	+	TCTGCCAATCTGGTCTGATATCTGCATCTGAGGAT[C/T]GCACCATCTGCATCTGGGATGCCACCACTAGGGCA
2,403	5	5034	53.35	89866284	F1Dsnp	PHR	A	G	5	4,950,563	+	TTGTGTTCCAAACTTACCAGAGAGTTTAGCACGAA[A/G]GGTTCCATTTGACACATACTCAGAGACAAGGTACA
2,404	5	5034	53.35	89810318	F1Dsnp	PHR	A	G	5	4,951,551	+	CCACTTAACGAATTCGAAGCCAAATTCAAGTAGCT[A/G]ATGTATGGCAATGAGAACAATGCAGCAAGAGGTGT
2,405	5	5034	53.35	89866285	F1Dsnp	PHR	A	G	5	4,960,217	+	AGAAGAAATCAAAGAGTGCAGCTACAGAGAATGGT[A/G]ATGCTATGACTGTGGATGAACCAGCTACAAATGGA
2,406	5	5034	53.35	TP7380	GBS				5	5,016,873	5,016,936	TGCAGGTCTTTGTCATCCAGGTTATTTTGTTCCTCGGAATGCCGCCGAGTATGCAAATCAGCAG
2,407	5	5034	53.35	3_1515220	GBS				5	5,025,344		AACTCAGATTTCGCAAGCAACGCAGGCAAGTRCGTAGCTAGACGACATGCAGCAGACAAGTCGA
2,408	5	5034	53.35	89893085	snp	PHR	T	G	5	5,114,366	+	TTCCTGGGTGGGGATCTGCATGGAAGAAACCATTC[G/T]TCAAAATCATTTGTCCATATGCTAGTGTCAAACTT
2,409	5	5034	53.35	89810319	F1Dsnp	PHR	T	C	5	5,116,796	+	CACATAGCATATATCTTCTCAGCCGCAACTTCATG[C/T]TGCCTCTCCCACATTTCCTCTTGTCTCTTCACATC
2,410	5	5034	53.35	89866286	F1Dsnp	PHR	T	G	5	5,155,518	+	TACACAAGTCCTTCCGATGGAGAAGAGGACACTAC[G/T]TCTGTGACTTTGCAATCACTGAGATATGATGGCGG
2,411	5	5034	53.35	TP4877	GBS				7	12,081,193	12,081,246	TGCAGCTACTGTACATCAACTTCGCAGATTAAACTGGGAAGATTCAGGAGGAACAAGCAAACAA
2,412	5	5034	53.35	TP2630	GBS				NGH			TGCAGATTTGCGATTTGGCTCAACTGAAGATATACAAGGTACGTAGTGTATAGCTAGGCACATA
2,413	5	388	55.79	89866268	F1Dsnp	PHR	T	C	5	4,075,783	+	ATCCCTTCTTACATAGGAACAGCCTCCACGAGCCT[C/T]GAAAAATAAAACTGTGTAGTTGTTAGTCCTCTCTT
2,414	5	388	55.79	89810304	F1Dsnp	PHR	T	C	5	4,076,047	+	TCAGCCTTGCTCTGTGGATAATGAATCAAAACATC[C/T]AGACACACTACTGTGTCATACTTCCCTCCCAAGCT
2,415	5	388	55.79	89866269	F1Dsnp	PHR	A	G	5	4,076,392	+	GACGGTGACGCCAGCAAGCGGGCCTTCATCCAACA[A/G]CATCTTCATCACATTCTCGACGGTCTTGGAGTGGC
2,416	5	5018	58.31	89809378	F1Dsnp	PHR	A	G	2	19,523,212	+	CAGAGGAAGGTGAGGTTGTGGATGTTAGTGAGAAG[A/G]TTGGTGAGATGAATGAGGACATAACGTATAGGATG
2,417	5	5018	58.31	89866287	F1Dsnp	PHR	A	G	5	5,215,427	+	CATGTGATGGAGTTGGACCCTGAAGATGGTGGTGT[A/G]TATTCAATCATGGCTAGTGTTTATGCCAATGCAGA
2,418	5	5018	58.31	89810320	F1Dsnp	PHR	A	G	5	5,262,691	+	ATCGAATCGCCTTTGATCCCATGCTTCCTGGCCAA[A/G]GCGTCGAACAGTTTTCCGGCGAACTCCTTGCAGTC
2,419	5	5018	58.31	TP9683	GBS				5	5,291,081	5,291,144	TGCAGTTTATTGATGAAAGCATTATCAATACAACAAAGCCAAAATCCAAAGTCCACTCACGGGG
2,420	5	5018	58.31	19_842549	GBS				5	5,311,198		ACCTAAGACGGTGGCTAATTTGATATTACATCATCCACTGCATTTTACATACACAGAGGAATGA
2,421	5	5018	58.31	TP6489	GBS				5	5,311,321	5,311,254	TGCAGGCCAAATATAAAAATGATCAATGGAGTAGGAATGAGCTAGGCACATTCCTAATTCATTC
2,422	5	5018	58.31	89866288	F1Dsnp	PHR	T	C	5	5,353,659	+	ATCCAATTCTGAACAGCTTTCTCAATGCTAAGCTC[C/T]CTATGCGGAATGTTGTCATACCAGGCAAAATCCCT
2,423	5	5018	58.31	19_930211	GBS				5	5,402,157		TTAATGGTGATCACTGAAAATGGTGATAATTTAAAATGATGATCACTTTGCTTCAAGTTTATAG
2,424	5	5018	58.31	19_943653	GBS				5	5,426,208		GTTGCCAACAACGAGTAGAGATCACGGTAAACTGACCGTAACGCAGCAAATGTCACAGATTGAA
2,425	5	5018	58.31	89866289	F1Dsnp	PHR	A	G	5	5,436,404	+	AGCCAAAACCAGGCTGACTTGATCCACCATTACTC[A/G]ATGATGGTTCATTTATGGTGATAGTAGTACTGGAA
2,426	5	5018	58.31	89866290	F1Dsnp	PHR	T	C	5	5,455,050	+	TTATGGCCTGGTGTATCAGACTTGACAGGATCTTT[C/T]AGGTACTGAGTTAATTATTGCATTGAGATATGAGG
2,427	5	5018	58.31	89866291	F1Dsnp	PHR	A	G	5	5,462,852	+	CTTTTAGTGGAATATGGATATCCCATTAGACCTCG[A/G]CGTTGCAAGGAAAGTGGCAGGCAGCATTTTAGGTG
2,428	5	5018	58.31	89866292	F1Dsnp	PHR	T	C	5	5,472,313	+	AACCCACTTGGACCTCTTCATTGACTTCACCAGAC[C/T]CTTGTGATTCCTTGCTCAAATCCTTGTCTAATGTC
2,429	5	5018	58.31	19_999273	GBS				5	5,473,425		ACGATGCTTTTCCAGATCTGGAGTCTGGTTTGTTAGATACCTGCATAACAGTTTCTCCCTCGAA
2,430	5	5018	58.31	89810321	F1Dsnp	PHR	T	C	5	5,507,796	+	AGACCTTTCTCAAGTTTTGTGGCATCAATTTCTCT[C/T]GGAGTGCTCTCCATAAGAACCTCCAAAATGTTGCG
2,431	5	5018	58.31	TP260	GBS				5	5,525,784	5,525,850	TGCAGAAATAAAACCACCTCAATGATCAAAGTAATGAAGGCTCTGAACCCAGGCATACTAATTA
2,432	5	5018	58.31	89866293	F1Dsnp	PHR	A	G	5	5,526,680	+	CGATGCCAAATCCACTGCATTGTACACTGTGATCA[A/G]AACAAGTGGATACCTGATCAAGTGTTCACAAGCTA
2,433	5	5018	58.31	89810322	F1Dsnp	PHR	T	G	5	5,530,708	+	AGTACCAGGAAAGTTTTGTTATTTCCTAAAGTTAT[G/T]GAAGTAGGAAATGCTCGATCCATGGTGCTTGCTGC
2,434	5	5018	58.31	89810323	F1Dsnp	PHR	T	G	5	5,545,670	+	GATGATGAGTTTCGAGCAAAGTGGGATGACATGCT[G/T]ATCCATGCTTCTACTTTGGAAGAATGCCCGACTAC
2,435	5	5018	58.31	89810324	F1Dsnp	PHR	A	C	5	5,546,962	+	CTTTCCCGGTGTGCTAAAATGGCCCAGATCAACAC[A/C]AAAGTCAGTGCAGATTACTTGAGATCGGTGGAGAA
2,436	5	5018	58.31	89866296	F1Dsnp	PHR	T	C	5	5,589,234	+	ACTGCCCCCATATCATCGTCAGACACATTCCTCGG[C/T]GAACTGCGTACAGATGGCAAATTGCGATCATTAGC
2,437	5	5018	58.31	TP9576	GBS				5	5,589,651	5,589,714	TGCAGTTGGGGAAGCCAGCTGAGGTAAGCTAGACGCATGACGAACTCGTGGTACACGAGGTACT
2,438	5	5018	58.31	89810325	F1Dsnp	PHR	A	C	5	5,589,995	+	TGCACTTGAAGCTGAACTTTTATTCTGCCCATGTA[A/C]CTTCTCACTAGAGCCGGCAGGAACTGCAGTATCTC
2,439	5	5018	58.31	89810327	F1Dsnp	PHR	A	C	5	5,641,279	+	GGATAAAGGATTCCATGTCTGCAAGAAGAAGATGA[A/C]AACGTCTCCAGACACCTTGTGTCTCGATCCCCTCC
2,440	5	5018	58.31	89810329	F1Dsnp	PHR	A	G	5	5,682,893	+	ACTTAGACACTGTTCGAGACCAACTAAAATGCGAT[A/G]TCAATGTGTTCCATGGCAGAGATGATGAGCTTATC
2,441	5	5018	58.31	89810330	F1Dsnp	PHR	T	C	5	5,740,903	+	TGGCGGAACCTTAGTTTCCAGTTCCTTTGGGACTG[C/T]CCTGAAAGAGAAAATTCATGGAGTCATATAATGTG
2,442	5	5018	58.31	89810332	F1Dsnp	PHR	T	C	5	5,769,917	+	CATCTGTTGACAGTTGAAACAACAGCTAAATGCTG[C/T]ATCTGAGCAAGAAGAAAATGGGGACAAAAGATAAC
2,443	5	5018	58.31	89810333	F1Dsnp	PHR	A	G	5	5,772,239	+	GATAGAGGCAAGTATTAAAAATGGAGATCTTCAGG[A/G]ATTTCAATTCTTCAATGAAGCTGCAAAGCATGTTT
2,444	5	5018	58.31	293_189447	GBS				5	6,134,827		TTCATGCAGTGATAGTTCCACATGCCAAGACWCGATAGCTGGCCAACTAGCTTCACTCCCTCCT
2,445	5	5018	58.31	89866303	F1Dsnp	PHR	T	C	5	6,142,038	+	TGAAAGGAGTGATGTGGTACAAGATCAAATGGAAA[C/T]TGCAGCTGGATTAGATGTACTGAGTTTGCAGGGAT
2,446	5	5018	58.31	89810337	F1Dsnp	PHR	A	G	5	6,320,072	+	ATGGAAGCTGCACGTGACTCTGCAGAATCAGCATC[A/G]ATGAACTCAAGCCTCTTGTATACCTCCTGAAGCCT
2,447	5	5018	58.31	89810339	F1Dsnp	PHR	T	C	5	6,406,123	+	AAAGCTGGAGAATCCAACACTTACCTGGATGGTAT[C/T]TACCTACTCTTTACCTACTTCACAAAACCCGAGTC
2,448	5	5018	58.31	TP965	GBS				5	6,549,694	6,549,757	TGCAGACAAGAGAGAAAAACCCTAGGTTTCTGAGTGAAGGTATTTATAAGGAGGATGGAGATGG
2,449	5	5018	58.31	TP3625	GBS				5	6,567,624	6,567,558	TGCAGCATCTATATGACTATATGCATCGCTGATTGGTGAATTTGAGACTTTGAGTTGAATACCA
2,450	5	5018	58.31	TP4713	GBS				5	6,578,851	6,578,888	TGCAGCGTCAAACATAGCAGCTGCAATTGACACTCCCGAGATCGGAAGAGCGGTTCAGCAGGAA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,451	5	5018	58.31	89866307	F1Dsnp	PHR	T	G	5	6,605,240	+	TTAACGAGAAGAACAGATTTGAAGTTTGGCTCAAA[G/T]CCTAGATGGAATTCAAAATTTAATATGGTGTTACA
2,452	5	5018	58.31	86_265083	GBS				5	6,605,271		ACACCATATTAAATTTTGAATTCCATCTAGGMTTTGAGCCAAACTTCATATCTGTTCTTCTCGT
2,453	5	5018	58.31	89866309	F1Dsnp	PHR	A	C	5	6,725,184	+	CAAATCCCTTAGTGAAGCGGTACTTGATCTCAGAT[A/C]TTTTCCTGGGTCACAAAGTTGGGATGAACCTGTAC
2,454	5	5018	58.31	89810344	F1Dsnp	PHR	T	G	5	6,725,443	+	TTCACGTCGCTGCTGATAGAATTTGTTGCAAGGCT[G/T]CAAAATCTTGTTGACTCCTTTGAGGAATTGGGTGA
2,455	5	5018	58.31	89866310	F1Dsnp	PHR	T	C	5	6,725,455	+	CTGATAGAATTTGTTGCAAGGCTTCAAAATCTTGT[C/T]GACTCCTTTGAGGAATTGGGTGAGACGGCACTTTT
2,456	5	5018	58.31	86_102859	GBS				5	6,738,223		AGCTGTGGCTTCCAGAGTGAAGATCGAGGAASAATTGCCTTAAAGGAGTGAAGTTTTTAATCCC
2,457	5	5018	58.31	89866312	F1Dsnp	PHR	A	G	5	6,828,649	+	TATGCCGGTCCTCTTAAATGTAGAAAAGGCCAGGG[A/G]TGTTAGTGCATATGAAGCTGAAACTGAACCCTGTT
2,458	5	5018	58.31	89810349	F1Dsnp	PHR	A	G	5	6,847,922	+	CCGACAACTTTGTTTATAGACCTCAGCTCTTCGTG[A/G]AACTCCGGATGCAACACCAACGCAGAGTAATTCTC
2,459	5	5018	58.31	89866320	F1Dsnp	PHR	T	G	5	6,902,419	+	TTTCTTTGTTCTCATTGAGTGCTTCCTCTACAGAT[G/T]TAGGGATAACTGACCCTGTGACAACAGCAAATCAT
2,460	5	5018	58.31	89810352	F1Dsnp	PHR	A	C	5	7,018,279	+	ACACCCTTCGCTTTGAGGGCGACTTCCACCATCTT[A/C]GCGTAGGGACTAAACCAGGTTCCGTATAGGATCAC
2,461	5	5018	58.31	89810354	F1Dsnp	PHR	A	G	5	7,043,518	+	AGTGTACATTGGAGCCATGAGGCATTATGGAAGGA[A/G]AGGAAAGATTGAAGAAGCTGTGAATGTGTTTCACC
2,462	5	5018	58.31	89810355	F1Dsnp	PHR	A	G	5	7,044,604	+	GGGTTATGTGTCTGATGCCAGTAGACTTGTTGATG[A/G]TGCTATTGCCAAAGGTTACCTTCCTGACATATTTA
2,463	5	5018	58.31	89810357	F1Dsnp	PHR	A	C	5	7,048,956	+	ATGGATGGTTTAGCACATGCAGTGAGTATGCTAGT[A/C]ACAGTAAACTTATTTATTTCCTCTCCCATTCTTCT
2,464	5	5018	58.31	89866323	F1Dsnp	PHR	A	C	5	7,099,762	+	CAGTAGAAGCCTATAGCTTGCATGTACGTTTGCCC[A/C]CATTGGCATACTGACAACCGAACAAGACAGACAGG
2,465	5	5018	58.31	89866325	F1Dsnp	PHR	A	G	5	7,132,915	+	TAGCTGTTGCATGCTTTAGGGGCAAGGCAGCTGAT[A/G]GTGTTTGGTTTAGGACCAATGGGTTGTATCCCACT
2,466	5	5018	58.31	89866326	F1Dsnp	PHR	T	G	5	7,239,118	+	CGGCAGGTTATGGAGGTGGCGGCGAAGCCGGTGGT[G/T]TTGGTCGTGCCACTGATGTTGGTTCATTCGTTAAC
2,467	5	5018	58.31	89810360	F1Dsnp	PHR	T	C	5	7,274,408	+	ATCGATTAGTGAATTGTACGTAACAGCATTTGCAG[C/T]AACTCCCTTCCTTATGTTTTTCAACAACTGATATG
2,468	5	5018	58.31	TP3239	GBS				5	7,275,683	7,275,746	TGCAGCAGACTCCAAAATCTGATACAAATCCATACACAAATTCTAGTTCACGGTTTCGCTCAGA
2,469	5	5018	58.31	89866327	F1Dsnp	PHR	A	G	5	7,275,842	+	CGCTCCGAGTTTTTGGGAATGTAGAGAATCCGAGT[A/G]TCACTGTGTGGAACCAGATGATCAGAGGATATGGT
2,470	5	5018	58.31	89836356	snp	PHR	A	G	5	7,320,006	+	CCTTGTGCTGCACCAGTATGCAGATAATGCAAGCC[A/G]CGAGCAGCGCCAATGCAAACCTCGAGCCTTTGCTT
2,471	5	5018	58.31	89861823	del	PHR	-	AGA	5	7,321,820	+	TCTTGGGGAGCGCCACAGTCGATGAGGAAATTATC[-/AGA]AGGAGTGAATGTCAACGTACCAGAATTTGAATGTG
2,472	5	5018	58.31	89866329	F1Dsnp	PHR	T	C	5	7,434,698	+	GAGTCACATTGGCAGTACTTGAACAGGAGTTTGAG[C/T]CGTGTTTCATCTACAACAAATGGAAAATATGATGC
2,473	5	5018	58.31	89810361	F1Dsnp	PHR	T	C	5	7,435,735	+	CAACAGTATCTCTTCAGATGAGGAGTTGGAAACAA[C/T]TGTTCCTGAGACTAAAATTAGAGAATGGAGAGTGT
2,474	5	5018	58.31	89866330	F1Dsnp	PHR	A	G	5	7,436,971	+	ATGAGCCTCTCTGTAAACTCTGCCAAACACCATGC[A/G]AGTAAGTCCTGTTCAAATGATCTGTTAATGTGCTG
2,475	5	5018	58.31	89810362	F1Dsnp	PHR	A	G	5	7,441,169	+	TCCATTTATTACAAATCCTGATGGTGAAACTAGAG[A/G]TTCAGAGGAGAACCCTGCAAGTGATAACTCTGAAG
2,476	5	5018	58.31	89866332	F1Dsnp	PHR	T	C	5	7,459,831	+	GAGGCTAGACACCACAGCAACATCCCAAGAAGAGC[C/T]CTCAGGACTAGCAATATCCCCAGTACACAAGATTG
2,477	5	5018	58.31	89810363	F1Dsnp	PHR	A	G	5	7,460,504	+	ACGAAGACGGCAAAGTCCATGGTTGGATTAGTACC[A/G]AGTCATCTGTGGGATTTTGGCTGATCACACCAAGT
2,478	5	5018	58.31	89849444	SnpSnp	PHR	T	C	5	7,470,224	+	GCTGTGAAAATAATTAACTTGCCTCTTTTATCACT[C/T]GTTACAGAAAATCCCAACAGAATTTCTCCAGCATT
2,479	5	5018	58.31	89810365	F1Dsnp	PHR	T	C	5	7,585,483	+	AAGCTGTGTCGTCAAGATAAGCCTCTTTTTGGACC[C/T]AAACATTGGTGGTCCATCTTCAATCATTTCACTTT
2,480	5	5018	58.31	89810366	F1Dsnp	PHR	T	G	5	7,614,744	+	ACACCTGAGAAGTTAAACATGGATGAAGCATTTGG[G/T]CTCACTCTACAACGAGCTGCACCGTTAATGATGCA
2,481	5	5018	58.31	89810367	F1Dsnp	PHR	A	G	5	7,680,675	+	GACATCGAGGGCTTCAAATCCGGAGAGCTTGCATT[A/G]TGTGCTCCATCCAAGAATTATGCCAACACAATAGT
2,482	5	5018	58.31	89866333	F1Dsnp	PHR	A	G	5	7,726,614	+	AACCATACATGATGATCACAATGTGATGAGTTTTG[A/G]GCACTATTGACAATATCTTTGAGGATGCCAATGAA
2,483	5	5018	58.31	89794753	snp	PHR	A	G	5	7,738,122	+	CCTTGTCAAGTTATTGGAACATTCAGAGATCAAAT[A/G]CACAAACAAAGTTTTGATGTTAATGGCTCCATTGT
2,484	5	5018	58.31	89866334	F1Dsnp	PHR	A	G	5	7,740,171	+	GAACTTATTGAAGCAATAAGGAGAGTACCTCCAAT[A/G]AACAGCTTAGAACTTGCCCCAGTTGTCATGCATCT
2,485	5	5018	58.31	89858334	mSNP	NoCls	A	G	5	7,758,196	+	TTTGGATTGGAATTTATTGTTTCAGATGTATGATT[A/G]TGATAAAATGTGAGATGGTTTCGCCTCCTCTTGAG
2,486	5	5018	58.31	89810368	F1Dsnp	PHR	A	G	5	7,759,357	+	CTCGACTGCAGGAAAAAAGTGGTTGTGGTTTCTTT[A/G]TGGAATGATCTTGCAACTGGTGTTGGCCAGGAATT
2,487	5	5018	58.31	89810369	F1Dsnp	PHR	A	C	5	7,811,576	+	CACATCTAATGGCTCACAAGAACCACTGAACCTCA[A/C]CATCATATTTGAATCATTGGTGGCTGTATGCTTTT
2,488	5	5018	58.31	89836544	snp	PHR	T	C	5	8,023,895	+	ATTAGGATCTTTAACACTGACAGGCATGCAGGGAA[C/T]ATTCTGGTTAAAATGCCTGATGGGGAATTTGGTCA
2,489	5	5018	58.31	89810371	F1Dsnp	PHR	A	G	5	8,028,203	+	TGATGCTCTAGACTTGGTCCCTCGTCGGTTTTGAT[A/G]TACCAAGGTGTATCAGACACATATTTGGGTATATG
2,490	5	5018	58.31	89810372	F1Dsnp	PHR	A	G	5	8,028,347	+	ACGTTCCTGCGATACTCTTGCCTGGATTTAAAGGA[A/G]GCCAGGTTTTGCGACACCATATCAAATTATAAGAG
2,491	5	5018	58.31	89849466	SnpSnp	PHR	T	C	5	8,210,347	+	GAAACAGTTTCAATAGTCAGAAAGCATTCAATTCT[C/T]GGATGCTTATAATCTACTATACTTCACTCCGTGGA
2,492	5	5018	58.31	89810375	F1Dsnp	PHR	T	C	5	8,212,588	+	GAGATAAGCAACTTTAGTGTTAAACAAATCCTACC[C/T]CTGGATTGGACACCGAAAATTCCTGGAAGTCAGAA
2,493	5	5018	58.31	TP1196	GBS				5	8,331,611	8,331,668	TGCAGACGCCGCATGCGCACAAACTTGAAGGCCTCTCAAACCCGCTGGCCATAAACCGAGATCG
2,494	5	5018	58.31	TP4708	GBS				5	8,405,041	8,404,978	TGCAGCGTAGATTTTGGGTTTGTACCGTGTACTTCAAAATTTTCTTTTACATGAAGTAGATCTT
2,495	5	5018	58.31	89866342	F1Dsnp	PHR	T	C	5	8,430,081	+	GCTTCAAGGGATGCACAACTGAATGGCTGCCAGAA[C/T]TTCCAGTTGCAACTCTAATCTCTTCATCTGTCCAG
2,496	5	5018	58.31	TP8393	GBS				5	8,437,217	8,437,154	TGCAGTCCTTCCCCCAAATCGTCTCCATCCTCCCCATCGCATAGACATGGTACGTCACAAACCA
2,497	5	5018	58.31	183_222692	GBS				5	10,271,588		TTTAGGAAACAACCTTCCATGAAAAGATCCCAGAACTGCAGCCGCGAAGTATCGCCTATCTTGA
2,498	5	5018	58.31	89810111	F1Dsnp	PHR	A	G	5	10,280,629	+	AAGGACATGGAGTGTTTCCTGCATGCTAGAGCACA[A/G]GAGATTGTATGTGGAGGACTAATGGTGCTTACCTA
2,499	5	5018	58.31	89866070	F1Dsnp	PHR	A	C	5	10,281,969	+	GCACATCCTATGAAAGGTGGAGATGGCCCCAATAG[A/C]TATATGAAAAACTCCATTCTGCAGGTTTCTTCTTT
2,500	5	5018	58.31	89866071	F1Dsnp	PHR	A	G	5	10,490,333	+	TAATGTTTTTTTTTCCTCCATGTTTAGCTTGCCAA[A/G]TGTGTTGAGATTGGATTGCCAGAGCTTGTCATTTT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,501	5	5018	58.31	89866072	F1Dsnp	PHR	T	G	5	10,575,651	+	GTAGGCTGATGGCACCATTGGACCAATCATCACAA[G/T]GGGCCAAAGTCCCAACATTTCATTCACCAGCTTTT
2,502	5	5018	58.31	431_23448	GBS				5	10,583,316		TCGGTATATGAGCTTTTTCACTTCTGCAGACTGAAAAGGAAGCGACACGGACAAGTGCAATGTC
2,503	5	5018	58.31	89866073	F1Dsnp	PHR	A	C	5	10,644,340	+	TGTCAAAACATTTAGTTCAGAAGAAGAAGCTATTG[A/C]ATTAGCAAATGACACCCAGTGAGTCGACTCTTATT
2,504	5	5018	58.31	89810117	F1Dsnp	PHR	T	G	5	10,816,849	+	AGCCATTCAAATGGCTTCACAACTAGCTCAGCATG[G/T]AAATGTTGCTCCTTACTGTTGAGATATATATCCCA
2,505	5	5018	58.31	89866075	F1Dsnp	PHR	T	G	5	10,856,081	+	CTCGTTAACAGAGGTCGTGATTTCTATTACAATGA[G/T]TCCATATGTGAATCTCACAAGAAAGATGTTTCCTA
2,506	5	5018	58.31	306_17971	GBS				5	10,867,969		TCAGTTTCCATATTGAACAACATGATTACATRCTTTTTCACTCTTCGCTTTCCAACTCTCTTAC
2,507	5	5018	58.31	89810118	F1Dsnp	PHR	T	C	5	10,920,596	+	CTGCTGGCTGATGATCCTGAGGATCCACTGAACAT[C/T]ATTATTTTGAATATGCGCAAGGTCTTGTTCGACAT
2,508	5	5018	58.31	89866076	F1Dsnp	PHR	T	C	5	10,950,865	+	TTTGTTTTAACTCTCAGTGCTGGCTTGGAGGGTTA[C/T]CATGTTAATGTTGATGGGAGGCATATCACCTCTTT
2,509	5	5018	58.31	89810119	F1Dsnp	PHR	T	C	5	10,951,107	+	ACGTCACATCCTAGTTTTGCTCCACAGAAGCATCT[C/T]GAGATGTCACCCAGATGGCGTGCCCCACCTCTTCC
2,510	5	5018	58.31	58_676394	GBS				5	10,951,138		GAGGTGGGGCACGCCATATGGGTGACATCTCAAGATGCTTCTGTGGAGCAAAACTAGGATGGGA
2,511	5	5018	58.31	89866078	F1Dsnp	PHR	T	C	5	11,005,933	+	CAGAAGCTTCTTTGTCATAGATGAACCCGATTACC[C/T]TCACTGAGAAAATGTAAGACCCAACAGGGCTGGCT
2,512	5	5018	58.31	89810121	F1Dsnp	PHR	T	C	5	11,017,082	+	AAAAAATGGGTGCAGCTCATCATAATCTTGAACAT[C/T]TTCTGATCCCATGGCTAGTGTCTGCGAAACACCAA
2,513	5	5018	58.31	89810122	F1Dsnp	PHR	T	G	5	11,032,896	+	ACTGTAAGTAAATGTGTCAGGCGAAAGACCAGCCT[G/T]TTGCATCCTATCATACAGTCCAAGGGCAATATCAA
2,514	5	5018	58.31	89866081	F1Dsnp	PHR	A	C	5	11,118,954	+	ACCACATTTACCATAAACAAACCACCCAGATTGTA[A/C]TTTGTGGTCAGGTACACAGACATGTTAGCTATCAA
2,515	5	5014	60.75	89810378	F1Dsnp	PHR	A	C	5	8,618,043	+	ACAAATCTTGAGACAGAGCAAGGAAATACAATGGT[A/C]GAGGAATTGAAACTTGCATTTGCACAGAAGGATGG
2,516	5	5014	60.75	TP1591	GBS				5	8,722,561	8,722,501	TGCAGAGCCAACTATAGAATTGGACAAACCAAAATGGTTCTCATCATAAGCACCGAGCTTCCGT
2,517	5	5014	60.75	89810380	F1Dsnp	PHR	A	C	5	8,866,707	+	ATGAAGATAACTGATGTTGGAGGACAGGCAATCTC[A/C]GCAATTCGGACCCTCAAGAAGTTGAACTTGGAATG
2,518	5	5014	60.75	89810381	F1Dsnp	PHR	T	C	5	8,879,124	+	TGATAATAGAAATTAACTTGCCTGTAAATTCTGGT[C/T]TAGTATAATGATCAGCAGGCTTATTGGAGACGGTA
2,519	5	5014	60.75	89836724	snp	PHR	A	G	5	8,883,469	+	AGTGGGTCAATGATTTCCAAATTCTGAACACTGAC[A/G]TCAAATTTCAACTGTAAAAGTTATTACCACATACT
2,520	5	5014	60.75	TP2782	GBS				5	8,936,952	8,936,889	TGCAGCAACACAAAGATGGACTTAGTATGCACGACATTGTAATCTACCGCGAGAAAATCAATAT
2,521	5	5014	60.75	TP3742	GBS				5	9,045,536	9,045,599	TGCAGCATTTTCCCCCGACACCATAAGAGCCCCAACTAGACATGCATTCAGTGAGTTCTTCTAT
2,522	5	5014	60.75	TP2094	GBS				5	9,075,217	9,075,278	TGCAGATATGCAACAAAGATATTTAACACGATATATAACAATCCTATGGATGAGATTACCAATT
2,523	5	5014	60.75	307_201734	GBS				5	9,170,859		GGTTGACATTTGCTTCTGGGTTCTGATTGTCGTCTCGTCGTGCAACTTATGGCTGACGACATAT
2,524	5	5014	60.75	TP1709	GBS				5	9,175,349	9,175,304	TGCAGAGGACCATTTCGCTTCGTTGGCTTGAAGGAAGATGTGCCCGCCGAGATCGGAAGAGCGG
2,525	5	5014	60.75	89836807	snp	PHR	A	G	5	9,276,088	+	GCAGCGGAAGAAGTAGAAGAGAAGGAAAGACTGGT[A/G]AAAATGGGATCGTACGGAGGAATGGTCCGGCAGCT
2,526	5	5014	60.75	89866352	F1Dsnp	PHR	A	C	5	9,537,250	+	TTTTCCTTCAGTGACAAGCCCCGAATGGCTGCAAG[A/C]AGATAAGAGGCCAATGAAAGTTACATCATCCGGCT
2,527	5	5014	60.75	89866354	F1Dsnp	PHR	A	C	5	9,562,737	+	CTCACATCGGATCTTGTCGTTCTCTGATCGAAGCA[A/C]AGAGTTATCAGCTCTTTCATGTTGGGCCTGCCGTA
2,528	5	5014	60.75	89810388	F1Dsnp	PHR	A	C	5	9,633,628	+	TATTATCCTTGTACCCAGGAAGTTGAATTGTCAGC[A/C]TTGGAGGATTCTGATTCGATGTAGTAACAGTAAGC
2,529	5	5014	60.75	TP5521	GBS				5	9,657,853	9,657,914	TGCAGCTTACGTCATTTCTTACAGCTAGCTGGCTATGAAGAGTTTCTAAAATCTTTGACTCATA
2,530	5	5014	60.75	89810399	F1Dsnp	PHR	T	C	5	9,999,352	+	GGTGTTTCAGGGGGATCCAAACCTAATTTGGCTGA[C/T]CTAGCTGTTTTTGGGGTGTTAAGACCTATCCGTTA
2,531	5	5014	60.75	89866069	F1Dsnp	PHR	T	G	5	10,079,718	+	GATGCACGGCCAGCATCAGATGTAAGAAGACCAAG[G/T]GCCTCAAGAAGGTAGCCTAGACTGATCCAGAACCC
2,532	5	5014	60.75	89791561	snp	PHR	T	C	5	10,100,239	+	ACTCTTGTGAAAAATGCTGCTTTTTCGAATTTGAT[C/T]GAGTCCATGTGTAGAGAAGGGTATTTTCAAGAAGT
2,533	5	5014	60.75	89810108	F1Dsnp	PHR	T	C	5	10,112,387	+	CCTCTCTTTAAGTCTTCGGAGGTAGAACTCCTGGA[C/T]ACTTCACTGGACTCAGGCTTACCCCTGACAGTACT
2,534	5	5014	60.75	89810110	F1Dsnp	PHR	A	G	5	10,166,741	+	CATCTTGAAGAACACACTTCCTGGGGTCTTGCCTC[A/G]GGCTTCATAGTTCAAAATGGTCATGGACCATCTGA
2,535	5	5014	60.75	183_359585	GBS				5	10,177,867		AGTTACGACCAGATCGATCCGATGATGATCGGAGGGAAATGTATATACCGGTGAGTGATTTCCA
2,536	5	5014	60.75	183_343745	GBS				5	10,186,921		CTCTTAATATATTAACATGAATAACCAAGAGCAGACTTTAGTTTCTTTAATTCCGGCAGGTTTA
2,537	5	5014	60.75	TP4816	GBS				5	12,688,072	12,688,009	TGCAGCTAATGAAGTAGCAGTAGTTAAACTAAGTGAGCTGAATGTCTGATGTATAGGCAGCCCC
2,538	5	5014	60.75	89866097	F1Dsnp	PHR	T	C	5	12,710,548	+	CCCCTTCATGATTACCCTTTTGGGGCTCTTCATAA[C/T]CATCTTTACATCTGAAAGAAGAAAAGAAGTTGAGA
2,539	5	5014	60.75	89866098	F1Dsnp	PHR	T	C	5	12,752,587	+	GTCGTCCCGTCCTTGCTATTAAAAGGAGCCCAGCC[C/T]TTGTCTATCAACCTATGACGATGATGACTCGCATT
2,540	5	5014	60.75	89866099	F1Dsnp	PHR	A	G	5	12,756,033	+	TACTGCAGATACTCACCAAACATCAAGGAGTTGAA[A/G]GTACTTAGTCACAGGAAGGTCAGAAGGGCAAGGCT
2,541	5	5014	60.75	89866102	F1Dsnp	PHR	A	G	5	12,794,263	+	CCGATGACTTCCACCAGCCCTCCTTCAATGCCTCC[A/G]ATGACTTCTTCTACTCCTATGCTCAGCCCTACAAG
2,542	5	5014	60.75	89866104	F1Dsnp	PHR	A	G	5	12,806,791	+	AAGAACCCTGTTAGAGTGATCCGTGGCTCCGAACT[A/G]GTGGATGGAAGCAGGACATATTTCTATGATGGATT
2,543	5	5014	60.75	89866105	F1Dsnp	PHR	T	C	5	12,916,732	+	AGGTGAGAAGGCTCCCGATCTGCTTCCCAGTGGGG[C/T]AGACACCCAGAATGAAAGGCAAGGACAAGACTACT
2,544	5	5014	60.75	89810141	F1Dsnp	PHR	A	G	5	12,918,626	+	CTTGATGATTTTGTAGATGTTACCAAAGATGAAAA[A/G]CAGCTGATGCATCTTTGGAACTCTTTCGTGCGGAG
2,545	5	5014	60.75	89866106	F1Dsnp	PHR	T	C	5	12,918,653	+	GATGAAAAGCAGCTGATGCATCTTTGGAACTCTTT[C/T]GTGCGGAGGCAAAGGTACTCTTGCTTCTTTGGGCT
2,546	5	5014	60.75	89866107	F1Dsnp	PHR	T	C	5	12,961,284	+	CTTCAACAGCTTTGTTGAAACAAAAATGGTGGGTG[C/T]TTTCAGAGTTCTAAGCAAGTCCCTCAGACACTACA
2,547	5	5014	60.75	89866108	F1Dsnp	PHR	A	C	5	12,985,497	+	TGACATTTTGGTATATGTGTTTTATAGGGCATAAT[A/C]AGAGGGAAGTTGGATCATTTGAAAAGATCTGTTGA
2,548	5	5014	60.75	89866109	F1Dsnp	PHR	A	G	5	13,115,621	+	GTGGCAGGAGGATCAGAGCGTCCTTTCACAGCAGA[A/G]GAATATATGTTGCTGCACACAACTATCTTCAACAT
2,549	5	5014	60.75	89810146	F1Dsnp	PHR	A	G	5	13,143,050	+	CTGTGGTCACTGTGGTTTTGATCTTGACTGCAGCA[A/G]CAACAGAACCACAATCCACATCCCATCTTATGGTG
2,550	5	5016	63.29	89866082	F1Dsnp	PHR	A	G	5	11,179,051	+	GGGTAAATAGTTGACAGCTCATGTTGATCTTTGCC[A/G]AGCACATTTACAAGGGAAAAAAGCTGCATAAGGCC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,551	5	5016	63.29	89866083	F1Dsnp	PHR	T	C	5	11,219,849	+	GACCCATGTAGCATGCAGGCTTGTAATTTCGTCAA[C/T]AACCAACAGTCTTGAGGGAAAACCCATGACAACCT
2,552	5	5016	63.29	89810125	F1Dsnp	PHR	A	C	5	11,222,490	+	ACAGGATCTAGCACTGACTTGGGTGATGTATTCAT[A/C]ATGTGTAGTTCCGGGCATGACATCTGCCCTTCCTT
2,553	5	5016	63.29	89810126	F1Dsnp	PHR	T	G	5	11,237,996	+	GGGGCTGAATCAAATTGAATCCGAAGAGGTGCTTC[G/T]AACGAACACCTCCTCAGGCAAAAGAGAGAAAGAGA
2,554	5	5016	63.29	89810127	F1Dsnp	PHR	T	C	5	11,388,025	+	CCCTGTTCAACTGATTCATTCCTTTGAAAGCTGGT[C/T]GAGCCCATTCTGGCATGGCAGATATTTTTACAAGT
2,555	5	5016	63.29	89866084	F1Dsnp	PHR	A	G	5	11,546,499	+	AAGTGGAACTGGCATTATATTCTTAGCTTTGAGGT[A/G]CATCAAATCTCAAAGTTCTTTCTCTGTTTCTTTTC
2,556	5	5016	63.29	89810128	F1Dsnp	PHR	A	G	5	11,563,016	+	CAAGTGGAGTGGCTTCCAATATCAATAGGGAAATT[A/G]TCAGATGTCACTGAATTGGATTTGTCCGAAAACCG
2,557	5	5016	63.29	89866086	F1Dsnp	PHR	A	G	5	11,669,218	+	CGTGATCTCAAGCAAGAGTTATCGGCACTAGGCTT[A/G]TCGGACGACATCTTGGCATCAGAATTTGAGCAGGA
2,558	5	5016	63.29	89832474	snp	PHR	T	C	5	11,672,446	+	CATAATGTAAATGAATTCCGGTACCCTTTCCTTGT[C/T]TTCCTTGAAAAGGTTGAAACCAACAAAGTGTTTTT
2,559	5	5016	63.29	89810130	F1Dsnp	PHR	T	G	5	11,735,137	+	ACCATTCTCTACTCGGTGGTTTTCACACAAATGGC[G/T]TCTCTGTTTGTAGAGCAGGGAGCTGCTATGAAAAC
2,560	5	5016	63.29	89810134	F1Dsnp	PHR	T	C	5	12,040,652	+	CCTTTTTCTTTGCACCCACATTTAGTCCCAAATCC[C/T]CTTCTAAAGGAACCCTCCATAATTATTTCTCAAAG
2,561	5	5016	63.29	89810135	F1Dsnp	PHR	A	C	5	12,074,057	+	TAGCGGATTCAGTCAGCTAGTTACTCTTTATCTGT[A/C]TCGTGTTATCATTCATCCAACTTTTACGTCAAATC
2,562	5	5016	63.29	8_967269	GBS				5	12,168,009		TGCCTGCCACAACAGAGGTAGTTCATCATATRTATGTATAGACTCCGGGCATGAGTGAAAACAA
2,563	5	5016	63.29	89810137	F1Dsnp	PHR	A	C	5	12,273,753	+	CCCACCCGATAGTCCTACGCCTTTCATTTCCTCAT[A/C]ACACGCGTCGACTCCTGATTCCTCCAGCTGTGAAG
2,564	5	5016	63.29	89832604	snp	PHR	T	C	5	12,289,554	+	TATGATGACACTCAGCACATCACTGATGGAAATAT[C/T]GGAAATTTTAATGATATGAATTTAGTTCCTACAAT
2,565	5	5016	63.29	89866091	F1Dsnp	PHR	A	C	5	12,386,019	+	GAAATCATCTTGTATATAATCATCATCAACTTCAC[A/C]AAAAAACTCATTTCCTCTCAAATTGCAAAACCATG
2,566	5	5016	63.29	89866092	F1Dsnp	PHR	A	G	5	12,416,203	+	CTTATGAATAAGAAAACCCTCAGGAAAGCCATGCA[A/G]CCTTTTGAAATCAATAAATGATTCCCATACTTCAT
2,567	5	5016	63.29	89810138	F1Dsnp	PHR	A	G	5	12,516,264	+	TATTTGAAGAAGGAAAGGTTGCTGCATTGGTAGAT[A/G]CTGGTTCTACCACTTTGACAAGGGAAGAAATGCTG
2,568	5	5016	63.29	89866093	F1Dsnp	PHR	A	G	5	12,544,591	+	GTGGGGTGCTGCTGTGAAGTGGGGCTCAGAGTTTA[A/G]GTTCAATTCTTCAGAGGAGTGTTGTCAGGCTTGTA
2,569	5	5016	63.29	89810139	F1Dsnp	PHR	A	G	5	12,552,486	+	CAACTCTCACCATTTCAGGTCATAGTGGACATGAG[A/G]GAGTTCATGAGCAGCCTTCCAAATGTTCTCCACCA
2,570	5	5016	63.29	89866095	F1Dsnp	PHR	T	C	5	12,556,180	+	GGGGTTACTCAGAACAATCCAATCATGAATACAAT[C/T]GAGTTTTGGATATCTCATGAATGCCTCCATTTACC
2,571	5	5016	63.29	TP6466	GBS				6	460,585	460,532	TGCAGGCATGTACTAGGTGAAGCTCTTAGCACTTTGAATGCCAAGGAATTTAAGAACCTAGAAG
2,572	5	5022	65.75	TP6054	GBS				4	4,902,509	4,902,560	TGCAGGACTTCCAAGCATCCCCAGCTGCTGCCTTAGTCGCCACCTTCACCGAAATCAAAACCAC
2,573	5	5022	65.75	TP3512	GBS				4	7,941,490	7,941,527	TGCAGCAGTGGCTTCCGAGCCTTGCTGCGCCTTGTACACCGAGATCGGAAGAGCGGTTCAGCAG
2,574	5	5022	65.75	89810152	F1Dsnp	PHR	T	G	5	13,648,831	+	ATCTCTCCTGACTTGCATCAGCGCTGTGTAAGAGA[G/T]AAGCCATTGACTCTTCACGTCGGGGTCGGGAAGGA
2,575	5	5022	65.75	89866118	F1Dsnp	PHR	T	C	5	13,649,488	+	GGATTTGGCGACTAGAAAAGGGGCCGCAGCGGTAG[C/T]ATACCCTATGTTGGGAAGCTTGACAACTCTGACTC
2,576	5	5022	65.75	89810154	F1Dsnp	PHR	A	C	5	13,776,398	+	AGAAAATGCTGAAGGAAATACCGTTTTCTGGAATT[A/C]TAAGCAACAGGCAATCGTTAAATCCAGGTTTGATT
2,577	5	5022	65.75	TP2759	GBS				5	15,781,098	15,781,152	TGCAGCAAATGCAGCACAAATTGTTACTTTTCTCGGACATTAAGTTAAGTAAATGATGGTATCG
2,578	5	5022	65.75	51_383148	GBS				5	15,897,793		GAGGATCTTCAACTCCATCAATGGTAGGTTCSGTGAAAAAGTGGCAGAAGTCTGACCCCGAGAA
2,579	5	5022	65.75	51_342776	GBS				5	15,938,708		AAGCCTCCACGGACGGCAACAACGCCGTTTCRTTCTCATGGGCCGGTGGCCATTTTCGAGAGGC
2,580	5	5022	65.75	89810278	F1Dsnp	PHR	T	C	5	28,122,500	+	AAGCCAAACAATGGGAAGGAAGAAACCCAAGGACC[C/T]GGAAACCGACGCCGTTTCGGGTCAGCCCGACATCT
2,581	5	5022	65.75	89810279	F1Dsnp	PHR	A	G	5	28,153,196	+	TCCCAGTCCATGTAATAGGAAACTAGAGCCTGAGA[A/G]ACACCAAGAGCGAAAAGAGGCATCTGAGCTCCAGC
2,582	5	5022	65.75	TP8498	GBS				5	28,159,207	28,159,268	TGCAGTCTCACTCTGAGAATTGAATTATGGAGTGATCGGTGGATGGATGAACATGTTTTCTGTT
2,583	5	5022	65.75	89810280	F1Dsnp	PHR	T	C	5	28,336,261	+	CTTTCAGTTTCTTGTTCTTCTTTATCCTCAACAGG[C/T]TGCTTTGCATCTGCATACATACTCACTTGTTCAAG
2,584	5	5022	65.75	89866246	F1Dsnp	PHR	A	C	5	28,395,937	+	TGGCTCGCTTACTTGTCTGGACATTGATCTCAAGC[A/C]TGTCCAAGAATGGAATGATATTATCCCAATCAAAC
2,585	5	5022	65.75	89810284	F1Dsnp	PHR	T	C	5	28,406,582	+	ACAGCAATGGTGAGGAGACGTCAATGAAGGAGTTC[C/T]TCAATGAAATGAGAGCACTAGTAGAGATACGACAC
2,586	5	5022	65.75	89866250	F1Dsnp	PHR	A	G	5	28,428,440	+	CGTATGCAAAGACAAACAGAATTTCTACTTGAATC[A/G]TTTAGACTTCAGCAACGTGCAACAGACACCGCACA
2,587	5	5022	65.75	89866251	F1Dsnp	PHR	T	C	5	28,429,759	+	AGGCCAATAACACCACAGGAAGCCTCAAGCAGAAG[C/T]TTCTTCCAGCAACTGCTTCACCTTTGTAATATAAT
2,588	5	5029	68.24	9_679161	GBS				0	6,670,556	6,670,619	GCAGCGTAGCCTCCTCGTCCTCCGACGAGGCCGTCGTCGCTCTTTCTTCGGTACTGATGATCAG
2,589	5	5029	68.24	89865116	F1Dsnp	PHR	T	C	1	3,354,739	+	TTTCTAGATGATGAGGCAATATTGGCTCCTTTAAC[C/T]GAAGGAAACTTTAACGCATCAGATTCCCGCACACC
2,590	5	5029	68.24	89779768	snp	PHR	A	G	1	3,708,638	+	AGATGAGGCGTTGAAGGACAAACTTATGCAGCTTC[A/G]TAACTCATTTGCCTTGGTTTACCTCAAACAAGCTT
2,591	5	5029	68.24	89809151	F1Dsnp	PHR	A	G	1	3,830,618	+	TTCTTCTCATTCTTCTTTTCACCTCCTTTGTCCTC[A/G]TCTATCTGATTATCATCATCTTGATTTTGCTGTGA
2,592	5	5029	68.24	89809152	F1Dsnp	PHR	A	G	1	3,855,016	+	TTTTCATTTCTATGTTCTGGATCCCATACTAGACC[A/G]ACCCCTGTGTTCTTCACAGTGAAACCAGTTCCAAT
2,593	5	5029	68.24	89809154	F1Dsnp	PHR	A	C	1	3,961,671	+	TCCCAGGTTCGTTTGAAAGAGAGCTCCACCTGATC[A/C]TCATTTTCCACTATAACATCAAATTCTGTACCTTT
2,594	5	5029	68.24	TP8606	GBS				1	5,056,457	5,056,394	TGCAGTGAAAGAGTTTTCAGCAAACAAAATTGACCTGGTGTGTGTCATACTGTCATTGATAGTT
2,595	5	5029	68.24	89865136	F1Dsnp	PHR	T	C	1	5,088,584	+	CTCTAGTTGTACTCTTCCAAGCTTTTCTCTGCGGA[C/T]TATTTGGGTACTAATTCATGACTTAGTAATCTAGG
2,596	5	5029	68.24	102_182420	GBS				3	11,688,342		GACAAGAAGCAAAGCAAATCAGAAAATAATAAACGGAACAACAAACCTTCTGTTGGGAGCTCCC
2,597	5	5029	68.24	89809510	F1Dsnp	PHR	A	G	3	11,688,399	+	CTTATGACAGTGTTCCAGTGATTCTTGATTTCAGT[A/G]TCTGTTCTCCCTGGAAGTCTCCTTGAAATGAGAGA
2,598	5	5029	68.24	TP2386	GBS				3	11,688,443	11,688,380	TGCAGATGGTCTCTCATTGCAGGGAGACTTCCAGGGAGAACAGACACTGAAATCAAGAATCACT
2,599	5	5029	68.24	89865473	F1Dsnp	PHR	T	C	3	11,701,753	+	CCTGGGCTGTTCAGATCTGAAATTACAGAAGGTCT[C/T]ATGCAAAAAGATTGGCTACACAATGTGGCTATGAG
2,600	5	5029	68.24	89809511	F1Dsnp	PHR	T	G	3	11,713,970	+	GACATTGTGGTACTGGACATTTTAGATTCTGTTTG[G/T]CACTGTGTTCTCAATAATGAAAACAGTCGATGGAA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,601	5	5029	68.24	89865474	F1Dsnp	PHR	A	G	3	11,771,153	+	CACCCTGACTAATTTCTAGACCGTGTATAGGGTAT[A/G]CTACATGATGGGAAGGAAATAGCTGTAAAAAGACT
2,602	5	5029	68.24	89809512	F1Dsnp	PHR	A	C	3	11,896,226	+	TACACACCTCCAAGGCGATTAAGGACGGATGAAAT[A/C]CCACATATTGTCAATGACTTTAGACTTGCTGCAAG
2,603	5	5029	68.24	89810334	F1Dsnp	PHR	T	G	5	5,995,727	+	TTTGCATCACTTGTAGAGGAAGTGGGGCAGACAAT[G/T]AAAGAGGACAACTATTTGGTACAAGCTATACTAAT
2,604	5	5029	68.24	89866301	F1Dsnp	PHR	A	G	5	5,995,733	+	TCACTTGTAGAGGAAGTGGGGCAGACAATTAAAGA[A/G]GACAACTATTTGGTACAAGCTATACTAATAACTGG
2,605	5	5029	68.24	89810336	F1Dsnp	PHR	T	C	5	6,212,820	+	GAGTCGGGAGTGACTACTGTCATTTCCCTCAATTC[C/T]TCAGCACTTGGAATCTCAGGAATTTCCAGAAAATT
2,606	5	5029	68.24	TP1535	GBS				5	13,629,845	13,629,782	TGCAGAGATGTCGCTTTCTTGGTTGATAATGGGTGATTTCAATGAAATTTTAGAAAGGGCAGAA
2,607	5	5029	68.24	89810159	F1Dsnp	PHR	T	C	5	14,290,584	+	GGCAGCATGAAATTTAAAAGCGAGAAGATTAGACA[C/T]CAAATGATTTGTTAGCCTTATAGGTTATAACTGCT
2,608	5	5029	68.24	198_32979	GBS				5	14,302,846		AAGTATTTTTGAACAGTAAATGAATTGCATGYCTCTGTATTTCCTGTGTCCGGAAGCTGGAGAC
2,609	5	5029	68.24	89866121	F1Dsnp	PHR	A	G	5	14,331,391	+	AAGGCAGATGCTGCTAAGGCTGATATCTTTTACTT[A/G]CTGTCTGGTATATGGAGAACATCAGTAGAACGGTA
2,610	5	5029	68.24	89866128	F1Dsnp	PHR	A	G	5	15,012,924	+	TGCTAGAGCCTCTTCCAGCTACTCCACCTCCTTCT[A/G]TTACTCCCCCGCCAAGTTCTATTTCAGGTTATTAC
2,611	5	5029	68.24	89810166	F1Dsnp	PHR	A	G	5	15,123,117	+	CACGAAGCGTCAGCCTTAAGCACAGTCTTGAGTCC[A/G]GTGCAGCAACTCGCTTCCGGCTTCTCTGTCTTGCT
2,612	5	5029	68.24	89810167	F1Dsnp	PHR	A	G	5	15,151,750	+	GCAGCTTTCTCGCTCTCGTCGCCGAATCGGAAGAC[A/G]ACGCTGCCGTCCAAGCACTCTGAATCACAAATCCA
2,613	5	5029	68.24	89810168	F1Dsnp	PHR	A	G	5	15,190,384	+	GCTACTTGCTTTTTTGTTCGCAGACATCGCATAAG[A/G]CGAGAAAGGCCTCAAGCTTCTCGGGTCCGAGAATT
2,614	5	5029	68.24	89866134	F1Dsnp	PHR	T	G	5	15,305,502	+	GCATCTGAGACTAGCAATTTGCCTGGCTTTAGGGA[G/T]TCCATTGATGTACAAAAGAGCAAGTTCCAAGCTCT
2,615	5	5029	68.24	89810169	F1Dsnp	PHR	T	G	5	15,305,533	+	GGGATTCCATTGATGTACAAAAGAGCAAGTTCCAA[G/T]CTCTTGGTCTCAACACTCAAGATCTTGTCACGCTT
2,616	5	5029	68.24	89848911	SnpSnp	PHR	T	G	5	15,344,434	+	CGACAGCCAGATGATGTGACCCGATTAGCCCTATC[G/T]TGTGAGGGACACATCCGGTATTTCAGCCCAGGAAA
2,617	5	5029	68.24	89810170	F1Dsnp	PHR	A	C	5	15,349,232	+	GTAGTGTGCTCTTTCCACATGCCTAATGGAATGTT[A/C]ACTGCCATACCCAAGGCTGCAATAACAAGCATTTT
2,618	5	5029	68.24	89810171	F1Dsnp	PHR	A	G	5	15,503,984	+	AAGAAAATTACTATTCTGGTCCGTGTGGCTTTCTC[A/G]GGAGATATCAAGATGTCACAAAATTCTCGTATTAG
2,619	5	5029	68.24	89866135	F1Dsnp	PHR	T	C	5	15,524,424	+	AATGATTTTTGAATGCAGAAATGATTTGCAGTCCT[C/T]CTGAAAAGACTGAACACGACATGGATATAGGAGGT
2,620	5	5029	68.24	89810172	F1Dsnp	PHR	T	C	5	15,605,923	+	CACCACGAGATGCATCCTTCAGTATCTTCTGGATC[C/T]ACATGTGCCACCAAGCTTAGTGTTTCACCCTGCTC
2,621	5	5029	68.24	89810173	F1Dsnp	PHR	T	C	5	15,619,668	+	CTAGCCTTGCTTGGTAAGTCATCTGCACCAAACGA[C/T]TAAGAGCATACCTTCCCAGAGAAGCCTTATCAAAT
2,622	5	5029	68.24	89810174	F1Dsnp	PHR	A	G	5	15,654,712	+	GCCTCCATAGCCATGGGGTCAATCTTCTGCCTTCC[A/G]GCTGGTTCATTCAAAAACATATGGATCTTCCCACC
2,623	5	5029	68.24	89866136	F1Dsnp	PHR	T	C	5	15,773,710	+	ATCTTTGGGGTAGAAGATTCACTAAATGATTTTTC[C/T]ATAACAAAATTGTTTCCAACAGGTCTTCAGCTGCT
2,624	5	5029	68.24	89866141	F1Dsnp	PHR	A	G	5	15,936,664	+	CTCTTACCACAACATCTTGAAGCATCAACTGGTTC[A/G]CACTAGATATGCTTGCATGATGGATTTTCAGTTCA
2,625	5	5029	68.24	89866142	F1Dsnp	PHR	T	G	5	15,938,523	+	GTTGAACAGTCCGACGTCCATGTCCATATCTTCAT[G/T]GAACAAAGCTTCCAGTTCTTTGTTGATCCTCTTCT
2,626	5	5029	68.24	89866143	F1Dsnp	PHR	T	C	5	15,983,662	+	TCGAAACCATCCATTTCAACCAGTAATTGATGCAG[C/T]GTCTTCTTCGTGTGGCCTTCCCATTGTTTCCGAGT
2,627	5	5029	68.24	89866144	F1Dsnp	PHR	A	G	5	15,988,977	+	CTCCGGTCGCAATGCGCAGGGAATCGACGTGTTCC[A/G]GCCGCTGAATCTCAAGTTTCTTGATGAGGAGACAT
2,628	5	5029	68.24	89866145	F1Dsnp	PHR	A	G	5	16,006,026	+	GCTCGAGAAACTTCAAACTGAGAGAGATGCCCAAG[A/G]AGAAGAATCTCCAGCATCTAAAGGTCCCCTCTACA
2,629	5	5029	68.24	89866147	F1Dsnp	PHR	A	G	5	16,091,252	+	ATTTTCCACCGGTTCATCATCTCTATTCTCTCTCC[A/G]GAGTTTCATAGCTTTGATCTCCTCTCTAGCATTGA
2,630	5	5029	68.24	89810176	F1Dsnp	PHR	T	C	5	16,123,712	+	AAGAAAGAGGTGAAGATTGAAGGGAAGATGGTTTC[C/T]GACGGAATTGATGCGTCCCAGGGACAAGTTGATGA
2,631	5	5029	68.24	89866148	F1Dsnp	PHR	T	G	5	16,306,083	+	AAGAAAATTATTGATCACCTCCAAGGTCTGAAATA[G/T]TTCTGGCCATGAGACTGGCAACCCTTTCACATTGC
2,632	5	5029	68.24	89810178	F1Dsnp	PHR	A	C	5	16,517,716	+	GTAAAGGTTCACAACTTCAACTGGGAAAACATTTA[A/C]AGGAGTGCTTTGCAAATCCAACACATTAAGCAGCG
2,633	5	5029	68.24	89810179	F1Dsnp	PHR	A	C	5	16,551,406	+	GCTTATTTGTGGATTGCTTGAACACATTTTCAGTT[A/C]CTGGGAAATCGAGCGTGATTGAGATTCAGTATCCT
2,634	5	5029	68.24	89866150	F1Dsnp	PHR	A	C	5	16,564,764	+	CAGAAGGGAACAGGAGATTGTAGCAGCAAACATCG[A/C]GGATGTGGAGATTAGAGAAAATGGAGATGAAACTT
2,635	5	5029	68.24	54_180590	GBS				5	16,575,439		CCAAGACTACTCTTCCCRAGTAACCGAAGTTKTCAATCAAATGAGAACCCTTGGAGAAGACTTR
2,636	5	5029	68.24	89810180	F1Dsnp	PHR	T	G	5	16,652,509	+	CCTGTAAGTGCACGTCTATCTCCAACATCTTTAAT[G/T]CCATAAGGACCAAGCACTATTTCCTTATTAAACCC
2,637	5	5029	68.24	89866151	F1Dsnp	PHR	T	C	5	16,669,679	+	CTTGGTGGAAGATTTGATCGATCTCTGTGGCAAGC[C/T]TATGTTTCTGTCAACAAGATATTTGCAGATAAAGT
2,638	5	5029	68.24	89810181	F1Dsnp	PHR	A	G	5	16,670,798	+	CTGCAGGATCTTGAAAGGGCATGTAAAGATCATAT[A/G]AGGAGGAGATGCTGGGGAATTGGTTTTGGTTTAGG
2,639	5	5029	68.24	TP969	GBS				5	16,746,460	16,746,522	TGCAGACAAGGCAAGTCGTCCAATCTCAGATTGGAGGAGCTTCAGATCTGCAAGGATTCGAGCG
2,640	5	5029	68.24	89810183	F1Dsnp	PHR	T	C	5	16,954,526	+	CTTACAACCTCCATATAATGAATCCTATGGTTTTG[C/T]ATTGAGTGATGTCACCGGTGAATATAAAATAGTCC
2,641	5	5029	68.24	122_211855	GBS				5	17,239,912		GGGAAACAGATTGGCTACCATTTTCAACAATGTTGACATTATCAGAATCTTCAGCCCGGTCGAT
2,642	5	5029	68.24	TP1040	GBS				5	18,101,217	18,101,280	TGCAGACATCAGGTCGTGGTACAAGCAATGTACTGAATGAGAACGGGGGTGAGAGTCGGGGTTT
2,643	5	5029	68.24	89866155	F1Dsnp	PHR	T	C	5	18,104,194	+	ATTAGTCTTACCCCTCAACCGCTATCTAGTCAGAC[C/T]GTCATGTCTACAGTATCTGCAATTCAAAATCAGAC
2,644	5	5029	68.24	89866156	F1Dsnp	PHR	T	C	5	18,331,576	+	GGTGTGGTCATAGGATTGGTAACAAGCGCCCACAT[C/T]AATCGTCATTTGGGTGCACAAACCGAGACTTATTC
2,645	5	5029	68.24	89866157	F1Dsnp	PHR	T	C	5	18,331,696	+	CCACCACCACTGGAGCCTAATTATTGTCCAGCAGT[C/T]GTGCAAAATTGCGAGAAGGTTGATTGTTTGAGCAT
2,646	5	5029	68.24	89810187	F1Dsnp	PHR	T	G	5	18,401,464	+	TCATGACTTTCAGGAAAGATTCAGTAAACAAATAC[G/T]ATCATATACTGAACTTGAGGTAAAAGCATATATAT
2,647	5	5029	68.24	89810188	F1Dsnp	PHR	T	G	5	18,504,864	+	ACTTATCATTCTGCTTTGCTCTAAGATGGGCAGTT[G/T]CAGGACAGGTCAAAGCTATGATGATCTCTGGATAT
2,648	5	5029	68.24	89810189	F1Dsnp	PHR	T	C	5	18,547,980	+	GAGGTGAAAAGGAAAATAATAGGAAAAGAGTTCAT[C/T]TGCATTTTTGATGCTTTTGCACATGAACTTGAGAA
2,649	5	5029	68.24	89810190	F1Dsnp	PHR	T	C	5	18,549,516	+	ACAGAACGAAAACAAGAAACACTAAATCACAAAGT[C/T]GACTTGCCATGTCTGACAGACCCATCAAAACTGAG
2,650	5	5029	68.24	89866159	F1Dsnp	PHR	A	C	5	18,551,670	+	AAAGGTACTGAGGTTCATACCTTTGACTTATGTCG[A/C]TTAGCAGCAACAAGTTGGGAAACTTTACTTGCACT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,651	5	5029	68.24	89810192	F1Dsnp	PHR	A	G	5	18,551,875	+	TATAAGAGCAAGGACATACCCATTTAATGGCTTCA[A/G]ATGTTTCTGGGGTCTATCAGTTCTTGGAGTGATGG
2,652	5	5029	68.24	89810194	F1Dsnp	PHR	T	C	5	18,632,154	+	CTCGAATTACGTCATGCATCTTCACAAATCCACAG[C/T]ATGCACTGTCCAAAAGCAAGCTAGAAGCTTTCAGG
2,653	5	5029	68.24	89866160	F1Dsnp	PHR	A	G	5	18,633,752	+	CAGAAAAACATCATTCTTCCTGCGAGGAACTGATG[A/G]TTCAGCTGATGAAGTCTGAGATGCAGAGGCTCTTT
2,654	5	5029	68.24	89810195	F1Dsnp	PHR	A	G	5	18,649,837	+	GAAAGCTCAAATATAACATGATTAGTTACCTCATC[A/G]AGTGTTGAAAAGGTGCATTGCTGGGACTTGTAAAA
2,655	5	5029	68.24	89810196	F1Dsnp	PHR	A	G	5	18,659,737	+	GACTGGGGCAGTGAAGCATTTTGTGCCTGATATGG[A/G]CCTTAAATACATTGCAGAAGGGAATCATTTTGTGC
2,656	5	5029	68.24	89866161	F1Dsnp	PHR	A	C	5	18,663,910	+	AACAGTGGATTGTGGTTATACGATCCAAAAGTCTC[A/C]GCTCCAACACTGCTAATCCAGGGTGAGAAAGACTA
2,657	5	5029	68.24	89866162	F1Dsnp	PHR	A	C	5	18,664,099	+	CCTGAGAAAATTAATGAGCTAATCCTCACTTTCCT[A/C]GCCAAACATGGCATCTGATTCAACGTTTCTCCATG
2,658	5	5029	68.24	89866163	F1Dsnp	PHR	T	C	5	18,672,674	+	GCTAAAGACGTTAACCAGTTCCTTGGAAGGTGGCG[C/T]GTCAAATGTTCATCAACAATTGCAAGACGAGGTGA
2,659	5	5029	68.24	89810198	F1Dsnp	PHR	T	C	5	18,673,542	+	CAGATAAGCTAGGAAGGGAATCTTCTCATCAGCCA[C/T]AGAATCATCATCAAACGATAAATCTAAAGAACTGC
2,660	5	5029	68.24	105_98324	GBS				5	18,673,846		CTGGGGATCAGCCTATTTGTGCTCGAACTGCTTGGGCATATGGAAATGCCGGTGGTCGAATCTC
2,661	5	5029	68.24	89866164	F1Dsnp	PHR	A	G	5	18,765,426	+	TCTTGACTTCGGCAGCTTGATGACCATCTCCGCCC[A/G]TCTAATCTACTCAAAGCTTCCAAATCAAGCTCCCC
2,662	5	5029	68.24	89810199	F1Dsnp	PHR	T	G	5	18,791,951	+	GAAATGTAGGTTTCAGAGAATGTAAACGAGGTTAT[G/T]GGAGTAAGTGGAGTTGGGCAGGCTACTCTCCAGGG
2,663	5	5029	68.24	89810200	F1Dsnp	PHR	T	C	5	18,792,634	+	CCGCTTGTTTTTGATAGGATTCAGGAATTCTCTTC[C/T]AGTATTTGCAGGTCAAGAAGAGCAGATGATGTTCA
2,664	5	5029	68.24	89810203	F1Dsnp	PHR	A	G	5	19,101,619	+	GATGGAAATTGTACATGGGCAGTCCCTGACTTTAC[A/G]GGCTGTGGTGCTGGTATGTCACTTTGCAAACAAAT
2,665	5	5029	68.24	89810204	F1Dsnp	PHR	A	G	5	19,202,177	+	CGGAGACGATGGTGAAGGAGACGGAATATTACGAC[A/G]TCCTCGGAGTAAAGCCCACCGCCACCGAAGCCGAG
2,666	5	5029	68.24	89810206	F1Dsnp	PHR	A	G	5	19,266,389	+	GGATACCTCCTAATAGATGTGGTGACAGGGTGGAG[A/G]AGGTCACAGTATTACCTCATGAAAATGTAAGTTAC
2,667	5	5029	68.24	89810208	F1Dsnp	PHR	A	C	5	19,533,882	+	CTCACTGATAGAATCCTCTTTCTTCTCCAATTCTG[A/C]TTTCTCAGCCTTCAAAATAAAATCATAGTACTCTT
2,668	5	5029	68.24	89810209	F1Dsnp	PHR	A	G	5	19,538,184	+	GGAGATTATATGGCCCTGGCAGCAGATCATTACAT[A/G]TTTGTGCTCCTAACCTGAAGTATTTGAAGTGGAAA
2,669	5	5029	68.24	89866171	F1Dsnp	PHR	A	C	5	19,621,579	+	TACCGCCATTGAAAGTGAAGCATATGCCATTCCAG[A/C]AGTATAACAAACATCAGCAGCTCCAAATGGACTCC
2,670	5	5029	68.24	89866173	F1Dsnp	PHR	A	G	5	19,881,316	+	TAGATCCTACAGCATATCTTCGTAGCCTAGTAGTC[A/G]AATCAGTATTTAGACTGGCACGTATGCCCTGCAAC
2,671	5	5029	68.24	89810212	F1Dsnp	PHR	A	G	5	19,926,961	+	TTCTTGTTTGCAAACTCCGACATGATGGTGGCCGA[A/G]AGAGGGTAGTCTCCGCCGATGCCGACACCGAGAAG
2,672	5	5029	68.24	89810214	F1Dsnp	PHR	T	C	5	20,243,452	+	ATTTTATCAAAAATCTCCTGAGCCTTCCTCACATT[C/T]TTGGATTTGCATAAAGCACTAAGCAGGTCATTGAA
2,673	5	5029	68.24	89810217	F1Dsnp	PHR	T	G	5	20,495,526	+	TATTTTTTGTGCGCATGCAGAATGCCTTTGAGATG[G/T]CAACATTTCTCTGGTCCTTGGTAAGACACTATATT
2,674	5	5029	68.24	89866176	F1Dsnp	PHR	T	C	5	20,520,805	+	GGCTCTGGAAATCTATGATGGTATCTGTCCTTTTG[C/T]GCAGGTTCCCATGAAGCATGTACTGATGTGGGTAA
2,675	5	5029	68.24	89810218	F1Dsnp	PHR	A	G	5	20,521,159	+	ACTGCTAGGGTTTTGGGTTTTACTGGCTCTTCTTC[A/G]AGAAACCCTAGTGGCAATTTTGCTTTTGCTGCTCG
2,676	5	5029	68.24	89810219	F1Dsnp	PHR	T	C	5	20,521,588	+	TGAAGCTCTAGCTTATTTGAAGAGACAAAGGATGA[C/T]ATGCCTGTGACTTACAAAAGGAAGCTTGGTCGCTC
2,677	5	5029	68.24	89810220	F1Dsnp	PHR	A	G	5	20,525,368	+	CTCGATGCTCAGAAGGCTAACATTGCCGCCGGTAA[A/G]GCCGTCGGCAAAATCCTCCGCACCTCGCTCGGACC
2,678	5	5029	68.24	TP6764	GBS				5	20,529,225	20,529,162	TGCAGGCTTCCCTCCATCTCCTTGCTTTGAATTTACCATTATTACCAAACAAACCCATATACTG
2,679	5	5029	68.24	TP2349	GBS				5	20,561,987	20,562,046	TGCAGATGCGGACCCAGAAGATCCAAGAAGTATAGCAGAGGCACTTATGCTGTCAAGAGAAGGT
2,680	5	5029	68.24	89810221	F1Dsnp	PHR	A	G	5	20,620,385	+	ATGTGCAGCCTTATTCATGCACATCAGCCAATTTC[A/G]CAGTGTACACCGGATTGTTATTGCCAGGTGATAGA
2,681	5	5029	68.24	89834074	snp	PHR	A	G	5	20,625,015	+	GCAAGAACTACGAGAAGGTATGTGAAATGTGTCAC[A/G]TTACTGTCAACAAGATCACCATTTTTGGTGATAAT
2,682	5	5029	68.24	89866177	F1Dsnp	PHR	T	C	5	20,629,344	+	CTCAAGCAAATATAGGCCAGAATTTGATCCTTCAA[C/T]CTTGGAGGCAAGCGATTGCGGCTAACAAAGTTTGA
2,683	5	5029	68.24	89810222	F1Dsnp	PHR	T	C	5	20,737,408	+	CAACGAGCAGAAGCTGTTAGAATTTTACAAGATTG[C/T]TCTTATCAGTAACAAGCGACCGTGTTGATTACATT
2,684	5	5029	68.24	89866178	F1Dsnp	PHR	A	G	5	20,839,906	+	ACCCTTCACTCAATCCAAGCAAATTGGCCCCCACA[A/G]TGATCTGGTTAGCAATTTTACAACTCTGCCCGGAC
2,685	5	5029	68.24	89866179	F1Dsnp	PHR	T	C	5	20,877,875	+	ACACCTGCTGGATCTATTGTCCGGAGTGCCTTGAT[C/T]GTTGAAACATATTGATGCAAAATGTCATTTGTTGA
2,686	5	5029	68.24	TP7442	GBS				5	20,877,920	20,877,861	TGCAGGTGCCTCAACAAATGACATTTTGCATCAATATGTTTCAACAATCAAGGCACTCCGAGAT
2,687	5	5029	68.24	89866180	F1Dsnp	PHR	A	C	5	20,877,970	+	TTGTAGTGCCGAAATAAATGACTCCACAAGCTTAG[A/C]ATGTTGACCAGTGTACTCAAGACACTGTTTCAAAT
2,688	5	5029	68.24	89866181	F1Dsnp	PHR	A	C	5	20,882,273	+	ATTTGACGGTCCCTGCCCTTCTTTTTCCTTCTCTA[A/C]GGGTTCCATACATGCAGAAATTCCATGGTCTTGTA
2,689	5	5029	68.24	89866182	F1Dsnp	PHR	T	C	5	20,882,441	+	AGGAACTAATGATTTGAAGCCACAATAATCCATCT[C/T]ACAATCTTTGAACACATGAATCTCTGCAATAAAAA
2,690	5	5029	68.24	89866183	F1Dsnp	PHR	A	C	5	20,994,658	+	GGGCGATGTCGGAGCTTTTCAAGCATCCAAGTGTT[A/C]TGAAGAAATTACAAAATGAGGTTAGAGGAATAGTC
2,691	5	5029	68.24	89810223	F1Dsnp	PHR	A	C	5	21,559,223	+	TTCTTACGACATTGGTTGTGACGGTTGGAGCTGTG[A/C]GAAAAACTGTTTCCCGTCTCCTTATCCTCACTGTT
2,692	5	5029	68.24	89866186	F1Dsnp	PHR	A	G	5	21,616,998	+	ACATCACATTAATTCTTGCACCGCCTCTAGCTTGA[A/G]CCATTTTTGAGTAGAGATTTAAAACAGATAAGAAA
2,693	5	5029	68.24	89866193	F1Dsnp	PHR	A	G	5	22,078,598	+	CTTCTTCCAATATCAATTTCTTTAGAAACCTCTCA[A/G]CTTAACCAGATTTGCATGGTGGATGCTTCCGATTG
2,694	5	5029	68.24	89866195	F1Dsnp	PHR	A	G	5	22,554,483	+	ACTCGTTCTGCTCCTTCACCGGAATTACCTGCAAC[A/G]GCGTCAATTCCGTCCTAGAAATCGATCTATCCAAC
2,695	5	5029	68.24	89810231	F1Dsnp	PHR	T	C	5	22,612,024	+	ATGAATTAAGCAAGGACCTCAAGACCATTTTGTGG[C/T]TTGCCTTGTCCTGAAACTTTGTCATTTGCTGCAAC
2,696	5	5029	68.24	89810232	F1Dsnp	PHR	T	C	5	22,841,732	+	ATCTTGTTGCATATTCCCCCATTGATTACTATTCA[C/T]CCCCTCATCGTCGAAGTCATTAGAGAACATCATGG
2,697	5	5029	68.24	89866200	F1Dsnp	PHR	A	G	5	23,361,607	+	CTAGGTTTTCCACTGTAGTAAAATCCAGTCAAATC[A/G]AGTGCTTCACTTGCCACAGCACCCAGAACAGCTAA
2,698	5	5029	68.24	TP575	GBS				5	23,365,176	23,365,209	TGCAGAAGATTCTTGATCTCTTGCGGAGAATACACAACCGAGATCGGAAGAGCGGTTCAGCAGG
2,699	5	5029	68.24	89810234	F1Dsnp	PHR	T	C	5	23,409,805	+	GATGTATATATAGGCTCACGGCCATGGCAACTAGA[C/T]CGAAGAATATGAGTTCTTGGGATGCTGGTTCTGTT
2,700	5	5029	68.24	89891822	snp	PHR	T	C	5	23,582,633	+	ATTCCTGATGGTTTCATATATCTTAGAGCAAGTCC[C/T]GATACTTGTCACAAAAGAATGATGAAACGCCACAG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,701	5	5029	68.24	89866203	F1Dsnp	PHR	T	G	5	23,727,735	+	TTGAAAGATTACAGTGTACCTTATCTATTTCAAGA[G/T]GACTACTTTGATGTTTTGGACAAAGATAAGCGACC
2,702	5	5029	68.24	89810236	F1Dsnp	PHR	A	G	5	23,746,170	+	TTCGAACATTTGAAGATGAAGTTTTGAAGAAGTTA[A/G]CAAAGGCTGGGCAGCAGCAAAAACTTGATAAACAA
2,703	5	5029	68.24	89866205	F1Dsnp	PHR	T	C	5	23,852,407	+	CTGGAGTCTTTCCAAAATGACCGTTTATCAAGTTC[C/T]GGAATTACAAGAGTGGCATTTATGATACGGGCTAC
2,704	5	5029	68.24	TP7973	GBS				5	23,985,009	23,984,946	TGCAGTAGATGTCAGAGCTCAGAAAATCAGATCCACACTAAATCTTTCTTCACCTTTTCAAATA
2,705	5	5029	68.24	89866206	F1Dsnp	PHR	T	C	5	24,069,343	+	CATCTTAAATATGTTGATCTCAGCTTGAATGAACT[C/T]TTTGATACCATCCCAGCTCAGATAAGTTCCCTCTC
2,706	5	5029	68.24	89866207	F1Dsnp	PHR	T	C	5	24,077,503	+	TAACAACATTGTGAATAGTATAGCTGACCTTTCAA[C/T]TTGAGTAACGGGTACCATTTGTTCTTCGTAAAGGG
2,707	5	5029	68.24	89810239	F1Dsnp	PHR	A	G	5	24,132,096	+	TGGAAGTGTTCGTGGAGGGAAGAATGGTATTGATC[A/G]GTTTGAAGGAAGTTCGCGGTCGAACCGGTGGGGTT
2,708	5	5029	68.24	297_103313	GBS				5	24,135,834		GGTACGGGTTAAAGAAATGGAAGAAAGGGTGRAGAGACTGAGCCTGTCCGAGTTGACTCGGGTG
2,709	5	5029	68.24	89866208	F1Dsnp	PHR	A	G	5	24,215,727	+	TCCAGGTGTGGAACTAGAATCACAAGAAGATGACG[A/G]TAAATCAAATGGTTCTGATAAAGATTCTCGTCGTC
2,710	5	5029	68.24	89866209	F1Dsnp	PHR	A	G	5	24,238,350	+	TTCTGAGTCCTGCAAGTATTTTTGATTCGGAAGGG[A/G]TAGAAAAATCTCAAGATGATAACATCAATGAAGAG
2,711	5	5029	68.24	89810241	F1Dsnp	CRBT	A	C	5	24,239,218	+	AATTGAACAGTCTCCCAATATTTTCCAAAATTTAA[A/C]CAGCACAATTGATGATGATCCAGCTGAGGGATTGA
2,712	5	5029	68.24	89866210	F1Dsnp	PHR	T	C	5	24,239,591	+	GGAGTTTATGAAGATGACAAAGAATATTTGAGCCT[C/T]GAAGAACCTTCTCCTGGTGAAATGGAGCCTTCAAC
2,713	5	5029	68.24	89810242	F1Dsnp	PHR	A	G	5	24,239,670	+	AAAGTGCCTCTGTGACTGTTGATGATGATGATCCA[A/G]ACGTGCTACAATTTCATAACAATGAGTACGACGAA
2,714	5	5029	68.24	89866211	F1Dsnp	PHR	T	C	5	24,245,256	+	CCATCACTACCCACCGCCAACCTGGGCTACTCCTC[C/T]AGCTTCACCACCATCAGTTCCAGCACTGCCACCGC
2,715	5	5029	68.24	89810246	F1Dsnp	PHR	A	G	5	24,357,193	+	CTTAAGGCAGTGAACCCATCAACGAGCAAAGTCAA[A/G]GCAGCTGAGAAATACATCCAGGTCATCTCTGTGGA
2,716	5	5029	68.24	89866214	F1Dsnp	PHR	T	C	5	24,490,298	+	ATATTATCCACTGAAGAAGGAACTTTATGGTGGCA[C/T]GCTCATAGTGAATGGACAAGAGCCACGGTTCATGG
2,717	5	5029	68.24	89866215	F1Dsnp	PHR	T	G	5	24,637,720	+	TCATCGACGTTGGCGGTAGCGGCACCAACTGGTTT[G/T]CCAAGAATTACCCGACTCGCAACAAGAATTTCGAG
2,718	5	5029	68.24	89810247	F1Dsnp	PHR	T	C	5	24,648,030	+	CTGGAGCCCATGACAAGTAAATCAGCATGCAAATT[C/T]TCAACAGCTTCACAAATCTTCTCTTTCGGATCCCC
2,719	5	5029	68.24	89866216	F1Dsnp	PHR	A	C	5	24,665,860	+	TGATCCAAATGTTGATGGGGAAAGTGATGAAGGCC[A/C]GAAGGTGACCAAGAAAAATCTTGAATCTAATGCTG
2,720	5	5029	68.24	89810248	F1Dsnp	PHR	A	C	5	24,711,732	+	CACTTGATCTATTTTCTTTGGCCTTCTTCAGCAAC[A/C]CATCTTGCTTTATGGGTTTACCATTTGCTTTATCC
2,721	5	5029	68.24	89866217	F1Dsnp	PHR	T	C	5	24,765,883	+	GGTATAAAAACAGATCTACACAAGAAAACATTACA[C/T]CTGGAAGATACTGGACCTATTGGGCCACGAACACG
2,722	5	5029	68.24	89810250	F1Dsnp	PHR	T	C	5	24,969,903	+	GAAAGCAAGAGAAGAGATGGATCGAGCAGTTGGAA[C/T]AGAAAGATTAGTCGGAGAGTGGGATCTTCCAAATC
2,723	5	5029	68.24	198_313481	GBS				5	26,230,934		ATCCAGGGTTAATTTTATATGGATTAAATATTTTCATTGAAATGTCGCCCAACAGCGAAAGAAA
2,724	5	5029	68.24	89866227	F1Dsnp	PHR	A	G	5	26,256,283	+	GGCGAGAAGTACCATGTCTCAATCTCATATCTTCC[A/G]AGTTCTATAGTCGCTATATTTTTCACTTTAGTAAA
2,725	5	5029	68.24	54_13316	GBS				5	26,289,710		GTATTGAGCTCGGGCATTGTCTTGTAAACAAGGCAAAGATAACCACTTCACAGCTTCCTCTAAA
2,726	5	5029	68.24	89810258	F1Dsnp	PHR	T	G	5	26,349,379	+	CTCCTTTGTTCCTCTTATGATAAGGGATGCCGCCC[G/T]TATATGTGTGCTACTGACCATCGCTATTCCAACTG
2,727	5	5029	68.24	TP5622	GBS				5	26,350,012	26,350,062	TGCAGCTTCTATTTCTTCTGTTGCACATCGACGCAGTTTCCCAAGAAACCGAGATCGGAAGAGC
2,728	5	5029	68.24	89810259	F1Dsnp	PHR	A	G	5	26,352,692	+	TCGCAGTCTGAGGAGGCTTTCTGGAGATTTTCTTG[A/G]GATTAATCTTCTTAAAGGGATGATGTGAGAGGGAA
2,729	5	5029	68.24	TP3741	GBS				5	26,353,593	26,353,530	TGCAGCATTTGTTTGTGTTTATTGAAAGAAAGAAAATGGAAAGAGGTTTGAAATGTTTTGCTCA
2,730	5	5029	68.24	54_85619	GBS				5	26,377,214		CGCTCTTTGATGGGTCGCCTTTCTCTTATCCYGATCTCTCTCAAGTCTGAGTTTATAGAGAGAT
2,731	5	5029	68.24	89866231	F1Dsnp	PHR	A	G	5	26,453,173	+	TGGCTCTCAAAAGGAAGAATCACAAGGCGGCAAAG[A/G]GCACCATGACCTTTCAAAGCATTAAAGAAACGATC
2,732	5	5029	68.24	89810263	F1Dsnp	PHR	A	G	5	26,482,550	+	CCCGACCGAGTGTACATTTCTCAACCAGCTGCTCC[A/G]GGGTAAAAATCTTATTCTCAGTGCCATCACCCCAA
2,733	5	5029	68.24	89810264	F1Dsnp	PHR	A	C	5	26,485,708	+	CTTGATATATATCCTTTGACATTGCAGATTAGAGG[A/C]GATCTACATATCTGTTTGATGGGTGATCCTGGAGT
2,734	5	5029	68.24	89866232	F1Dsnp	PHR	T	G	5	26,603,120	+	TCCAAAGAATTTGGATCCCTTTCAGAACCATCCAT[G/T]GCTTCCTTGTCATCTTTGTTCCTGCTCTTATAATT
2,735	5	5029	68.24	89810266	F1Dsnp	PHR	A	G	5	26,647,842	+	GTGGATGTCTTGAAACGCTTCCACCATGCTAGAAA[A/G]CCTGCATTTCGGTTTTTCTGTTGGGCTGGGGAGAA
2,736	5	5029	68.24	TP4085	GBS				5	26,654,740	26,654,677	TGCAGCCCTGCTGGTGAACTGTCCTGCTGTATTTTCCTATTCCTTGTAGGGGTGTGGTGTAACC
2,737	5	5029	68.24	TP3766	GBS				5	26,711,385	26,711,448	TGCAGCCAACAATATTCCAGTGTCGAGTTTTATCCATAGCCTGCAAGTTCAAAACCTAGACAAG
2,738	5	5029	68.24	89866236	F1Dsnp	PHR	T	C	5	26,711,439	+	GTGTCGAGTTTTATCCATAGCCTGCAAGTTCAAAA[C/T]CTAGACAAGTAAAATATGAACTATATTAGATACTC
2,739	5	5029	68.24	46_584136	GBS				5	27,114,535		AGGGAAATGGCTTTCCCCTTGCAGCAGGTAAYCATCCGTAAGGAAGTGTGGATTTCCTGGCCCA
2,740	5	5029	68.24	89866239	F1Dsnp	PHR	T	G	5	27,146,812	+	AGGGAACCTAAAATCTCTTTTGGCTCTAGGATTGA[G/T]TGATAATCAACTCAATGGTTCAATTCCAAAAATAC
2,741	5	5029	68.24	89810272	F1Dsnp	PHR	A	G	5	27,291,162	+	CTTTGAAGGCTTTCTTGAGCTGCTCGGAGTCTTCG[A/G]CCGGAGAAGGAACTTGTGCTGGGACTGCAAGGGTG
2,742	5	5029	68.24	89866240	F1Dsnp	PHR	T	C	5	27,576,784	+	AACAAGTCACGAAATTCTCGAAAAGTTGGCACTGA[C/T]GGTTATAAATGGAGTGAGACTGAAACTTTCAAGTC
2,743	5	5029	68.24	89897239	snp	PHR	A	G	6	2,834,363	+	TGCTGGTCTCCCGGTTGCATTAATAGCAGTTGCCA[A/G]GGCACTTGGAGATAAAGATATAGATGATTGGACTG
2,744	5	5029	68.24	9_749021	GBS				6	17,053,394		CTGCCTTAGTCGCCACCTTCACCGAAATCAAWACCACATCACCTCAGGTCCTCTCTAGCCAAAC
2,745	5	5029	68.24	89810479	F1Dsnp	PHR	A	G	6	19,629,887	+	CCCCTCAGTGGACAAACTCAAGATGCAAGCGGCCT[A/G]CTCACCACACTCCAACAACAGCAGCAACAAACTGG
2,746	5	5029	68.24	89903686	snp	PHR	T	G	7	8,075,647	+	TTGGGGCTTTCCAACGAGATCCTCCATGTATTTGA[G/T]CGGAATAAGGTGAGAAACTGTACGTGTAAAGCTGA
2,747	5	5029	68.24	89864974	ins	PHR	-	GTTC	7	8,136,378	+	GGTATAAGTACCTCATTGTGGAAATGAACTAAAAT[-/GTTC]TGAAATTCTCATATACATGTGTCCTCTTGTTGACT
2,748	5	5029	68.24	89866982	F1Dsnp	PHR	T	G	7	8,138,848	+	TCAACAGAAGTGATGAACATTTCCTTTAGAACCAC[G/T]TGCCCTGGTGTAGAGGTTCAAAGAAGTGGAGTTCG
2,749	5	5029	68.24	198_150353	GBS				7	8,190,724		GACATATCATAAAATTTTGAACAAACATTTATACTCCTCAATCCAATCCTCATGTGGTCGATGA
2,750	5	5029	68.24	TP1368	GBS				NGH			TGCAGAGAAAGCTCTCCCTGCCTGTACGAAGCCGCAGTTTTCGTCTTGGTAGACATTGAACTCC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,751	5	5029	68.24	TP9276	GBS				NGH			TGCAGTTCAGTAGTGGAATGCACGGAAAATCGTGTACACTGAAGTGGATTACAGTTCATTTCTT
2,752	5	5029	68.24	118_210402	GBS				NGH			GCTTTCCAAGAAGCTCATTGGGAAGGTCCTCCTTAATGCCCTTAAGGTAAAATGTGTAGAAGAG
2,753	5	5029	68.24	9_56639	GBS				NGH			ACGGAAAATCGTGTACACTGAAGTGGATTACAGTTCATTTCTTAAAGAGGTTAGCACAGGTTTG
2,754	5	5029	68.24	TP3434	GBS				NGH			TGCAGCAGCTTATTTTCCCCTTCAAGCTCTTCTACACATTTTACCTTAAGGGCATTAAAGAGGA
2,755	6	346	0.00	89866758	F1Dsnp	PHR	T	C	6	92,815	+	GGAGCTCTCCCAGTGGGATTCTCAATCAAAAGAGC[C/T]AATCAGCAAGATTTCGTTCGGGCATTTCCCTCTTT
2,756	6	346	0.00	89810429	F1Dsnp	PHR	T	C	6	1,445,104	+	ACCAGTATCAAGGTTACGGTTCTAACAAGAGGCGG[C/T]TGGTGTACAGAGATGAGAATTTACAGAAGCCCCAG
2,757	6	346	0.00	89866392	F1Dsnp	PHR	T	C	6	1,445,118	+	TACGGTTCTAACAAGAGGCGGTTGGTGTACAGAGA[C/T]GAGAATTTACAGAAGCCCCAGACCATGAAAGTTTA
2,758	6	346	0.00	89866395	F1Dsnp	PHR	T	G	6	1,468,194	+	CAGCGTGTTAAAGACGCCAAATTGCCAGATGTTGA[G/T]GTTGTGCGTATCCTGTGGGATGTCATTATGGATGC
2,759	6	346	0.00	89866396	F1Dsnp	PHR	A	G	6	1,477,009	+	AAAGCTTTCAGAGTTATGGACAGGGAACTACGAAT[A/G]CAACCAAGTATTGATTGCTTTTGTAGTGGGACAAC
2,760	6	346	0.00	89866397	F1Dsnp	PHR	T	C	6	1,478,815	+	CTGGAAGGAGTTTCTCGTGTTAACACATTGTTGAC[C/T]CTGCCAAGATTTGTACCTGGAAAAGAAGACATTAA
2,761	6	346	0.00	89866400	F1Dsnp	PHR	A	G	6	1,481,344	+	AAGCTTAAGGGTAAGTTGCTGCTTTTGGTTGTTGT[A/G]GAAGTAGTGTTCCCTGATTTAGTTCCAGGGTCGTG
2,762	6	346	0.00	89810430	F1Dsnp	PHR	T	C	6	1,481,855	+	GTAACCCTTGAGATTTAGAACCGGTTTTGTTCCAT[C/T]TTGTATACCTAGTAGTTGTAAGCAAGATCATCCAT
2,763	6	346	0.00	89810435	F1Dsnp	PHR	T	C	6	1,500,495	+	CTGTTATTGATCTGCAGGTGCGGTCCTTGCAAGAT[C/T]ATAGCTCCAAAGTATCAAGAATTGTCGCAGAAATA
2,764	6	346	0.00	89810437	F1Dsnp	PHR	T	G	6	1,507,554	+	AATCACTTCTTGTTTTTGGGAGAGGATTCAACTAC[G/T]CAACAGCTTTGGAGGGTGCTTTGAAGGTAAAGGAA
2,765	6	346	0.00	89866412	F1Dsnp	PHR	A	C	6	1,509,437	+	CTGATGATACTGAAGAAGCTGAAGATGATGCTAGT[A/C]TAGTTAAAGAGGAGGATAGTAAAGCTAAATCTAGG
2,766	6	346	0.00	89810438	F1Dsnp	PHR	A	G	6	1,509,865	+	GATTTTTTTAAGAATAAGATGTGGTTGGACAAGGG[A/G]AGTCAGGGAAGAGGTGGTGTTGAGGTAAGGGAGGA
2,767	6	6011	2.44	89866371	F1Dsnp	PHR	T	C	6	1,153,020	+	ACTCTTCCGAACCCACCTTCTCCTAGAAGGCACTC[C/T]TGACGGAAGTTCTTTGTTGCTGTTGCTAGCTCACG
2,768	6	6011	2.44	89866372	F1Dsnp	PHR	A	C	6	1,179,660	+	TTGATGATGCAAGATGGCATTTCATGTTATCTGAT[A/C]AGAATATTGGCTCAGAAACTATGCAGCGTCTATCA
2,769	6	6011	2.44	89810409	F1Dsnp	PHR	T	C	6	1,182,170	+	TGATGCCCAAATCCTTCACTAGCCATCATCATTGG[C/T]ACTCCTCCATTGTTGATTCCTTCAAAACTGATCTT
2,770	6	6011	2.44	89810410	F1Dsnp	PHR	A	G	6	1,188,771	+	GGAAATGTGTCATTTGGTGAAATTGTTTGGGCGGT[A/G]GTAGATTTAAAGTACATGGTCAGGAGCCCCATTGT
2,771	6	6011	2.44	89810413	F1Dsnp	PHR	A	G	6	1,202,182	+	CCATCCGCCCTGTTTTCATTCGGAAATTTAACTTC[A/G]TTGATGTCATGATTTCTTGCAAGCTGTCTTTCCAT
2,772	6	6011	2.44	89810414	F1Dsnp	PHR	T	C	6	1,202,211	+	AACTTCATTGATGTCATGATTTCTTGCAAGCTGTC[C/T]TTCCATTTTTCTTTGGGGCACCAGAATCGCAGTCT
2,773	6	6011	2.44	89894556	snp	PHR	T	C	6	1,211,208	+	TCAACAATACGATGAACAACTTCTGAGGAGAGTAC[C/T]GGAAAAAAATTGTTCATATCAATGTACTCTGACAA
2,774	6	6011	2.44	89866376	F1Dsnp	PHR	T	C	6	1,227,272	+	CCCCAACTCTCTATACCAGATTTTACAGCCAATTC[C/T]TTGTACTCCACATCAATTTCTTCTAGAGTTTCAAT
2,775	6	6011	2.44	89810418	F1Dsnp	PHR	A	G	6	1,270,189	+	CTAGCCATTACTATATAACTCATGGGACAATATCG[A/G]CATATAATGAGCATTTGAAGCCAACTATGAGGGAT
2,776	6	6011	2.44	89810420	F1Dsnp	PHR	A	G	6	1,273,722	+	AAGAAGACATATACGCTGTATTTCATGTGTGATTC[A/G]TATTTGGGGTGTGATGAAGAACATAACTTCACTGT
2,777	6	6011	2.44	89866379	F1Dsnp	PHR	A	G	6	1,292,796	+	GTACGTATCGTCAACAATCTGAGCAATGGACAAAG[A/G]CTTTATCACCATTGTGAATCTAAAGACGATGATCT
2,778	6	6011	2.44	TP5394	GBS				6	1,303,659	1,303,722	TGCAGCTGCTTTAACTTACATTAAGTAATTATACAGCAAGACCCTGCAATAACATTATTTATTG
2,779	6	6011	2.44	89866387	F1Dsnp	PHR	A	G	6	1,360,955	+	ATATCTGAAGGGTTCAAGCCTACTAGAGATTGCTC[A/G]TTGCCAGAATACAACTTAAAAGCCTACCATCTTGG
2,780	6	6011	2.44	TP660	GBS				6	1,425,913	1,425,976	TGCAGAAGGCATCTGCCTAGGCTCTGATAGTGAAAGCCTCCTAGGCTTAGCTGATCCTGCTTCA
2,781	6	6002	4.93	89866757	F1Dsnp	PHR	A	G	6	911,595	+	AATTTTGGCATCCTTCATGACTTATGCGTCAGAGC[A/G]CCTTGCGACTAGATCATTCTTGAGAGGCCTTGAAG
2,782	6	6002	4.93	TP5201	GBS				6	914,641	914,702	TGCAGCTCTTGAACCACCATGGTCATGATCTCTATTCGATTCCAGACAACTCAACTCAGTGACT
2,783	6	6002	4.93	89866759	F1Dsnp	PHR	A	G	6	931,607	+	GAAACTTTTTCCAATACAGTTTGTAGCTCCAGAAA[A/G]CCAGCAAAACAATGATACCGAGTACCATTCGTGCA
2,784	6	6002	4.93	TP1022	GBS				6	952,550	952,607	TGCAGACAGGTTGACTTTAAATTTATAGTATAATTAGGGAAAGAAAAAAGAGGAGTACGTTTTA
2,785	6	6002	4.93	89866761	F1Dsnp	PHR	A	G	6	965,565	+	GAGGTATTCGAAGGATCATTTCGGACTTTATAAAC[A/G]AGAAGTCTCCCAAATGCCTTGGTTGAAGTTTCACG
2,786	6	6002	4.93	89810802	F1Dsnp	PHR	T	C	6	976,978	+	ACAGCTCATTCAACGCAGGTCCAATAGAGGATTGA[C/T]AAGCTTGTACAATACCAAGAACATGGTAAAGAACC
2,787	6	6002	4.93	89866762	F1Dsnp	PHR	A	G	6	983,647	+	CTAGAGAATGCATTCTTGGAAACTGTGGTGAACTT[A/G]CTCTTGCTGAGAAGAAGACATGACCACTGGAGAAG
2,788	6	6002	4.93	89810402	F1Dsnp	PHR	T	C	6	1,037,597	+	TAGTTTCTTTTTCTCTCTTAGGTGGACCATTGTTT[C/T]GACATATTTGTTTCAAAACTCTGTGATACTATTTT
2,789	6	6002	4.93	89866366	F1Dsnp	PHR	T	C	6	1,085,751	+	TGCAGACTTATGATAGGCCATTCATCCAGAGGTTG[C/T]TGAATGAAGGTAGCCAGATATGCCCTCAGACCAAG
2,790	6	6002	4.93	89810404	F1Dsnp	PHR	A	C	6	1,086,161	+	TTGATCACGACTCTACTAAACCTTTCAATTCATGA[A/C]AACAATAAGAGATTAGTTGCTGAAAACCCATTGGT
2,791	6	6002	4.93	TP8190	GBS				6	1,107,648	1,107,585	TGCAGTCAACTTGTCAAATTACCAGATGAAGAGGCGATGAGGAAGCTGACCAAGCTAAAGCATC
2,792	6	6002	4.93	89866433	F1Dsnp	PHR	A	G	6	18,547,341	+	GACGCCAGAATAGCAGATTTCGGGTTGGCAAGGAT[A/G]ATGATGCACAAGAATGAGACAGTTTCAATGGTGGC
2,793	6	343	7.37	89866730	F1Dsnp	PHR	T	G	6	643,910	+	CCTAAACCCTAAATCGGGGGTGTAGCTGCCCTCCG[G/T]CGACGTCGTCAAGATGAGGATCATGATCAAGGGCG
2,794	6	343	7.37	89810759	F1Dsnp	PHR	A	G	6	646,130	+	GCTATCATGATGGAAGCTTCAAATTTGGCAATGTT[A/G]AGAGAGTCTCAGACACCATTGTTAGGAGGAGAGAA
2,795	6	343	7.37	89799558	snp	PHR	T	C	6	654,926	+	AAATCGAATCAAAGGAATAAGAGTGGATACTGAGA[C/T]GGTTGAGACAAATATTGTGAGTATTTTAGTACAGT
2,796	6	343	7.37	89842589	snp	PHR	T	C	6	753,799	+	TTACTGGGGTTTTCAGCATGCAAATTGGCATGAAT[C/T]GTGCATTCAAAAGTGCATTGTTCCTGGAAAGTTAT
2,797	6	343	7.37	89810778	F1Dsnp	PHR	T	C	6	771,017	+	CCAGAATCGGATTCATTTAGTAAAGCACTCCAAGC[C/T]GAATACAACAATGAGACTCTCTCACTGGTGATGGT
2,798	6	343	7.37	89866745	F1Dsnp	PHR	A	C	6	771,101	+	AGCGAATCGACTTCCACTCTCTCTGTTACCTTCGG[A/C]TTAGAACTGCAGTCTGTGCATGTAAACATATCTTT
2,799	6	343	7.37	89810784	F1Dsnp	PHR	A	G	6	814,285	+	GAAGTTCTTGTGTCCAACGCATTCTAGCTTTGGTT[A/G]AAGGTGCAGTGGACTCTGGGTCAGGGCTAGTGAAA
2,800	6	343	7.37	89866754	F1Dsnp	PHR	A	C	6	864,902	+	GATTGGTTGAGCGCTTTAATGATCCTTTAAACAAG[A/C]GGGTGAAATGCACTCTAATATCTACCAAAGCTGGA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,801	6	343	7.37	89866755	F1Dsnp	PHR	T	C	6	865,508	+	TTGTTCGTTTATTTCAGGTATGGCCAAACAAAGCC[C/T]GTGTTTGCTTACAGATTGATGGCACATAGAACTAT
2,802	6	343	7.37	89850345	SnpSnp	PHR	T	C	6	871,176	+	ATTAGGCTTCTCTTAAAATTTGCTCTACAAAAATGG[C/T]ATCCATGAGGGTGTAGTGTTGTTGATATGCTTCTT
2,803	6	343	7.37	89866756	F1Dsnp	PHR	A	G	6	890,461	+	TGGCCTGAGGAAATTGATCAAGCTGTTGACTCAAC[A/G]TGGTACTTGAAATGGCAATCTGAGGCAGAAATGAA
2,804	6	343	7.37	89810794	F1Dsnp	PHR	A	G	6	895,596	+	CTATTTTAAAGCTAAAGAAATGCTCAATCAAAATC[A/G]TCGAGTTCTTGAAAAGATAGTTGAGGAGTTGCTTG
2,805	6	343	7.37	89810795	F1Dsnp	PHR	A	G	6	898,788	+	TTTCGACTAAGACAAGGTCAGGGAGATTATCGATC[A/G]TCGATTTTGATGATCGCTGTGGCTGTTCATTGCGG
2,806	6	6017	9.83	89866520	F1Dsnp	Other	T	C	6	292,295	+	GGAGGAACTGTTAAATCCATTCAAGAATTATCTAA[C/T]TGTATAGTTAGAGTTCTTGGGTCAGGTGATCTTCA
2,807	6	6017	9.83	89810577	F1Dsnp	PHR	A	G	6	303,764	+	GATCTGTGCCAAGTCTGGGAAACAAAGGTGGAACC[A/G]ATCTTTAAACGTTATGGCCTAAAATGCCAATTGAA
2,808	6	6017	9.83	TP1610	GBS				6	366,457	366,394	TGCAGAGCCTAATGGAAACCTTAAACTCTACAGAGCCACATTATATCAGATGTGTAAAGCCAAA
2,809	6	6017	9.83	TP4757	GBS				6	420,954	420,891	TGCAGCGTGGGACAGTGCCACTGCAACCTGGTCAGCCACAACTTCCACTATCTCCATTTCATGA
2,810	6	6017	9.83	TP2313	GBS				6	422,569	422,632	TGCAGATGATGCAAGGCAATATCTGGATATCCATGAATCCGATCAATCTCGCAGAAAGCATGAC
2,811	6	6017	9.83	89866712	F1Dsnp	PHR	T	G	6	431,151	+	CAACTGCCCTCCGCCGTTGGGAACCAAACTTGGTG[G/T]CAAATTGTAAACCCCGGGCGGCATAGATGAATTCG
2,812	6	6017	9.83	89810740	F1Dsnp	PHR	T	C	6	466,896	+	GGTGGTGGAGAGGGGTGAACTGTAGGATTGGGTTT[C/T]GGAGGCGGCGGTGGAGACCTGCGGCTGACCCTGTG
2,813	6	6019	24.03	89809102	F1Dsnp	PHR	T	G	1	19,778,018	+	TAAGGAGCCAATGTTGGTATCCAGGTTCTTAATCT[G/T]TGTTGTCCCTGCATGTATATGTATGTGGAAATTAG
2,814	6	6019	24.03	89809103	F1Dsnp	PHR	T	C	1	19,812,223	+	ATTGCCCAATTTGACCCTGGGAATTTGGATCTTGC[C/T]AGCTTCACTCATCCTTTCAATATTTTCTGACTCTT
2,815	6	6019	24.03	TP4197	GBS				1	19,848,453	19,848,516	TGCAGCCTAATGTCGTTCACTCGCAGCTGCTTAAATAGGGACTTAAGTGAGAAAAGTGCTAATT
2,816	6	6019	24.03	89809106	F1Dsnp	PHR	T	G	1	19,854,627	+	GTAATCAGGAGTTATCTTGAGAAAAATGAGCTAGA[G/T]TTGGGGTTGCCACCATCTGAAGGAAACGAGCCAGC
2,817	6	6019	24.03	89865078	F1Dsnp	PHR	A	G	1	19,854,739	+	ACAAGAGTGCTCTGAAAGAAGGCGAAGATAATTTC[A/G]GAAATCTTGTGAAGAAGATCCTTGAGAAACTGGCT
2,818	6	6019	24.03	89809107	F1Dsnp	PHR	T	C	1	19,868,247	+	AAATCATAGTAACACTAGCAGCAGTGCAGCTTCGT[C/T]TAAGCCTCCTAATGTTCCTGTGGATTCTGAGGAGT
2,819	6	6019	24.03	89809108	F1Dsnp	PHR	T	C	1	19,884,236	+	GCTTCTCAGTGTAATGGTTGTTCAAAGACAGTGTT[C/T]GAGTATTTGAGCATGTATCAGTATGGGCGAGGTAT
2,820	6	6019	24.03	89865079	F1Dsnp	PHR	T	G	1	19,884,257	+	TCAAAGACAGTGTTTGAGTATTTGAGCATGTATCA[G/T]TATGGGCGAGGTATCCGCCTTTTAAGTTCAGCTTC
2,821	6	6019	24.03	89809109	F1Dsnp	PHR	T	G	1	19,884,731	+	CACTGTCATGCCATTGTTACCGGTTTGTTGTCACA[G/T]GGATACCTGCAAAACAGCCTCATCAAGATGTATAT
2,822	6	6019	24.03	89809110	F1Dsnp	PHR	T	C	1	19,884,836	+	TTCCATCATCTGCCAACACCAGATAGGGTCTCATT[C/T]AATATCATGATCGTTGGTTATGCTAGGAAGGAATA
2,823	6	6019	24.03	89865080	F1Dsnp	PHR	T	C	1	19,885,661	+	AACGGGGTGACTATTGTAGCCGTTCTGACAGGTTG[C/T]AGTCATAGTGGACTTGTGGAAGAAGGGCTCAGCAT
2,824	6	6004	29.11	89809098	F1Dsnp	PHR	A	G	1	19,199,538	+	TGATTTAATCCGGGATTATGTCCACCATATCCATA[A/G]TTAGCTCTACGACTGATAGGAATTCCAAACTGCAC
2,825	6	6004	29.11	TP39	GBS				1	19,200,346	19,200,283	TGCAGAAAACCTCCAAGGCTAAACTACAAGAAAAGGCAGATCAGAAAGCCTCCAAGGTTGAACA
2,826	6	6004	29.11	89809099	F1Dsnp	PHR	T	C	1	19,203,507	+	TCTTCACGTTCAATCTCCTGGCTATGCTTCTGAAT[C/T]GATCTCTTTAATTCTATAACCTCTTGCACTTTCTC
2,827	6	6004	29.11	TP6345	GBS				1	19,248,086	19,248,149	TGCAGGCAAAGAGGAGCTCACTATTCGACACGTGTACTATCTGAGTGAAACAAAGCAAATCGAA
2,828	6	6004	29.11	89865070	F1Dsnp	PHR	T	G	1	19,295,866	+	TTAGAGGCAGTGCTGATGGGGGGAAATCTTTAAAA[G/T]TTTCTCTTATGCTTCTTTTGTAAGGATCTCGGGGC
2,829	6	6004	29.11	89865071	F1Dsnp	PHR	T	C	1	19,300,707	+	AGGTCACTAATTTCGGTTCCCATAGATATAACAGC[C/T]GCTTCCTTCAATTCAGTCTCAACCTCGTCCGATAA
2,830	6	6004	29.11	235_311897	GBS				1	19,381,114		ACTTGAGATATGTAGGCGTGAGCGAAAGAGTCAGCATTGAGGTTTCCTTCCAGAGATTCAGTTA
2,831	6	6004	29.11	89809100	F1Dsnp	PHR	A	G	1	19,443,121	+	CAACGATCATCTGTGAAGTAAATCGAGTTTTCTTC[A/G]CACCCTGAAACATCTTTAGTGGACAGCGATATCGA
2,832	6	6004	29.11	89865074	F1Dsnp	PHR	A	G	1	19,606,249	+	TTGAGGAGCTGGCCAGGGCGGGGTTGAGGAATCCG[A/G]TGAGGGTTAAAGTGGTTGCGGAGTATATAACACCT
2,833	6	6004	29.11	89809101	F1Dsnp	PHR	T	G	1	19,610,864	+	GATCTCTAAGTTCCCTCAACTCAATCTGGTGCTTT[G/T]CCTTGAGCCACCTCAATTCCTTTTGAATTTCATGC
2,834	6	6004	29.11	89865075	F1Dsnp	PHR	A	G	1	19,611,854	+	CAAAACCATAGCCATTCGAGTATCCGTTACTAAAC[A/G]AACTGTTGTTTTGATGAACCTCGTAAACAGGCTGC
2,835	6	6004	29.11	89865076	F1Dsnp	PHR	A	G	1	19,632,186	+	AACGCAAGAATTCCATGTATGGGAGCTCCAATTGG[A/G]AACCGAAAATCAAGTTCTGTGATGGAAAATTAATC
2,836	6	6004	29.11	89817297	snp	PHR	A	C	1	19,642,160	+	TGATCCGTGTCTCATTGTCCGTGTGGACAGTAAGA[A/C]GGTGATGCAGGTGAAGAGACTTCGGTGGAAGTTTC
2,837	6	6005	31.58	89865064	F1Dsnp	PHR	A	G	1	19,110,398	+	ATGCTTTTTGCGCTCTTCAGCAATCTTACTGAGTG[A/G]CACCAAACATTTTTTCTCTTCATCTACTGACTTCT
2,838	6	6005	31.58	89809095	F1Dsnp	PHR	T	C	1	19,138,494	+	CAGAGGTATCGAATGTGACTGTGGATAGCTTGGGA[C/T]ACAAGTAGGCGATGGATAGGGTGGCGGTCTAGCAA
2,839	6	6005	31.58	89865065	F1Dsnp	PHR	A	G	1	19,138,574	+	CTGTCAGCTGAGCATTATATTCAGGCTGTTGTTGT[A/G]GTTGAAACATGGGTGTAGGAGTGGTAGGACAACTC
2,840	6	6005	31.58	89809096	F1Dsnp	PHR	T	C	1	19,138,608	+	TGGTTGAAACATGGGTGTAGGAGTGGTAGGACAAC[C/T]CCGCTTCTTCCCTATACTCTGCTCTTGTAGTTCAA
2,841	6	6005	31.58	89865066	F1Dsnp	PHR	T	C	1	19,141,189	+	TTCTAGTAATTTCTAAATCAAAATCAGTGTCCCTG[C/T]TGTTCATATTTGTATTTGAGCAATGAAATCCTTGC
2,842	6	6005	31.58	89809097	F1Dsnp	PHR	T	C	1	19,141,369	+	AGCCTCTACCATCCCAAGTTACTTCAGATTCAGAA[C/T]GGAGGACATTAGGCTCCTCTTTCGATTTCTGACCC
2,843	6	6005	31.58	89865068	F1Dsnp	PHR	A	C	1	19,187,073	+	TACCAGGGATCTTATCTGCATATGGAAGTGTCTGA[A/C]AGAATTCTAAAGCCTCTTTATTCTGAGAAATCATC
2,844	6	6005	31.58	89865069	F1Dsnp	PHR	T	C	1	19,187,903	+	CCTATATCAGCTGCTTCACCTGCTTGTTTACCTTG[C/T]GAAACAGTAGACAGAAGGCTTTTAAGTTCCTTGGC
2,845	6	6005	31.58	TP2387	GBS				6	2,648,018	2,647,955	TGCAGATGGTGAAATAAAGGATCTAGCTGATCGTATCCATTATCAGGGGTTTAGGAAATCTTAC
2,846	6	6005	31.58	89866486	F1Dsnp	PHR	A	G	6	2,648,471	+	TGCACCATGAAAAACAAACAATCGTTGGAAGTCAG[A/G]TCAGAGGTACCACCAAATGTGGCTTTAATCCTAGT
2,847	6	6005	31.58	89866487	F1Dsnp	PHR	A	C	6	2,650,684	+	GAGAGAAAATGTGTCGAGATGATTAATAGACGTTA[A/C]GGAATCCAGTAATGCATTGACATGTCCGTCATATT
2,848	6	6005	31.58	89810539	F1Dsnp	PHR	T	C	6	2,651,148	+	TGAGACCACACAGCAATGTACCTAGATTGCTCCTC[C/T]GTTGAGCCGAGTCTAAGAATCCTTAATATGGATGC
2,849	6	6005	31.58	89866488	F1Dsnp	PHR	T	C	6	2,651,583	+	TTCCTGCAGAGCTTTATGAAGTTCGTTAAGGCATG[C/T]ATTTCTTGGTGAATGATTCCCTGACTGGAATTGAT
2,850	6	6005	31.58	89810541	F1Dsnp	PHR	A	C	6	2,652,338	+	TGGTCAAGATGGTAGAGTGCAAGAAAATATGATTC[A/C]TGTTTCAACTTGCAGTATAATTCCACAAAGTCATC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,851	6	6005	31.58	TP9441	GBS				6	2,669,088	2,669,154	TGCAGTTGAGGAAGGAAAAGATCGGAGTGTCTTGTACTCTTGCATCATGCACACAATGAGAGAG
2,852	6	6005	31.58	89810544	F1Dsnp	PHR	T	C	6	2,670,785	+	ATGCTTGAAAGCTGGAAACAGTCTTCAGCAATGAT[C/T]AACTGAACTGGTCTGACAGGATGCGCATCAGGAAT
2,853	6	6005	31.58	TP9199	GBS				6	2,704,708	2,704,645	TGCAGTTAGATCAAACTCACACTTCAGCCTGTGAAATTCACATAAAAGAGGGTACATTTTCCAA
2,854	6	6005	31.58	89810546	F1Dsnp	PHR	T	G	6	2,709,988	+	TGCTGGAAATCAACTGGGCCAGGAAGGTGGAAGGA[G/T]ATAGAGAAGTAACCTGCTGGGGCAAGGTTCTGTGT
2,855	6	6005	31.58	89866500	F1Dsnp	PHR	A	C	6	2,754,046	+	TTGCTGAAGCCAATCCTCGAGTTCACCAAATCCAG[A/C]TGCACTAGGTTATCCTCCATCTGATGTGCCCCAAT
2,856	6	6005	31.58	89810548	F1Dsnp	PHR	A	G	6	2,755,096	+	TGAACAGGAGGGGTTCTCTTGAAAATCTGGGTCAC[A/G]TGGAGACCGGTAGCACCATCTTTCTGCACCTTGAG
2,857	6	6005	31.58	TP2775	GBS				6	2,857,690	2,857,635	TGCAGCAACAAGGACATCAAGCGCCGCCATCAATTGGGGAATCCCATCCAGCCCCGAGATCGGA
2,858	6	6005	31.58	89866507	F1Dsnp	PHR	A	C	6	2,858,608	+	CCTCCAAGGGACGTTCCAAACCAAGTGGGTGGGGT[A/C]GCTGGAGCTGCTAACTTTTTTGGACCTAGACAGCT
2,859	6	6005	31.58	89866508	F1Dsnp	PHR	T	C	6	2,859,055	+	TTTGGAGAAAATCAGGTCTGGGCCGCATATGATGG[C/T]GATGATGGGATGCCTCGATATTATGCTATAATTCA
2,860	6	6005	31.58	89866509	F1Dsnp	PHR	T	C	6	2,859,235	+	TGTGGAGATTTCAGAGTTGGCAAGTATGAAATCAA[C/T]AAATCACTCAATTCTTTTTCGCACAAAGTTCGGTG
2,861	6	6005	31.58	89866521	F1Dsnp	PHR	A	G	6	2,971,207	+	TGAATTATAGCGTTGAGTTAATCTTCTCAAAAGAT[A/G]AACCCCAAACCGAAACTAAAACCAAAGCCGGGAAG
2,862	6	6005	31.58	89866524	F1Dsnp	PHR	T	C	6	3,006,079	+	TACTCTAATCTCAGCTGCTTCTCCAGATGTGTCAG[C/T]ATTCTTCCCCCTAAGGTGCTGAAGAGCAGCTTCAC
2,863	6	6005	31.58	89866526	F1Dsnp	PHR	A	G	6	3,007,132	+	CTCCCACTCACTACTGCCCCTATCATCGCTCCAAT[A/G]GTCAATATTGAACCGAAAACTGAGTACTGCAAAAT
2,864	6	6005	31.58	89866546	F1Dsnp	PHR	A	G	6	3,089,462	+	AGAGAGAGAACCACAGAGGGCGACTAAAGTGCTCA[A/G]AACAACAACACTAGTGACTGAGGAGGATGAGGAGG
2,865	6	6005	31.58	89840537	snp	PHR	T	C	6	3,127,653	+	AGGGTTCAGAGAGTCTGCATTGCATTCCGTAACTT[C/T]GGTGAGGAGCACAACATTGAAGGGTGAGTAACATC
2,866	6	6005	31.58	89810603	F1Dsnp	PHR	T	C	6	3,242,174	+	GTATATGACGCGGTATAGACATCCGCTTCTCTTGC[C/T]CTATCTGCTAAAATTTGGCCAATGGCTATACAGGC
2,867	6	6005	31.58	89866582	F1Dsnp	PHR	T	C	6	3,305,914	+	GGAGTGTCATCAACGTTAGGCTTCATCCCCACAGA[C/T]GTAGTGTTGGCAAGAATCATTCCCTCTTCCGGATG
2,868	6	6005	31.58	89866584	F1Dsnp	PHR	T	C	6	3,320,073	+	CACCCTCTTATCAATAACACGAATCTCTTCAACAA[C/T]CGGCTCAAATTGTTTCCCTCTCAACTCAAACTTCT
2,869	6	6005	31.58	89866590	F1Dsnp	PHR	A	G	6	3,354,131	+	AGAACGACCTCCGGAACCGGTTGCGGGAAGTCAAG[A/G]CACGGGAAGACCGAATCGGAGTCAAAGAGAAGGAG
2,870	6	6005	31.58	89866592	F1Dsnp	PHR	A	G	6	3,357,284	+	TGGATGTGAAAATGAAAAGTTTTGGGGAAATGGAT[A/G]TGAAAATGAAAAGTTTTAGATTGCTTGAGAAATCC
2,871	6	6005	31.58	89866593	F1Dsnp	PHR	T	C	6	3,363,702	+	ACAAGATAATGAATGAACTCCTCAATGATGTTCAA[C/T]TGAAGGAAAAAGGCTTGGAATCATTTAAGGAATCA
2,872	6	6005	31.58	89866594	F1Dsnp	PHR	A	G	6	3,363,896	+	TCGGTACAAGAGCGTGAAAGAAATGTGGATTCACT[A/G]TACCATGGACTTCAAAGGAGAGAAAGGGAACTAGA
2,873	6	6005	31.58	89810619	F1Dsnp	PHR	T	C	6	3,366,141	+	GCTGTTAAATCTATTTGTGCCTTCAAATTAAATGA[C/T]AAGCTCCCCCCAGTGCCACTCTTAAGAGAATATGT
2,874	6	6005	31.58	89810620	F1Dsnp	PHR	T	C	6	3,366,387	+	AAGGCTGTGATTGGTAAGATAGCTAAGCTAAGAGC[C/T]GCCATTCAGTGCATGAAAGATTACAACCTCGAGTC
2,875	6	6005	31.58	89866597	F1Dsnp	PHR	A	G	6	3,366,428	+	TCAGTGCATGAAAGATTACAACCTCGAGTCTGAAT[A/G]CTCGAAGACTGTTGAAATCCAAATAGTTCAGCTGG
2,876	6	6007	34.07	12_708204	GBS				6	2,452,399		CATCCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAAATCCTAATACGGATTCATATACGTATACG
2,877	6	6007	34.07	89866467	F1Dsnp	PHR	A	G	6	2,460,707	+	GTGGTTTTTGGTTGTCTTCTTCCTCTGTGATGATC[A/G]CCATTGATGAAAGGTTGGAGCTTTTGAAATTGGAA
2,878	6	6007	34.07	89866472	F1Dsnp	PHR	T	C	6	2,530,851	+	ACTGATGGTTTGAGGGTCGCTGAAATTAATGGCTC[C/T]GATGTTGGTGTTGCTTTCTTCCTTCATTTTTCTGT
2,879	6	6007	34.07	89810528	F1Dsnp	PHR	T	C	6	2,536,366	+	CGTGGTGTGATTTTGCAGGGCATCCCATTGTTATA[C/T]GTGCCCCTTGAGGTTATATTGTCCAAGTACTATGG
2,880	6	6007	34.07	89810530	F1Dsnp	PHR	A	G	6	2,564,025	+	CAGGGATTGAAATTGACCCAAACATGGTTTCAGCA[A/G]TTCTTGGAGTATTTGGTGTTGATACTTCTTTAGGT
2,881	6	6007	34.07	89810531	F1Dsnp	PHR	T	C	6	2,566,356	+	CTGTCAACTATTTTACTGGAAAGATCCCACCAGAG[C/T]TCGGAGCATTAAGAAAGCTAGAGATTTTGTATCTC
2,882	6	6007	34.07	89866475	F1Dsnp	PHR	T	C	6	2,575,202	+	TATAATTCCGTTATTGAGTTCGACTCCTCCTTAGA[C/T]AATGAGCTGCAGGTCCTTTCCTCTGATTCTTCAAA
2,883	6	6007	34.07	89866476	F1Dsnp	PHR	A	G	6	2,576,462	+	ATTGAGGTTGAAGGGGAAAGACTGAAGGAATCTCA[A/G]TTTATAAATAAATCTCTCTCGGCCCTTGGAGATGT
2,884	6	6007	34.07	89810533	F1Dsnp	PHR	A	G	6	2,587,663	+	CATCTGCAAAGCAAAGCTTGAGCCCTAAACAAGCA[A/G]ATGTCAGTAACACAAAAGCGATGCCAAGAAAAGAA
2,885	6	6007	34.07	89810534	F1Dsnp	PHR	A	G	6	2,595,359	+	CCCTGATCACCACCATTGTAAGGCTTGATTTTGAA[A/G]CTTTTTCGCATTAGGTATTCGAACATGCATTGAGA
2,886	6	6007	34.07	89866480	F1Dsnp	PHR	A	G	6	2,607,858	+	GTTTCCTGATCGAATAATGGGGCTGTTGGGTGAAG[A/G]ACAGCTTTTTGTGCATAGTAAAAAACCTCTGGAAT
2,887	6	6006	42.16	89865010	F1Dsnp	PHR	A	G	1	13,341,150	+	GTATATGTTATTGGCGTGTAATATCAGATGACCTT[A/G]TTCTTTCATTTGATATGGGAAGTGAGCTATTTCAT
2,888	6	6006	42.16	89809050	F1Dsnp	PHR	T	C	1	13,362,262	+	CTTGGGAGAAGGTTATGGAATACAACCTTCGACCC[C/T]GAAATCAGCTCTAGTTCTCCCCGGTCCCCAGTGAA
2,889	6	6006	42.16	89809051	F1Dsnp	PHR	T	G	1	13,399,034	+	AGGTCCCAAAATATATTTCTTTAGCCCACACGTTT[G/T]CCCATGTCGATGACATAAGAACCGCCAACATACGA
2,890	6	6006	42.16	89809052	F1Dsnp	PHR	A	C	1	13,405,348	+	AGATCAACAGCTTATACAGTAAGAAGAAGCTTTCA[A/C]AGATTCATGAGAACGTTAGAGTAATGCGCTATCCG
2,891	6	6006	42.16	89865011	F1Dsnp	PHR	T	C	1	13,406,443	+	CATGAATCCCAAAGTTGAAGCTCTAGAACCAGATA[C/T]ACAGATGATGGATGATCTTATTCTATGGATCTTG
2,892	6	6006	42.16	TP9453	GBS				1	13,414,915	13,414,852	TGCAGTTGATAACCAAAATGTACTAGCATCAATGTGATGGTAGAATGTATAGCAAAAGATATGT
2,893	6	6006	42.16	89865012	F1Dsnp	PHR	A	G	1	13,447,132	+	TTGCAATCGCTTCATGATCTTATTACCTCGAAGAG[A/G]TACAGAGCATGGCAGAAGCCACTTGAAAAGATTAT
2,894	6	6006	42.16	89778661	snp	PHR	A	G	1	13,450,858	+	AAGCTGCATATCAACAACGTTTATTGGAAGAAAGC[A/G]TACTTCACGAGCGTGAGCAACAGGTATCAATATTT
2,895	6	6006	42.16	89865014	F1Dsnp	PHR	A	G	1	13,520,091	+	CTGATTCGAATGTCATCACCAGGAGCTTTCGGCAC[A/G]ACTCTAGCTGCTAGTCTGAACTTCCTGCTTCTGAT
2,896	6	6006	42.16	89865015	F1Dsnp	PHR	T	C	1	13,538,577	+	CATTTTGAGGAATGCAAAGTTGTGGGTCTTGATTG[C/T]GAATGGAAACCGAATTATGTTAAAGGTAGCAGACC
2,897	6	6006	42.16	89865016	F1Dsnp	PHR	A	G	1	13,638,652	+	TACCTTCTTGGCTTCGGGATCCTTGATTTTCTTTG[A/G]AGGAAGAAGATCCCAATCACTGTAGAGGCTGCCAG
2,898	6	6006	42.16	TP6383	GBS				1	13,642,278	13,642,341	TGCAGGCACATCAAAATGGCTCAAAACTCAAACTCACTCAAGCAAAAGGAATCATAATTTTGCA
2,899	6	6006	42.16	89865017	F1Dsnp	PHR	A	G	1	13,642,705	+	CCTTCCATGAGCCCTGGAATAGTATTGAACTGTCT[A/G]CGAACCTCTTCGACCATTTTGAGTGCTGCACTTCC
2,900	6	6006	42.16	89865018	F1Dsnp	PHR	T	C	1	13,669,864	+	GTAATCCGTAGCCGCCTATGACCAATAAGCACTAC[C/T]TGGTCTCCTTGGATGCTAGAAATCTGATACACCAA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,901	6	6006	42.16	TP6800	GBS				1	19,575,996	19,575,933	TGCAGGGAACATTTCCGAAAGAAATCTTTCACTTACCTACTCTCCGTAAGATTAGCCTTTCCGA
2,902	6	6006	42.16	89810488	F1Dsnp	PHR	A	C	6	2,080,722	+	CATTCCTCAGCTTTTGGTTCATACTTGGTGTAGGC[A/C]GATTTAGCAGCTGTGCAAGCCGCCTCTGGTGCCTT
2,903	6	6006	42.16	89810492	F1Dsnp	PHR	T	C	6	2,106,045	+	AAGTCGACTTGTGTAATATATACACCTTCAATAGT[C/T]TTCAAAATTTCGTTCACTCTTTTGACGCACGCATT
2,904	6	6006	42.16	178_401609	GBS				6	2,215,984		CAGCTTCATTCTCCTGAGCAAACACATCACCRTCCATGGTGGGAACACCAACATCTAAGCAGAG
2,905	6	6006	42.16	89810503	F1Dsnp	PHR	T	C	6	2,231,214	+	CCTATCTCTCTGTTCCTTGGGGACCCAATTCCGCT[C/T]CGTACTCCTCAGAAAACCATCACCGGTGAACAGAA
2,906	6	6006	42.16	89810507	F1Dsnp	PHR	T	C	6	2,262,154	+	GGAGCTATCCTCCTCCTGATCCTCATCAAGCTCAA[C/T]CCTCCCGATATCAAACACGTCATCCTCTTCGTCGT
2,907	6	6006	42.16	89810523	F1Dsnp	PHR	T	C	6	2,396,400	+	CATGTAGAATAGCAAAGGTTGTATGCAATTATCAT[C/T]GATGGATAAAGAGATTGAAAATCCAAAACAACTAC
2,908	6	6006	42.16	TP434	GBS				6	2,461,620	2,461,556	TGCAGAACTAAGGTTGAGAATTTATCCGTGTCTAATAGGCTTCTAAGATTGGCTGGCACAAACG
2,909	6	6006	42.16	89810629	F1Dsnp	PHR	A	C	6	3,406,112	+	ACCACTCAATGAACACTATCTCGGATCTTTTGTAC[A/C]GTCTCTAAGGTTCCACCACAAAGCTTGCACAAGAC
2,910	6	6006	42.16	89810648	F1Dsnp	PHR	T	C	6	3,501,889	+	ATGCTGAGGAATGCTACATGGACTTTATCTAATTT[C/T]TGTCGTGGCAAGCCGCCCACACCGTTTGAGCAGGT
2,911	6	6006	42.16	89810657	F1Dsnp	PHR	A	G	6	3,561,708	+	GAGAACATGCAGAGGGATGACATTAAGATGCTAGT[A/G]AAGAGGTGGTGGGATATCTACAACGATGAGTCATT
2,912	6	6006	42.16	89866618	F1Dsnp	PHR	T	C	6	3,565,087	+	GACCACTTGTTTGACTACCCGGACAACTACTTCTA[C/T]GCTGTGATGGATTGCTTTTGTGAGACCAATTGGAG
2,913	6	6006	42.16	89866621	F1Dsnp	PHR	A	G	6	3,580,405	+	AATATATAACAATGATGCATAAGATCACATACCCA[A/G]TTTCCCTACACCTCTCATTTCCACAAAACCAGTTA
2,914	6	6006	42.16	89810659	F1Dsnp	PHR	A	G	6	3,586,123	+	CCACAGATGTTTGTTTACAAAGACGGAGCTCCACG[A/G]TGGCGGTCTGTAATGAGGATCGGCCAGACATGGGG
2,915	6	6006	42.16	89810660	F1Dsnp	PHR	A	G	6	3,586,167	+	TGTAATGAGGATCGGCCAGACATGGGGTAGTGTAT[A/G]TACAGTGGTGAACAATGAAGATGAGGTCTCTATCT
2,916	6	6006	42.16	124_101623	GBS				6	3,622,433		GTGGGGTTTGTGTTGTGGTCTTTTGGTATYGTCGCTTTTGTTTAGTGGGGTTTTTATGAGGT
2,917	6	6006	42.16	89866625	F1Dsnp	PHR	A	G	6	3,624,322	+	CTAATCATGCAGGCATTTGACTTGGCAGCGGTGTC[A/G]TTTTTCAGCAGGGACTACAGCAGTGTGGAGAAGGA
2,918	6	6006	42.16	89866626	F1Dsnp	PHR	A	G	6	3,626,593	+	CAAAAAAGGTGAATCTTTGGAAATTACCAGTAAGT[A/G]ACTGGAAGCAGTGAAGATCAAAGGTATCAGCTTGA
2,919	6	6006	42.16	89866639	F1Dsnp	PHR	A	G	6	3,675,967	+	ACAATCGGATTTCTTACGGTGTCCATGTGAATGTT[A/G]TTGAATGTTATGCTTGACACAGATCCTGATCCACC
2,920	6	6006	42.16	89866640	F1Dsnp	PHR	T	C	6	3,676,426	+	ACGAGTGAGTTGTATATTTTCATATTGTTTGTGTT[C/T]TGAATGTGAATTCCATCTGTGTTGGGACTAAGAGC
2,921	6	6006	42.16	89810681	F1Dsnp	PHR	T	C	6	3,680,045	+	CTTTGTTTCAAATACTCAGGTAACTCGTCGCTGAT[C/T]CATCCATGCTGACTTTTCTCGTGACGTATGCAGTT
2,922	6	6006	42.16	89810682	F1Dsnp	PHR	T	C	6	3,681,190	+	ATAGACTTTGGAGCAGCCTTCGTGGTCGCATAGAA[C/T]TAGAACCCCACCGTCTTTGCAGATGAAGCACCAAT
2,923	6	6006	42.16	89866658	F1Dsnp	PHR	T	C	6	3,739,964	+	ACCTTGCTTATCTTGGAAATACTGTTTCCAGGAGG[C/T]ATTTGCCTCTTCAACAACTCTTTTGCAATCTCCTC
2,924	6	6006	42.16	89810693	F1Dsnp	PHR	A	G	6	3,742,013	+	AGTACCAAATACTGAACTTCACTCAACTTGAGGCT[A/G]CCACCGTTTATCAGGTCAATAAGCCGACCAGGAGT
2,925	6	6006	42.16	89915432	mSNP	NoCls	T	G	6	3,742,826	+	GACTCATACTCCGACTCCGAGTCTAGCTCCTCCTT[G/T]GAAAACCCACCAAGCCCCTTGAAGGCCTCCTCACT
2,926	6	6006	42.16	TP848	GBS				6	3,762,029	3,761,994	TGCAGAATGAGCCAACAAGTAGGCTGCAATTGGTATCACACTCATTATCTCAGTAGTCAGTATG
2,927	6	6006	42.16	TP3803	GBS				6	3,775,200	3,775,140	TGCAGCCAATGTGCAGAAGATCCCAGGTCTTAACACGCTCGGCGTGTCGATGGCTCGCATTGAC
2,928	6	6006	42.16	TP8232	GBS				6	3,779,144	3,779,198	TGCAGTCACCAAAGAGCCGAAGGTGTTGTTGGTGAGTCCTGGCTTGGCCAGTCCGAGATCGGAA
2,929	6	6006	42.16	TP5939	GBS				6	3,816,475	3,816,538	TGCAGGAATCACACAGCTCCAAAGAGTTGGTATTGGACTAGTTCTCTCGGCAGTTTCAATGGCG
2,930	6	6006	42.16	89866684	F1Dsnp	PHR	T	G	6	3,833,066	+	ACATATTTGCATCATATCAATTGCTACTATTTCAG[G/T]CTCTTATTTCTGGTTGTTCTGCTGGAGGTCTGACA
2,931	6	6006	42.16	89866685	F1Dsnp	PHR	T	G	6	3,833,956	+	AGTTGCAAATTAAATGTTACCAACTGTTCCCCGTC[G/T]CAGTTGCATATTCTGCAAGGTAATCCAACTTATGA
2,932	6	6006	42.16	89810731	F1Dsnp	PHR	T	G	6	3,944,158	+	GAGGAAGCAGGAAGCAGTGCACAGATCAAGGTCCA[G/T]ACGTACAAAGCCACCAAGATATATTTACTCCACAT
2,933	6	6006	42.16	89866707	F1Dsnp	PHR	A	G	6	3,994,696	+	TACAGCCCAACTATGCTACTTAAAATGTGAGTGGT[A/G]TTTTCTAAAGCTTTGGAAACCTCATCGGCGAATGC
2,934	6	6006	42.16	89866708	F1Dsnp	PHR	A	G	6	4,059,568	+	GAAGTCACACAGGTGATAAAAAACCTCCGGAAGCG[A/G]GTTGTGTCCAGGGAGAATGAGAGAGCTGAAAGGGC
2,935	6	6006	42.16	89810732	F1Dsnp	PHR	T	C	6	4,081,275	+	TATTTTGAAAAATTAACAATTTTCCACCAAGTTGA[C/T]TCTGCAAAAGCACACACATCCCCAGAAGTTATTGC
2,936	6	6006	42.16	4_259422	GBS				6	6,702,898		AGGATTTACAATTTTAAAACGAGTTTTATAGYGTCTGTTGCACTTTGGTTTTGAATGGAACCAG
2,937	6	6006	42.16	89866736	F1Dsnp	PHR	A	G	6	6,882,010	+	ATACTTGCTGACCCTTAATGGAAGCAGCAGATGAC[A/G]TGTTCCAGAACAAAATATCTCCATCTACATATCCC
2,938	6	6006	42.16	89866737	F1Dsnp	PHR	A	G	6	6,883,623	+	TAAAAACCCGCAAAGAGAAGAAAATAAGATATACC[A/G]CTTAACAAATCCGCAGAAATATGATACGGCAACTG
2,939	6	6006	42.16	89810767	F1Dsnp	PHR	T	C	6	6,912,637	+	TTCTGGAGTACTGGTGCTGATAAGAGGATCATGCG[C/T]GTGGTGGTCGAAGTGATAAAGAAAATGAAAGTTCC
2,940	6	6006	42.16	TP1453	GBS				6	6,933,695	6,933,717	TGCAGAGACTGATACGAATGAAGGTGTATAATCATACTGAGCTTCTATTTTTTTGTTTTTCCTA
2,941	6	6006	42.16	89866738	F1Dsnp	PHR	T	C	6	6,946,284	+	ACATTCATATGTTTGTGTGTACCTTCAGCAAGATG[C/T]TCCTGAGCTTCAACGCTAAAACCACCAGTTCCACC
2,942	6	6006	42.16	89810768	F1Dsnp	PHR	A	G	6	6,953,833	+	AATTTTGCTGTCATTAGGGCTTTGGAAGAGAAAAG[A/G]GCTCGTTTGGGTTTATTTGAGTGCGTCAACCATGA
2,943	6	6006	42.16	89810769	F1Dsnp	PHR	T	C	6	6,972,236	+	TTGCACTTTCTTCAAACAACTTCAGTGGCTCCTTC[C/T]CTCTCAACAGTGTCCAACAGCTCAAAAATCTTTCG
2,944	6	6006	42.16	89899702	snp	PHR	A	C	6	6,972,626	+	TTCAGGGAAAACTGCCAATTTTTCGACCAAGTGCC[A/C]CTTATCTGGACTACTCCAGAAATAATTTCAGCTCT
2,945	6	6006	42.16	89866739	F1Dsnp	PHR	A	G	6	7,003,100	+	GGACAGACTCTTGAGGTAGAAGAAGCGGTGGCGAA[A/G]AAGTCGCTTATGATCAAGAATATGATCGAGGACGA
2,946	6	6006	42.16	89810770	F1Dsnp	PHR	T	C	6	7,024,453	+	ATAGCTGGGCATTGTTCTTTTGTTTTGTATTATTT[C/T]TTGAGCCAAATTGCCATGGAGGAAGACATGACATC
2,947	6	6006	42.16	89842472	snp	PHR	A	G	6	7,033,062	+	TGCAGAGAGCTGCAGAGCTTTGTGCTCAGATGGAC[A/G]CCAATGATGATGAGCTAATGGAGTACGGTGACCAG
2,948	6	6006	42.16	89810771	F1Dsnp	PHR	T	C	6	7,034,805	+	ACTATAAGGAGGTCGTTATTTTTCTTACACCAGCC[C/T]TGCAGATTGACCAAGTTCTTATGCCTTAGACGTCC
2,949	6	6006	42.16	89866740	F1Dsnp	PHR	A	G	6	7,034,928	+	GTTATCTTCTTAACTGCAACTTCACATCCAGTAGA[A/G]GGCAAAGTACCCTTGTAAACTGCACCGAATCCGCC
2,950	6	6006	42.16	89842529	snp	PHR	T	C	6	7,252,709	+	TTTGTGTATATGAGCTGGAGATCCTCTTGTTCAGC[C/T]TTCTTTGCATCTGCTTGGAAGGGACTGAAGGTTCC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
2,951	6	6006	42.16	4_872286	GBS				6	7,268,015		CCATATCCTTGAATGATTTAACGAAACTGGCYTCCCATGAAGAAAGAGAAATATCTTGACTGCC
2,952	6	6006	42.16	4_872332	GBS				6	7,268,061		AGAAATATCTTGACTGCCTTGGCTGATGGGGKTTGTGTTACTTTCTTGGTTGAAGAAACTTGAA
2,953	6	6006	42.16	89810772	F1Dsnp	PHR	T	G	6	7,348,631	+	TCATTGAATTATCATCACCTTGGAAGAATGAGAAA[G/T]AATAGGTGTCTGTAAGCAACTTATTGCAGCAAGGG
2,954	6	6006	42.16	89866741	F1Dsnp	PHR	A	G	6	7,382,901	+	GAACTGAACTGGATTTTTACTGCTGTCACTGACAC[A/G]ATTGCATGGAATGTTCTTCCTCATGGTAATTTTTC
2,955	6	6006	42.16	89866742	F1Dsnp	PHR	T	G	6	7,394,449	+	AGCCATTGTCTCATCGAGCCTTCTTGAGGAATTGC[G/T]AGGCATTCCATATCCAGCTTGAGAAGGTCTTGGTA
2,956	6	6006	42.16	89810773	F1Dsnp	PHR	T	C	6	7,407,566	+	CTGTCGACCAGAGTTCGACGATCATGAAAGCTGAA[C/T]AAGGAGCCTTTGATCTGGAACATGAGATTTCCATT
2,957	6	6006	42.16	89810774	F1Dsnp	PHR	A	G	6	7,435,983	+	TTCCGGTCATACATGGTCAATTTGGTGAAGATGGT[A/G]GCATTCAGGTGTAGTGTAGTATAAACTTTACTACC
2,958	6	6006	42.16	89810775	F1Dsnp	PHR	T	G	6	7,439,168	+	GACAAAAATGAAGTTGATGCAACTTCCAGAACAGT[G/T]TGGTCATTACCGTAAGTTTCCCTCTCTGTTTATCT
2,959	6	6006	42.16	4_1071064	GBS				6	7,442,924		ATAAAGAAGATGGAATGAACCTCTGCAGAATRATTGTTGGCTTACATTTCATAGCGCACCAAAT
2,960	6	6006	42.16	4_1082146	GBS				6	7,447,212		CAGGAAATCCAACTATTGATTCACGGTGTTCATTCATATCCCAAATTGTGGAGGGAAGTCTTTC
2,961	6	6006	42.16	89810776	F1Dsnp	PHR	A	G	6	7,486,803	+	CGTTTGGTAGGTTATAATGCAAGTGATTCAGATTC[A/G]GATGAATTGAAGGGGGAATCGTAGCTGGACCAACG
2,962	6	6006	42.16	4_1195465	GBS				6	7,520,170		AACATTGACTGTAAAGATTGCCAACAAATTGYTGAATCCGTTGTAAAATATGTAAGATAAATTC
2,963	6	6006	42.16	89810777	F1Dsnp	PHR	A	G	6	7,532,624	+	GCCACATCAGCTTCTCTTTGGTTTTCATAAATTTT[A/G]ACCTCAGTGTTAACCCTAACCTCCTCCTTCTTTCC
2,964	6	6006	42.16	89866744	F1Dsnp	PHR	T	C	6	7,562,791	+	CGGGTGAGCTTCTCTGTTATTCACCGGAGACTTGT[C/T]CTTCTTCCGGTTTGTATATCAAACACGACAGCTGC
2,965	6	6006	42.16	TP368	GBS				6	7,781,181	7,781,118	TGCAGAACACGTTAGTTCAACATGTCATGGAAACTAGTGTTGACCCTTCAATATATGCTACATA
2,966	6	6006	42.16	89810779	F1Dsnp	PHR	T	C	6	7,819,606	+	TGCAGATTGGCATTCACTGCAAGAGTTTACGGAGT[C/T]TGCATGTTTTTGATACTATCATTGTTGTTGAACAC
2,967	6	6006	42.16	89810780	F1Dsnp	PHR	A	G	6	7,845,235	+	TAGATATCAAAGTCATGAAAATGGTGGTCACTACA[A/G]GAATGTTCTGTAACACCGACTTTGTTCTTTGTGTA
2,968	6	6006	42.16	4_1643540	GBS				6	7,925,644		GTATTGGGTTCTTGCTTTTTCTGTTTCTGTGGTAAGAGATAAGCATAATTAAACAGAGCAAAAG
2,969	6	6006	42.16	89866747	F1Dsnp	PHR	A	G	6	7,962,431	+	AACTGAGGATCGGCGGCGACTCTCGATCTCCACCC[A/G]TTCAGAAACATCCCCAAAAGCCCAAAACCCTCAAA
2,970	6	6006	42.16	TP534	GBS				6	8,001,228	8,001,165	TGCAGAAGACCACTCTCCCTCAACTGCCCAACTACTAAACCCCCTCCCTCCCTATCATTCTCCT
2,971	6	6006	42.16	89866748	F1Dsnp	PHR	A	C	6	8,003,042	+	TGCAATGGTCACCTCAGTTGGTTATTTTCAGATAC[A/C]TTGGTCCGGCAGGCAGCAATGGTGATCAAGTTTAT
2,972	6	6006	42.16	TP695	GBS				6	8,027,794	8,027,841	TGCAGAAGTACCTGGAGTAGATGGAATACAAGCAAAGTATACTGACCGAGATCGGAAGAGCGGT
2,973	6	6006	42.16	89810781	F1Dsnp	PHR	T	G	6	8,041,728	+	ATTAGGCTCTCCCATGTCTCCAGTAGTGCCATCGT[G/T]GATTCCTCCATTAAACCTACCATGCCCTACACATT
2,974	6	6006	42.16	89810785	F1Dsnp	PHR	T	C	6	8,214,002	+	TTCCCCAAATTATGAGCATTGTCCTAAATATGGAA[C/T]GACACTCAATCCTGGTCATGGAATGTGAGTCCAGT
2,975	6	6006	42.16	89866750	F1Dsnp	PHR	T	C	6	8,252,082	+	AGCATAGAAAGCAACACCAGGCCTAGAACTCCAAC[C/T]ACCAATCCTTTCCATCTCTTCTTTCCGGCGTACGC
2,976	6	6006	42.16	89810786	F1Dsnp	PHR	T	G	6	8,262,428	+	TGGAGAACCAAAGCGGAGCTTCAGATGGGTCAAAT[G/T]AGTTGTTACTAAGGTCTCTGAAAATAACATCAGTG
2,977	6	6006	42.16	TP6532	GBS				NGH			TGCAGGCCATTTACCAAGTAAATAAGCAAGGGTCAACAAGCAAAGCCAAAAATTCCAACAACCT
2,978	6	6009	44.70	89809176	F1Dsnp	PHR	T	G	1	5,159,954	+	CCATGGATGGAAATTCGGGATTCGACCGAATGAAG[G/T]AAGTGAAAGAATTCGACGAGTCAAAGATTGGAGTA
2,979	6	6009	44.70	89865671	F1Dsnp	PHR	T	C	3	3,438,293	+	ATTATCAGTTTCTTCTTCCTCCACTTTTTCCTTGT[C/T]ACTCTTCTGCCCTCCACCCATGTCTTTCCTTTGAA
2,980	6	6009	44.70	89865673	F1Dsnp	PHR	T	G	3	3,516,421	+	AGAGGCGGTGGCACTCGAGCAATCGTGGGTTGCAC[G/T]TTTGCACAATGAGATGTAAGAGTTCCTTTGCCACT
2,981	6	6009	44.70	89809698	F1Dsnp	PHR	T	G	3	3,517,675	+	GGAGCCTTACAAGGACCTTTGAAAACTGCTCCTTT[G/T]AGTTGAAATGTCCCTTTTGGAACAATAACTCTACT
2,982	6	6009	44.70	89865674	F1Dsnp	PHR	A	G	3	3,637,492	+	GCATTTGCCTCCCCTTGCCATACATATTGTTTGTC[A/G]GACTTCGGAGACTTTGTGGAGACAACAACCTACAC
2,983	6	6009	44.70	89865675	F1Dsnp	PHR	A	G	3	3,644,748	+	AACACTTGCTTGGCTTTAGCAAACTGATTGTCTTT[A/G]GACAAACCATGTATAATAGCATTGTAGCTTTCAAT
2,984	6	6009	44.70	89809700	F1Dsnp	PHR	A	G	3	3,645,576	+	TTCTCTATCATTTCATCAAGCATATCCAGTGCCTC[A/G]TCCACCCTCCCCTCACTGCACAACCCATTAATAAG
2,985	6	6009	44.70	2_46746	GBS				3	3,649,829		AAGCTGTCAAACCCTGAAAGAAGCCACCCAGCTCCACGCCCTCTCCCTCAAAACCGGCGCCTTC
2,986	6	6009	44.70	89809701	F1Dsnp	PHR	A	C	3	3,655,873	+	AACGAAGTTGGTGGCATATGCCCATGCATTGTTGG[A/C]CACGGGATCAGCAACGTGGTCATAGAGGTTCTCAA
2,987	6	6009	44.70	2_48402	GBS				3	3,665,140		CCGGGATGCAGTAGCATAGAGCACAGAGGTACGCTTCATGAGTTTATTGTAGGCGACAAATCCC
2,988	6	6009	44.70	89809702	F1Dsnp	Other	T	G	3	3,671,542	+	GGCCGGCAAATGCTGACTGCTGGATTTGAGAGGTT[G/T]CCATGGCTAGTTTTCTGTTTGAGGTGGGATGGTGT
2,989	6	6009	44.70	89865676	F1Dsnp	PHR	T	C	3	3,688,225	+	GCCGAAGCTCTCAGCATTGCTAAGGCTATCGAATT[C/T]TGTACCACTATTATTGATGAAGTTTCTGGTGACAA
2,990	6	6009	44.70	TP3559	GBS				3	3,701,055	3,701,118	TGCAGCATAGTGGCCTGTTCGTCACGAACGACCTGCGGAAACTCTCCGACGTATACAGGCTTGA
2,991	6	6009	44.70	89865677	F1Dsnp	PHR	A	G	3	3,708,071	+	TGTACAGCAGGGAGATCAAGGGTGAAAGTACATGC[A/G]GTGCACTTGCTGAGCTGAAAGATCCTTGCATTTGT
2,992	6	6009	44.70	89865678	F1Dsnp	PHR	T	C	3	3,711,178	+	TGTATCCTATCTAGATCAAACACCTTCAAGCACCT[C/T]GATTGCTGCGACGAGATTTGCTCATCGTCTCCAAT
2,993	6	6009	44.70	157_193171	GBS				3	18,703,313		TGTGAGAGGGGTTGAACTTATGAGGCATGGCAGGAAAGGCTAGGTTTTGCCCGAGTGTTCTTTG
2,994	6	6009	44.70	89809550	F1Dsnp	PHR	A	G	3	19,494,375	+	TGAAGGAAAGCTCCAAGAGAATTAGAAGGATGGGG[A/G]TTCAAGAAGGCAAGAGTTTCACCCAAAACGGGCCA
2,995	6	6009	44.70	89809573	F1Dsnp	PHR	A	C	3	21,671,736	+	CTTCCTCACTACCATTAAACTGATGTAACCCAGAA[A/C]TTTGGAATATCATTGCCAATGACAATACAAGTCCA
2,996	6	6009	44.70	89809574	F1Dsnp	PHR	T	C	3	21,672,564	+	CATATAACATGCAAAGGTGCCCACTAGAAACTGCA[C/T]TTCTCAAACACTTTTCGACAAGCTCCTTACACTTC
2,997	6	6009	44.70	89866034	F1Dsnp	PHR	T	C	4	44,835	+	TGTCACTGCATCTGATGGAGGAATCCGGTATGTGA[C/T]CAAAGAGAACGTAGTTTTGTTCTCTCCCTCTATTT
2,998	6	6009	44.70	89866062	F1Dsnp	PHR	T	C	4	88,322	+	GAGGTTGCTTCATCCAGAGGATATACAAAACAGGG[C/T]AGCTTATCCAATACTCTTATTCCAATTGAAGCTAC
2,999	6	6009	44.70	89810099	F1Dsnp	PHR	A	G	4	88,999	+	CTTACACCAGCCTTAAAAAGATGAATGACTGCATG[A/G]AACAACAAAGATACTCCTCCTCAGTTACCGAAGAG
3,000	6	6009	44.70	2_1366272	GBS				4	119,014		CAACTCCAGTATTTACTTTTCCAGTCACTTTCTTCATGTCTTGACTTGAACTGTTTTGTAGCAA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,001	6	6009	44.70	89848308	SnpSnp	PHR	T	C	4	122,947	+	ATTGGAAATGGAACTGATTCATTGTCTATGCCATT[C/T]GGTGCTTCAAATTATACCACAACAGGCAATGATTA
3,002	6	6009	44.70	2_1376116	GBS				4	161,908		TTTGCCTCTGTTATCAACTCTGATGGGCATGTAGTTGGTGGGTGCATGTCAACATGTGATGATC
3,003	6	6009	44.70	89865883	F1Dsnp	PHR	A	G	4	171,488	+	CAATAATTTATCATTTTGTGATTTGAATTTCAGAC[A/G]TTGATGAGTGCAAAGATGGTACTAAACGATGCTGG
3,004	6	6009	44.70	89809995	F1Dsnp	PHR	A	C	4	21,974,468	+	TTGTGCAGGCTGATGTATGCCATGCATACCAAGTA[A/C]TGAAGAGAGGCGGATTAGAAGATGAGAACATAGTT
3,005	6	6009	44.70	TP7894	GBS				4	22,511,437	22,511,414	TGCAGTACGTCTGTTTCCAACCAAACTTTCCTATACACGCAGGGCCGCTCACCTGCGGACCATA
3,006	6	6009	44.70	89865955	F1Dsnp	PHR	A	G	4	23,124,227	+	ATTTCAGTTTACCCCTTTACCTGTATGGCATGGTC[A/G]TGGTTATCGCTCCTTTGGATATCGTTTTGGTAATG
3,007	6	6009	44.70	328_167554	GBS				4	23,133,530		AAAGGCAGCTCAGATGGGAGCGACCATGAGCAGCAGCACCACCACATCAGGTTCGCTCTCGGTG
3,008	6	6009	44.70	89810009	F1Dsnp	PHR	T	G	4	23,146,304	+	TCCTTTGATTCTTGTTTTGATGACAAAGCAGCACT[G/T]GCTGCTGCCGACATGGCAGCTGCGGCTACACCTAC
3,009	6	6009	44.70	89810010	F1Dsnp	PHR	T	G	4	23,158,207	+	TTGTAATTCTCCACATGCACCTTGACACTTGATTC[G/T]AGGCTTGCTTGATTCATAGCCTCATCTGCCATGAA
3,010	6	6009	44.70	89810011	F1Dsnp	PHR	A	G	4	23,197,881	+	TGACCATGTCAACATATTCACCTAGGTCAGCACAA[A/G]CATCATGGTTAAAGCAGTGAACACTCCAAAAACCC
3,011	6	6009	44.70	178_264056	GBS				4	23,299,266		TGAAAGTTAAATATGGTTTCAGAAATTGTGTCGATTGACAATTTGACACTGACTAGACGAAGAT
3,012	6	6009	44.70	89810012	F1Dsnp	PHR	A	C	4	23,319,656	+	TATTCATGATCATATCTCATCTCTAGCATTAGATC[A/C]TGGGTCTGCCAGGTCACCAGGATCTGGAGGTTCAA
3,013	6	6009	44.70	89865956	F1Dsnp	PHR	T	G	4	23,345,680	+	TGGATGCATTACACTTCATAAGCTCATCATATTGC[G/T]TCTTGATCTTCCTCTGTGTAGCACTAGTGGATGAG
3,014	6	6009	44.70	89865957	F1Dsnp	PHR	A	G	4	23,491,496	+	AATTGAACAAGCTAATAAAGCCATGGATGAACTTC[A/G]TGGCACCATGTTACCATCTTCAGACCGTGGTGGCA
3,015	6	6009	44.70	89810013	F1Dsnp	PHR	A	C	4	23,516,296	+	GAGATATCACCCTTCAGCTCTGAGGTTGTTCCTGG[A/C]TGAGACTTCTTGTTAATACTCGCACAGTCCCCTGC
3,016	6	6009	44.70	89810014	F1Dsnp	PHR	A	C	4	23,625,729	+	AACATTAGCTTCAACGGAGGACAGTATAAGGAAGC[A/C]AGATTAGTAGGAGACTTGTCAATGTCATTCGCACT
3,017	6	6009	44.70	89810015	F1Dsnp	PHR	T	G	4	23,755,988	+	TGAGACCGTGCTGGCAAGCCTTCGGAAACTTTTCT[G/T]AACTCTCCGAAAGAGCTGTCCTTTAGGAGCATGGT
3,018	6	6009	44.70	89865958	F1Dsnp	PHR	T	G	4	23,756,084	+	GTACCAACCACCTCTTCCTTTTAAGCCAACAATTT[G/T]GCCTCCATCCACTGTGAAAGTAAAGGGTGTGCCTT
3,019	6	6009	44.70	89865959	F1Dsnp	PHR	A	G	4	23,804,884	+	CGAAAATTTCTTAAGTTGGAGATAGTATGTGATCT[A/G]AATGAATCACAGTTAGCTGAAGATGACGATGGCCC
3,020	6	6009	44.70	89865960	F1Dsnp	PHR	T	C	4	23,814,304	+	AACATTGGGGTGGTAAAAGTTTGGCCGCTGAGCAA[C/T]TGTGTCAAGTCCCTTTTATCATCAGTAGGCCTTTT
3,021	6	6009	44.70	89865961	F1Dsnp	PHR	A	C	4	23,833,026	+	TTTCAGTGACATCATCTCAACTGAATCTTTCGTTT[A/C]TGTCACATAGCTATCCTTTTTTCGAGCCAATTCTG
3,022	6	6009	44.70	89810019	F1Dsnp	PHR	A	C	4	23,836,693	+	AGTTTTATCTCATCACCTACGAAACAACTAGCACG[A/C]AACGCCAAATCCGAAAGACATGGAAATCTAAGAAT
3,023	6	6009	44.70	89810733	F1Dsnp	PHR	T	C	6	4,212,972	+	TCGCCAACTGCAACACTTGTGAAAGACTACCAATG[C/T]TTGGCCATCTTCCTCACCTTGTACATCTGAGGATA
3,024	6	6009	44.70	89866711	F1Dsnp	PHR	T	C	6	4,297,417	+	TTGTCCTTCATTATGAGCCAGCACTCCTCATCTGA[C/T]AGTTTTTCCAAATCACACCTGGGAAGGGTCTCCAT
3,025	6	6009	44.70	89810734	F1Dsnp	PHR	A	G	6	4,297,883	+	CATAGTTTGACTTGATCAAGGTTTCGACTATATCT[A/G]ACACGACCTCCTCCCTTCCAATGATGAGCTTCTCA
3,026	6	6009	44.70	89866713	F1Dsnp	PHR	A	C	6	4,367,911	+	GTTTGGGTAATGAAAGAATATGGTGTGCTTGACTC[A/C]TGGACTAAGCTCTTTAGCTTTAAGTTTCTGTGTCC
3,027	6	6009	44.70	89810735	F1Dsnp	PHR	A	G	6	4,422,451	+	TTATGTACTGCTATATGGATGTTTGAGTTTGATCA[A/G]TTGGGCCAGTTACTCTAGTCATGTGCCTTTTCTCC
3,028	6	6009	44.70	89810736	F1Dsnp	PHR	T	C	6	4,447,221	+	AATGAAGAAGCCTGTCCAGAAATCCAAGGGTGCTA[C/T]AGCTCGACCTCTAAAACAGAAATCCAAACGCTCGG
3,029	6	6009	44.70	89866714	F1Dsnp	PHR	A	G	6	4,450,145	+	TGGGTACCAGAGCAGATATATGTACTCTCATGCGG[A/G]ACTCGCAGTATCTACTGGAAGATGTCACTGATGAA
3,030	6	6009	44.70	TP1286	GBS				6	4,487,540	4,487,477	TGCAGACTGAAGATGCCTCGCCACGATGATCGATATGGGAATTCGCGTCTGTATGTTGGTCGCT
3,031	6	6009	44.70	89810738	F1Dsnp	PHR	T	C	6	4,579,233	+	AAATTTGGAGAGGTGGGATAGTCTGACCAGATGAA[C/T]GTGGTTGGCAAAGTTGGGAGCCTAATTTCCCAAGG
3,032	6	6009	44.70	TP4216	GBS				6	4,604,267	4,604,218	TGCAGCCTATGCCCATAAAAAGGAACAATAGCAGTGGAAGCTCACTGCCGAGATCGGAAGAGCG
3,033	6	6009	44.70	TP1538	GBS				6	4,640,155	4,640,218	TGCAGAGATTACGTGTTGGAGATTGCTTGCGAGGAAGAGGTAAGATAGGGACACTTCCTTGTAC
3,034	6	6009	44.70	251_226532	GBS				6	4,640,302		CACGTTGGTGACGACGGCTATATCTCTCCGTTTGGTCTGGCTCATACTTGTCCTTGTTTGCAAG
3,035	6	6009	44.70	89810739	F1Dsnp	PHR	T	C	6	4,640,815	+	CGCTCTCCGTTGAAGAGTATTGTCATAGACACCTT[C/T]ACTGCATTCAGCCAATTCTTGATTTTGAGCTCCAC
3,036	6	6009	44.70	89810747	F1Dsnp	PHR	T	C	6	4,804,125	+	AAAGTTCTTATGCTGCTATCATATAGGTTAGAAAC[C/T]AAGTTCAAAAGATGTTCGTCTTCCCCAAATGATGT
3,037	6	6009	44.70	89866717	F1Dsnp	PHR	A	G	6	4,804,132	+	TTATGCTGCTATCATATAGGTTAGAAACCAAGTTC[A/G]AAAGATGTTCGTCTTCCCCAAATGATGTATTCGAG
3,038	6	6009	44.70	89810748	F1Dsnp	PHR	A	G	6	4,871,818	+	TCGTTTCTTGAGATCTGTGCCTTCTCTTCTCCGTC[A/G]TCTCCGGCGAGATTTGGTGTTTGCTCCGATCGTTT
3,039	6	6009	44.70	89810749	F1Dsnp	PHR	T	C	6	4,914,786	+	TATAATACTCTGATTAGCACATTGTGCAAGGAGAA[C/T]CGGGTGGAGGAGGCAACTAAGCTAGCGCGTGTTCT
3,040	6	6009	44.70	89866718	F1Dsnp	PHR	T	C	6	4,930,116	+	TTCTCTCACCTTTTATGCTTCTGTGGTATCTTTGT[C/T]GAAGACAGTCATTAGACCTTTGTATGATGTGAGGA
3,041	6	6009	44.70	89810750	F1Dsnp	PHR	A	G	6	4,931,152	+	CAGTGAGCGGGGTACTTGGCACTGTATACCCTCTT[A/G]TAATGGCAGCTGCCTTGGGCATTGGTGATGGAGTC
3,042	6	6009	44.70	89810751	F1Dsnp	PHR	A	G	6	4,931,463	+	TCTCATTACAGGCAATGCTGGTGGTTATGCTTGTT[A/G]CAATCTCCATTGCATATGGTGGCTTTATTTTTCTC
3,043	6	6009	44.70	65_533287	GBS				6	4,986,862		ACATATTGGCCTCTTCCGGCCATGGTGTTGTTTCATCAGTCCTTGTGATTCAACAGCACGATGT
3,044	6	6009	44.70	65_533191	GBS				6	4,986,958		ACCTAATAATTGTAGGAAAAGGACGGTTCCCRTCAAGCATGGTGGTGGAATTGCCAGACCGGCA
3,045	6	6009	44.70	89866719	F1Dsnp	PHR	T	C	6	5,084,257	+	TTTGATCAGTTATGCACAATTGAGGTTGGGCCATG[C/T]GGCCATCAGATGTGTGCTCATTGCACCCTTGCTCT
3,046	6	6009	44.70	TP1263	GBS				6	5,084,764	5,084,702	TGCAGACTCGGTGCGCCGAAGGACATATATATTATCATATGCTCATAGCACTTAAGACCTCAAA
3,047	6	6009	44.70	89842077	snp	PHR	A	C	6	5,267,580	+	TTCCTATTTGACAAAACATTCTCCACTCCACAATT[A/C]TCCTTATCAACTCCTTCAATGAAGCCAATCTCCGA
3,048	6	6009	44.70	89810752	F1Dsnp	PHR	T	C	6	5,307,904	+	TAAGCTTGGAATGCAGCTTATCATGCACTTCTCTA[C/T]GGATGCAGACATACATATCTTCTTCCATTGTCTCA
3,049	6	6009	44.70	89810753	F1Dsnp	PHR	A	C	6	5,384,073	+	CACCTTGACCCGCTTATTCTTTTCAAGGAGTTCAA[A/C]CCAAGCAAATTCTAACAGTGCTGGATCCTGCACAA
3,050	6	6009	44.70	89866721	F1Dsnp	PHR	A	G	6	5,461,999	+	TGAACCAAAAAACTCCCAGAAGCAAGATTGTTGGC[A/G]CATACTTCATCAGCTCTCCAAACCAATTAACTTGC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,051	6	6009	44.70	89810756	F1Dsnp	PHR	A	G	6	5,641,308	+	AATTGCCTGTCTATACGATGGGCTTCCTAGAAACC[A/G]CTGACGGTAAATCCTCCATCCACACTAACAACCTG
3,052	6	6009	44.70	89866722	F1Dsnp	PHR	T	C	6	5,657,109	+	GCTCCTAACTATGTTAGAAGATACAGCTTTTCCCA[C/T]GACATTGTGAATAGCATTGAATCTATCTTTCATGA
3,053	6	6009	44.70	284_148633	GBS				6	5,715,002		TAACTCAACTTCACTTAGTTTACATGCTTTTTCTTAACTACAACAAAGATCAAGCCTTTCTTGT
3,054	6	6009	44.70	TP7463	GBS				6	5,739,506	5,739,443	TGCAGGTGGAACTTTTGCATAACTAAGGAGGTCTTGCAGCTTCTTTGTGGAGAAGTTGCTCACA
3,055	6	6009	44.70	89866723	F1Dsnp	PHR	A	G	6	5,836,228	+	GGCAGAATTCCTCTGTACAAGCCACGCAGGCCTTC[A/G]TTCCGGATTATGTGCCTAAAAGTTCCTACTATGCC
3,056	6	6009	44.70	89866724	F1Dsnp	PHR	T	C	6	5,922,380	+	TCTTGTGCAGCCATTGCACAAGGGGCAAGGCTCAT[C/T]GCCTCTTCATCTGGAGTCGACTTTCCACATGCGCT
3,057	6	6009	44.70	89810758	F1Dsnp	PHR	A	C	6	5,968,659	+	CCTCAAGTGCACTATGGTGAGGATGATTGCCCACT[A/C]TCAGCTCCCACAGACTTCCCAAAGGATGATGAACT
3,058	6	6009	44.70	89866725	F1Dsnp	PHR	A	G	6	6,138,013	+	TGAATATGAAGGCAGCCTGAAGAAGCTGAATCGCA[A/G]AACCAAAAAGGTATACTGTTTCTAGTATGAATTGT
3,059	6	6009	44.70	89866726	F1Dsnp	PHR	A	G	6	6,153,054	+	ACAAATGATGTGGAAACGTTTAGGCCAGTCTAACA[A/G]TGGTTCTTCCCTTGTTTGATCTGGCAAGTTCATCA
3,060	6	6009	44.70	89866727	F1Dsnp	PHR	A	G	6	6,167,815	+	GATCCGAATCAAGCGATCACCCTCACTAATGACCA[A/G]ATGAAGGCTGTTATCAATGTATGTTTATCTTTATT
3,061	6	6009	44.70	89866728	F1Dsnp	PHR	T	C	6	6,170,410	+	CATACACAGTGGGAACACCCTCAACGCAGAACAAA[C/T]ATCACTCTCAGACCAACCCCATCTCTTATACGCCT
3,062	6	6009	44.70	TP6408	GBS				6	6,277,113	6,277,175	TGCAGGCACTGCGACATTGCTCGCACCAAACAGATTGGGCTGATCAATAGCGTGATGGGCCGCT
3,063	6	6009	44.70	89810760	F1Dsnp	PHR	A	C	6	6,467,064	+	GGGGCTGTTGCTGGCTTCGCATCCTCAGCTTTTTC[A/C]TGTTCTTTGTTTAGCATCTGAAAAACCAGAAACCA
3,064	6	6009	44.70	4_104721	GBS				6	6,547,772		TACGATCAGGTATTCAGGTTCCAAAGTATTCKTACTGATTTACTTATGTTGGCCGGCCTGAAGT
3,065	6	6009	44.70	89810761	F1Dsnp	PHR	T	C	6	6,580,658	+	TTGAGTGCTGCATCCATTGTTGAGGAACTCAAGGA[C/T]TCGACCGTGAAATTTCTGCGTAAAATCATTGGACT
3,066	6	6009	44.70	89810762	F1Dsnp	PHR	A	G	6	6,583,255	+	GGAGAAATCCTTCAGAGTTATGAAGTCGGTGTCTA[A/G]GTACACACCTCCATACTTGTAGAGCACGGTAAGTC
3,067	6	6009	44.70	89810763	F1Dsnp	PHR	T	G	6	6,583,600	+	CTTTGCTGGCGAAAACCATATCATGTAGAACTGAA[G/T]GCTGCATCCATTATTGAGGAACTGGAGAACTCGAC
3,068	6	6009	44.70	89866733	F1Dsnp	PHR	T	C	6	6,583,788	+	AAACTTCATCCGGACCTTCATCAATGGTGATCTGC[C/T]CTTGGATATTAGTAGTAGTGATCAAGGTTGGTTCG
3,069	6	6009	44.70	89866734	F1Dsnp	PHR	T	G	6	6,583,979	+	GAGAAGACTGGGGAATTGGCAGGGCGTCTAAATAG[G/T]TTGTAATCAAACACTTTCTGTGACATTCTTTTCAT
3,070	6	6009	44.70	89810764	F1Dsnp	PHR	A	C	6	6,587,980	+	TCTCCATCGACAGGAATTCTCTGCTTCCGAAAGAC[A/C]TCACAGGTGAAATCCATGTCATGAAGAACTGAGTC
3,071	6	6009	44.70	89866735	F1Dsnp	PHR	A	C	6	6,631,161	+	CTCAGATCTTCCCACGCAGGCCGTAACCTCACTAG[A/C]ACACTTGTATCACGAACCTGCAGTGGGAAAATGAT
3,072	6	6009	44.70	89810765	F1Dsnp	PHR	T	C	6	6,632,554	+	AGAACTGAGAGAGGTGGACAGCGTTCACTTTGCTG[C/T]GAGATGTGGTGGATTCGAATCTCGTTGTTCGGGAA
3,073	6	6009	44.70	4_205022	GBS				6	6,657,756		AGTTGTTCCCGGTGAATTACACCGCCGAGACMTACGAGGTGCCTATTCTCGTGACCATACGTGT
3,074	6	6009	44.70	4_205054	GBS				6	6,657,788		TACGAGGTGCCTATTCTCGTGACCATACGTGTCATCACTTTTTTCTGGTTGGACGATAGCGATG
3,075	6	6009	44.70	4_205097	GBS				6	6,657,831		TCTGGTTGGACGATAGCGATGATGATGATGATGAGGACTCGAGTGTCACTCCTGCAGCTGAATC
3,076	6	6009	44.70	89810787	F1Dsnp	PHR	T	C	6	8,327,483	+	ATCACCAGCTATGCCTTCAATTTCCTTCACCCAGA[C/T]TTTCACGTTCTCACCCAGATCTTTTGTCAGATTCT
3,077	6	6009	44.70	89810788	F1Dsnp	PHR	T	C	6	8,459,132	+	TATGCTAAGTGTTCAAATCTCGATGATGCATTTGT[C/T]GTGTTCAAAGATATGAGAAATCGTGCTGCTTCAGT
3,078	6	6009	44.70	89866751	F1Dsnp	PHR	A	G	6	8,460,065	+	GTTGAAGATAGTTCACACCCAGAGAGGGGTCAAAT[A/G]TATGCAATGCTAGAGGAGTTGTGGTTGCAGATGTT
3,079	6	6009	44.70	89866752	F1Dsnp	PHR	A	G	6	8,461,415	+	GGAAAATCATAATTAATCACACAGTTGATGCCTTT[A/G]AAATCCATACCCCTAGCAATAACATCGGTGGCAAT
3,080	6	6009	44.70	154_299080	GBS				6	8,461,446		CCACTGATGTTATTGCTAGGGGTATGGATTTYAAAGGCATCAACTGTGTGATTAATTATGATTT
3,081	6	6009	44.70	89866753	F1Dsnp	PHR	A	G	6	8,467,183	+	TACACAACCACCCATGCAGCTTCAGTTGCTAACTC[A/G]TCGTCTCTGAATTTAACGAGTTTAATATACATAAT
3,082	6	6009	44.70	89810789	F1Dsnp	PHR	A	G	6	8,468,623	+	GAGGAAATTCTGATCTAGACAGTAAGCGCCTGAGT[A/G]CACGCAGGGTGCTCACCCTCTTTTGCCAAGCACCT
3,083	6	6009	44.70	89810790	F1Dsnp	PHR	T	G	6	8,478,732	+	GCCATGTGCTCATTGAACAGCAGGAAAGCCAAATT[G/T]TGGAGCTGGAATCCGGACTGCAGTCTGCCCAATCG
3,084	6	6009	44.70	89810792	F1Dsnp	PHR	T	C	6	8,884,179	+	CTTTCTTCTTTAAAAGGATTATATGTCAACTGCAC[C/T]ACAAGTTGGCCTCTTTTTTTCTTGTTTTGAGGATC
3,085	6	6009	44.70	TP320	GBS				6	9,013,699	9,013,637	TGCAGAAATTAAGCACTATTTCTCTAGTTTCACCAAGTTTGGGGAGATGGCATTGCATCATTCA
3,086	6	6009	44.70	TP835	GBS				6	9,127,134	9,127,182	TGCAGAATCTTGGTAGTTGATCTCGCTTATTGTGATAGAGTAGATATAAGTCCATTAAACCATA
3,087	6	6009	44.70	TP1367	GBS				6	9,287,511	9,287,546	TGCAGAGAAAGATCTAGTATGGCAAGGTAAAAAGATAAAAAACAAAAACGCCGATGCTGGGGAT
3,088	6	6009	44.70	89810797	F1Dsnp	PHR	A	G	6	9,434,569	+	TGTCGGAAACAACATAGTTGTGGTTGCATACCTCT[A/G]CAAAACTGGCAAGCCTGATATGTTTCTCTCCCAGG
3,089	6	6009	44.70	89814887	codon	PHR	A	G	6	9,436,578	+	TCTCCCATTTCGTCAAACTTCCAACTGCAGAAGGC[A/G]GGACCAATCTCGGACTTCAAGCAAAGTCGTGTCTC
3,090	6	6009	44.70	89810800	F1Dsnp	PHR	T	C	6	9,471,783	+	GTTGCAGTGGAATTAGAAATAGGGTATGATTATAG[C/T]GAAGGGAGCGGGACAGGTCCAAAGCACTGGGGAGA
3,091	6	6009	44.70	89810400	F1Dsnp	PHR	T	G	6	10,131,282	+	CCTTACACAGTGTAGACCATAAAATTTAGTGACCA[G/T]CGTGTTCTCGTATGCTCGAACATGGTTGTAATAGG
3,092	6	6009	44.70	TP2895	GBS				6	10,340,814	10,340,877	TGCAGCAAGCCTATTCCATAAGCAGCTGAAGCTGAAGGATGAGCCACTAAGTTGGTATTCATGT
3,093	6	6009	44.70	89866360	F1Dsnp	PHR	A	G	6	10,343,556	+	TATAATGAGCAATAAGAGCAGATAATTCATACCTT[A/G]TTTATTATGGACTTGAAATGGTCCATCACAGAATC
3,094	6	6009	44.70	89810401	F1Dsnp	PHR	A	G	6	10,348,628	+	AATGCAAGTTTTATCTCCAGTGAATTAGCAATCAG[A/G]TTAAGTATACGACCCCTTTGTGGCTCCCAGTTCCA
3,095	6	6009	44.70	89810403	F1Dsnp	PHR	T	C	6	10,396,847	+	AAATGCATTGAAAAACCTTCTTGTGGCATTCAAAT[C/T]CAGCTTGAGCAGAATGGACATGCCAAAACAGAAGA
3,096	6	6009	44.70	TP2290	GBS				6	10,412,431	10,412,369	TGCAGATGACCCTTATTATCACACCATTACTCCCTCGCCTTACGGGGTTATATATACCTGCACC
3,097	6	6009	44.70	89866361	F1Dsnp	PHR	T	G	6	10,542,475	+	AAGACAAAGAAGATCAAGTGGAAGGTACCACTGGC[G/T]TGCTTATAACCAACAATCCATCTTTTCCTGAAACA
3,098	6	6009	44.70	89866362	F1Dsnp	PHR	A	G	6	10,543,459	+	AAGTCGATATACCTGCTTCTGGAGCCACAGTTGAC[A/G]ACCAGCAAGAGACACATTCCATCAAGACTTGTAAC
3,099	6	6009	44.70	89866363	F1Dsnp	PHR	A	G	6	10,619,890	+	TTATATACATTTGGAAATGCAGCCTTCCCTTCCAC[A/G]AAAAGGAGAAAGTTTGAAACTCCAATAACCTTATG
3,100	6	6009	44.70	89866364	F1Dsnp	PHR	A	G	6	10,622,477	+	AATACCTTGTCAACAGTAGTGTTCTGCCTACAGAC[A/G]ATATTAGCAACACCGATATCACCTCTTGTAGAGAA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,101	6	6009	44.70	TP5597	GBS				6	10,782,837	10,782,900	TGCAGCTTCGAGACCCAATAAAACCCCCAAACCGAGCTCCTTTTTTCTCATTTATTCAATTTCG
3,102	6	6009	44.70	89866367	F1Dsnp	PHR	T	G	6	10,880,330	+	TTCTTTCAGTTTACCTACAGTCATTTCCATCAACC[G/T]CTGACTTGGAATAGGAGTTGGAATTGCATATGGAA
3,103	6	6009	44.70	89866368	F1Dsnp	PHR	A	G	6	10,958,336	+	AAGCTTGTGTTCCGGACCTCTTGAAAGTTGCACTT[A/G]CTTGTCTGGATAACATGGTGGATTCTGATGGATCA
3,104	6	6009	44.70	TP447	GBS				6	12,227,516	12,227,475	TGCAGAACTCAGAACGGTTATACAAACACATACAAGTAACACCCGAGATCGGAAGAGCGGTTCA
3,105	6	6009	44.70	89866375	F1Dsnp	PHR	T	C	6	12,235,674	+	TCCTCTGCTGAGAATGGCAGTGGCTATGTGCTTGG[C/T]CATGTCGGTTATGATCTTCGCCGAGAGGCTTTACA
3,106	6	6009	44.70	80_560689	GBS				6	12,235,705		AAGCCTCTCGGCGAAGATCATAACCGACATGRCCAAGCACATAGCCACTGCCACTCTCAGCAGA
3,107	6	6009	44.70	89866377	F1Dsnp	PHR	A	G	6	12,622,784	+	CAATTGAGATTGGCAAAGTTGAAAGCTGATAGTGT[A/G]TTCACTGCCCCATGCAATACATCAGTACTATATCC
3,108	6	6009	44.70	89810417	F1Dsnp	PHR	T	C	6	12,637,780	+	TTTTGGGTTTTGTAGATTGATCCAAGACACAGGTA[C/T]GGGCATAGCTTGCATGTGTATTATGAAGAATGGTG
3,109	6	6009	44.70	89810419	F1Dsnp	PHR	T	G	6	12,724,743	+	AGGAATCAGCTAATTTTAGAAGAGTTTCTTAAGTG[G/T]AGCTTTGAGGTTTGAATACACAGCGAACCATCCCT
3,110	6	6009	44.70	89866378	F1Dsnp	PHR	T	C	6	12,741,480	+	GTAGCTTGTCCTGCAGAATTCCTAGTATTTGCTGT[C/T]TCAGTAGCTACCATGGACTTCTTTATCTGTCAAAA
3,111	6	6009	44.70	89810421	F1Dsnp	PHR	T	C	6	13,076,732	+	ATGCGTATCAAAAAAATGCAAAAAGCTTTCTCTCT[C/T]AGTGCCCTCACTAAATATTGACGGATCTTCATCCA
3,112	6	6009	44.70	89866380	F1Dsnp	PHR	A	G	6	13,076,805	+	TACAAGAAATCCAAGTCGAAGCGGCTGAACTTGTT[A/G]AATCACTTGGATAGGTTCTTAATGCAACGTAAGGA
3,113	6	6009	44.70	89810423	F1Dsnp	PHR	A	C	6	13,110,612	+	GGAGGAAGTTTCCCATCACATTCTGTCTTTCCTTC[A/C]TGTGAAAGACCTCGTTCGCTATGGTGGACTGTCCA
3,114	6	6009	44.70	89810424	F1Dsnp	PHR	T	G	6	13,124,109	+	CCCATTTGATGAGGCATTTGCTTGACAAGATTAAT[G/T]GCTCTTTCAAGCTCCCCATTTTCAACAAAAACACT
3,115	6	6009	44.70	89810428	F1Dsnp	PHR	T	C	6	14,009,932	+	TCACTAGGAAGAGGACTGACTTCGCTTTTCTATAA[C/T]GTAGAGCAGAACCCGATTTTCTTTAGGGAAAATGT
3,116	6	6009	44.70	TP4503	GBS				6	14,322,581	14,322,518	TGCAGCGCCAGGGCATCGATTTCGAGCGCAACCGCGACAAAGGGATCGACTCGTACAAATTCGC
3,117	6	6009	44.70	89866394	F1Dsnp	PHR	T	G	6	14,680,665	+	TGATATCACCGGTGCCTGAAGGTCGTCTGTCAAAT[G/T]CCCTCAAGCATTTCGATTTCTTGTAGACTCGGCAT
3,118	6	6009	44.70	89837806	snp	PHR	A	G	6	14,726,038	+	AACAATTGTGCGACTGATGAATGAAGAGATTGTCC[A/G]CTTTCAGGAACAAAAGACAATAGATATGGGAGTTG
3,119	6	6009	44.70	89866398	F1Dsnp	PHR	T	C	6	14,804,561	+	AGTCAGCAACAGTTGGAGGTGATCCAAGCTATGCC[C/T]AAAAATCCAAGGTCTGCCCATTTCATCACCGCTCA
3,120	6	6009	44.70	89866402	F1Dsnp	PHR	A	G	6	14,871,064	+	ACGCTCTGACGGCGTTCACCGTCTGATCTACTACC[A/G]AGACGGGTATGCCGTGGTTGATCACTTGGAAGAAG
3,121	6	6009	44.70	89866404	F1Dsnp	PHR	T	C	6	14,877,855	+	GATTCCAACCCTAACCCTTCTGAAAGCAACTCCAT[C/T]ACAGTTTCACCCACCTTGGTTGCATAAACATCCCA
3,122	6	6009	44.70	89810432	F1Dsnp	PHR	T	C	6	14,878,397	+	CGACTCGTCGAATTCTTTCACTTCCTTCACTCGGT[C/T]GTATCTTGAAGTTGCATCAATGGCTGCCATTTTAG
3,123	6	6009	44.70	89866406	F1Dsnp	PHR	T	G	6	14,959,687	+	TATCACACCTTTCTTTCACTTTCCTCCTGATAGTA[G/T]CGCTCCTTTGGGATATAGACTCCATTCTTCTCACG
3,124	6	6009	44.70	89810436	F1Dsnp	PHR	T	C	6	15,013,700	+	AAACGTATAAGGGATTGTGGTTCACTTTACCTTAA[C/T]GAGCTGTTCCGTTAGAATAACATCTTTAGCCCCAC
3,125	6	6009	44.70	84_435867	GBS				6	15,047,141		CGAGGTCGACTACAGTTAGGAACGAGAGAATGTGATGTGCAACCTGATCCGGAAGATCACTAAG
3,126	6	6009	44.70	89866413	F1Dsnp	PHR	T	G	6	15,109,352	+	CAACACGTCTTTTTGTTTTCTTTAGTGAAGCAGCA[G/T]CTACTTCAACTTCAACATGCCTTTTTGTTTTCTTT
3,127	6	6009	44.70	89810439	F1Dsnp	PHR	A	G	6	15,211,601	+	TAGAAATAGTAGCAATATTGCCACTGAAAATGTAG[A/G]CTTGGAAGCCATCTAACTCGAGCTTTGGTTGAACT
3,128	6	6009	44.70	89810440	F1Dsnp	PHR	T	C	6	15,256,920	+	AAGGGCAACTGTCCAGGTTGAACTCCCTTCTCTAG[C/T]TCCAGCACTTTCACTATCCGGTTTACAGGAAAGCC
3,129	6	6009	44.70	89895145	snp	PHR	A	G	6	15,376,701	+	CTACCATGCTCGCAGCACAAAGCATCCAGTTGGGC[A/G]TCAATGATGTTGTTGTAGCTGGTGGAATGGAAAGC
3,130	6	6009	44.70	89810441	F1Dsnp	PHR	A	C	6	15,406,127	+	TCACTCTGTTTCACAATGGACTCTCCAACCAAAAC[A/C]GCTTTAACACCAGCTTCTTGCACATAGGCAATGTC
3,131	6	6009	44.70	89866415	F1Dsnp	PHR	T	C	6	15,410,703	+	TATACATTCAACAAGAATGCTAAAACTATCTCACC[C/T]CTTCAAATTGTTTGCTCATACTTGGAGGACTGACA
3,132	6	6009	44.70	89810442	F1Dsnp	PHR	T	C	6	15,434,136	+	GGCAATCACAGCGAGGAAGAAATCTATGCAATGCT[C/T]AAGGAATGTAACATGGATCCCAACGAGACCGCTCA
3,133	6	6009	44.70	89866416	F1Dsnp	PHR	A	C	6	15,484,027	+	GTTACCTCTTGTTCACCCACTAAACATGACCGTCT[A/C]TCATCAACAGGAGTCTCTCTTTTACCAGCTTCAGA
3,134	6	6009	44.70	89866417	F1Dsnp	PHR	A	C	6	15,788,385	+	TAACACGGCAAAGCTTGTCCAAGTCCACAGAGCTA[A/C]CTTCAATAGGTTTCACCTAAGGACAGTAACAGATG
3,135	6	6009	44.70	89866418	F1Dsnp	PHR	T	C	6	15,797,091	+	AGTGATTAACAAACCTCATGTGCAATAGGCCAGGA[C/T]AGATCATAAGGAATTGGACCACCACCACCTCCACC
3,136	6	6009	44.70	89866420	F1Dsnp	PHR	T	C	6	16,027,571	+	CGTGTTTTCCACATATTCCACATCCATAGTTAAAC[C/T]ATGAAAGTTCAAAGCCATGAACTAACTCATCGTAT
3,137	6	6009	44.70	89866421	F1Dsnp	PHR	T	C	6	16,055,592	+	TACTATTCATTTGTTGAAAAGATCTTCCAAGCTGA[C/T]GCTGTACTGCATTTTGGTACTCATGGTTCACTAGA
3,138	6	6009	44.70	89810445	F1Dsnp	PHR	A	G	6	16,057,682	+	GCAAGGACCAAGTTGTTGAATCCCAAGTGGTATGA[A/G]GGAATGTTGTCTAGTGGTTACGAGGGTGTTCGTGA
3,139	6	6009	44.70	89810446	F1Dsnp	PHR	T	G	6	16,062,641	+	CAAGGGACAAGTAGATCGCACCTTTCAGGCTCCAA[G/T]CCGACGGCGTTTTGGAGTTCCCAATCGCCAGGACC
3,140	6	6009	44.70	548_42524	GBS				6	16,747,984		AGGGCAATGATCCTTCTCAGCGATTATGGTGACTTCTCAGACATCATGAAGGTGCCACTTGATT
3,141	6	6009	44.70	89810451	F1Dsnp	PHR	A	C	6	16,865,440	+	TGCAGAAGGAATGTTATCCGTGAGTTCAAGGAGCT[A/C]AAAGAGCTGAAGCGCTTGCGGAAGGAGCCTCGCTG
3,142	6	6009	44.70	268_167301	GBS				6	17,168,372		ATTACTTTTCAAAGTGGCAACATCTTTCTGATTCTCGATCAGTTTGCTGTGGAGTACGTTCGTA
3,143	6	6009	44.70	89810459	F1Dsnp	PHR	T	C	6	17,464,850	+	ACCCTCGATTGAAGGGGAATGTCTTCAGTTAAACA[C/T]TGGGGAATGTTTCCACTCAAAGAATTATTAGACAG
3,144	6	6009	44.70	89866429	F1Dsnp	PHR	A	G	6	18,129,465	+	TCAGCTGATTCATCTCTATTTCCTTTCTTGTATCT[A/G]CCATGTAAAATTTGAAATCACCATCCACATGTGCT
3,145	6	6009	44.70	89810461	F1Dsnp	PHR	A	G	6	18,131,749	+	CATACTTTCATTCCCAGAGGGTTCTGGTAGTTCAT[A/G]TCCTTCCGGTAATCTCCTAGGAAATAGTCAACAAG
3,146	6	6009	44.70	89810462	F1Dsnp	PHR	A	G	6	18,133,204	+	ATTCACTCACTGGCTCAGGGTCTGAACTAAACAAA[A/G]TGTAGGCTCTCTTAAAAGAAGCAACCGCATTATCC
3,147	6	6009	44.70	89810463	F1Dsnp	PHR	T	G	6	18,312,685	+	ACAGAGACTGCAGAGAGAGTTGGGAGTCTTTTGCA[G/T]AGCTCGCAGGGGCAGGGAAGCAAGCAAGCTTTTGG
3,148	6	6009	44.70	89810464	F1Dsnp	PHR	T	C	6	18,314,085	+	TGCTATTTTGCACCACTGGAGTATTGCTTCGTCAG[C/T]TGGTAATATTTTTGTATCCTAGTATATTTCCAGTA
3,149	6	6009	44.70	89866430	F1Dsnp	PHR	A	G	6	18,319,216	+	AGTTTGTAGATCTATTATCAAACATTGGCTTTGTC[A/G]ACAAATCCAAGGGTGCTAGTGTAAGTTCCTAAACT
3,150	6	6009	44.70	267_132845	GBS				6	18,320,458		TAACAGGTCAGGTTATTATGTATACTTACATGCCAACTTTTACCGGGCTACTTGAATGATTTTG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,151	6	6009	44.70	TP9765	GBS				6	18,460,417	18,460,469	TGCAGTTTGATTTTCTTTTTGACATATGAAATTTTGTTGTAAACAAACACGGTTCAAAATATAT
3,152	6	6009	44.70	TP826	GBS				6	18,508,300	18,508,363	TGCAGAATCTGACGTGTCTGAGCTGCAATTTGGTGGGGCCCTTGCCCAAGTTTCTCGGGAATTT
3,153	6	6009	44.70	89810465	F1Dsnp	PHR	T	C	6	18,509,510	+	AGTGGTTCTGCAAGCAGAAACAGCAGTGGGATAGG[C/T]GAGTCTCATGTCATTGAAGCTGGAAATCTTGTCAT
3,154	6	6009	44.70	89810466	F1Dsnp	PHR	A	G	6	18,521,476	+	ATTTTGCGAAAGAACCAGTTCTTTTTAGAGGACAA[A/G]AGCAAGCTGAAGACTGCTCTTTCTGGGTTGGAGCG
3,155	6	6009	44.70	89810467	F1Dsnp	PHR	A	G	6	18,553,071	+	AATAAGGCCATCTCTAAGCTCGAAGATGAGTTTCG[A/G]CAGCTCCTTTCAAATTACAGGTTTCGCTATTTTGA
3,156	6	6009	44.70	89810468	F1Dsnp	PHR	A	G	6	18,571,054	+	GTCGAATGCTAATACCTTGATGGAGTTCAAGTTCG[A/G]CCTCAACAATGCCACGGCGCCGGCAGAGGATATGC
3,157	6	6009	44.70	TP2989	GBS				6	18,687,527	18,687,589	TGCAGCAATTCAACACAAATCACCTATCTATCTATTCTAACCTCGGTCCATAGGGACTTCAGTC
3,158	6	6009	44.70	89810472	F1Dsnp	PHR	A	G	6	18,783,033	+	CCCAGGGCAGACTAACAGTGTTACCGCTGTGAAGT[A/G]CTTCATCAAGGGATAAATTTCTGACATATTCATAC
3,159	6	6009	44.70	89810473	F1Dsnp	PHR	A	G	6	18,837,296	+	CATGACCCGATCCAAAAGGACATGGCAACTCAAAA[A/G]AAAGAAGCGCGGATTGCCGAGGCTGAGCAGCAGAA
3,160	6	6009	44.70	89810474	F1Dsnp	PHR	T	C	6	18,859,645	+	CAAGATATTAAACATAGTGGACACGTTTTTAACAG[C/T]CTCTGTTTCCTCTTCTTCAACAGTATCACCAAGCT
3,161	6	6009	44.70	TP3486	GBS				6	18,967,614	18,967,676	TGCAGCAGTAGTCGACCTTTGCTTGATCGGCTGAAAGACCAACGTAGCGGAGTAAACTTCCCGA
3,162	6	6009	44.70	89810477	F1Dsnp	PHR	T	C	6	19,362,755	+	TTTAAGCTAAGATACTGATCTACTTCATTTAGCAA[C/T]ATGATCATCACCTTCATCCTTTACAAGCTGAATAG
3,163	6	6009	44.70	89810480	F1Dsnp	PHR	A	G	6	19,793,930	+	GAGAAGTAATTATACGACAGGTTCAACGTCCCGGC[A/G]AGGCTTTCGAGCTCGGTGAGAGACTCCGGGAGGGA
3,164	6	6009	44.70	89866436	F1Dsnp	PHR	A	G	6	19,869,473	+	GTAGTTCTTCAGAACTCTCTGATTGATATGTATTC[A/G]AAATGTGGAAAGCTGAGTTACTCAAGAAGAGTTTT
3,165	6	6009	44.70	89810483	F1Dsnp	PHR	T	C	6	19,984,574	+	CTTTGCATTAATAAATGTGGCTTCTTTGGAAGGGC[C/T]ACTACAATGAATATGTGCTCCAAATGTTACAAGGA
3,166	6	6009	44.70	89810484	F1Dsnp	PHR	T	G	6	20,367,373	+	AAAGGAAATTACCGTCGGTATAGAACGGAGAGTTC[G/T]CCTCGGTTTCTGAGGAGGGCATGCTCTCCGGCAAT
3,167	6	6009	44.70	89866438	F1Dsnp	PHR	A	G	6	20,438,020	+	TCGATCCATTCCCAATCTAATGAGGAAAGAGCTTC[A/G]CCACCAACCTCAGATGGTCAGAAGACTGACAACAC
3,168	6	6009	44.70	89866439	F1Dsnp	PHR	T	C	6	20,441,433	+	GGCGGCCCCACATGGACCTCCTGGACTGGCTGGCC[C/T]TGTTCTTCGGGTTCCAATACGACAACGTCCGCAAC
3,169	6	6009	44.70	TP6732	GBS				6	20,442,353	20,442,416	TGCAGGCTGGATTGTTGTTTTCGGGGTCTGTTATGGGAGGATATGGTCCCAGAGAAACCTGGAT
3,170	6	6009	44.70	89866440	F1Dsnp	PHR	A	G	6	20,444,942	+	CGAATGCATTATGGTCATCCAGATGTCTTTGACCG[A/G]TTTTGGTTCTTGACTCGAGGTGGCATCAGTAAAGC
3,171	6	6009	44.70	89810485	F1Dsnp	PHR	T	C	6	20,463,786	+	CATTCAAGTCAGCTAGTCAAATGTGTGTTTTAAGC[C/T]GCACCTCGAAACTGCTCACAGTCTGTTGATCCATT
3,172	6	6009	44.70	89810486	F1Dsnp	PHR	T	C	6	20,561,397	+	GCTCCTCCATTGCGAATCACTACTCCAAAGTTTGA[C/T]AGGGGTAAGGCGGGCCCGAACGATAGGGGCAATGA
3,173	6	6009	44.70	89866441	F1Dsnp	PHR	A	C	6	20,726,461	+	TTCAGAATCAGACGGTGCCGGTGCCGGTGCCGGTG[A/C]AAGTGGTGCTCCTTCTTCTGGTGCATCTGCCACTG
3,174	6	6009	44.70	89810487	F1Dsnp	PHR	T	C	6	20,735,377	+	ACCCGAACCCGAAGAATCCACCTTCTGATGATGAT[C/T]GTCTTCTCTTTCTTCCGCGGTGCTTGTCTTGATGC
3,175	6	6009	44.70	89810489	F1Dsnp	PHR	A	C	6	20,908,232	+	TTTCATGTTTGGTACAGCTATCTCATCAAATTGTG[A/C]GGGGTCCTGAGCTTCCACCTTCTTCGTATATTCCA
3,176	6	6009	44.70	89810490	F1Dsnp	PHR	T	C	6	20,970,458	+	GGTGTCACAAATAGAGTTCCACGAGGTTCTAAACT[C/T]ATTAATGCATAGGATGTGATTGTACCATAGCCCAT
3,177	6	6009	44.70	89866445	F1Dsnp	PHR	T	C	6	20,974,620	+	TTGGGTGGTGACACAGAGAGCTCGAATCCTTCACG[C/T]CTCATATTCTCAATTAAGATACCTGTTTTGCAAAA
3,178	6	6009	44.70	89796411	snp	PHR	A	G	6	20,980,048	+	AGTTGAATACCAACCAGCATTTGGAAAGGTGCCTC[A/G]ATGTTTGCATTTGGTGGGGGAACATGTCTGATAAT
3,179	6	6009	44.70	89810491	F1Dsnp	PHR	T	C	6	21,039,068	+	CTTCCAAGAGATTTTTCATCAAGTGTGCCTCGTGC[C/T]CAAACCTAAACTTCTCTGTTTGGAGCTTTTGCTGC
3,180	6	6009	44.70	89866446	F1Dsnp	PHR	T	C	6	21,168,234	+	GGGCTCAACCGGCAGTTTACGAGGTTCTATATCAC[C/T]TGTTGTGTTACCACTTACAGAGTAGCTGATATGGT
3,181	6	6009	44.70	89810494	F1Dsnp	PHR	T	G	6	21,267,289	+	CCACATTCTCCTTGGTCCTTGACAGGCATCACAGC[G/T]CCTTTGGTTCTCCAGTCTAGTGAAGATGGCACTAC
3,182	6	6009	44.70	60_41649	GBS				6	21,285,793		TGAAACTAAAATTCAAAACCCAACACACTTCKGCCTGAAAATACAGAAAAGACCGAAAATTTTC
3,183	6	6009	44.70	60_41600	GBS				6	21,285,842		TACTCCCCAGTCCGCACACGAAAACTTTATAAAGCAATTCCCTCCTCCTTGAAACTAAAATTCA
3,184	6	6009	44.70	89810495	F1Dsnp	PHR	A	G	6	21,548,673	+	TGATTAGCCTGACCAATTCTCTCAAAAACCATCCT[A/G]GCCAACCCAACATCCCGACACTTGCCATAAAAATC
3,185	6	6009	44.70	89866448	F1Dsnp	PHR	T	C	6	21,631,980	+	AAACCACCAAATCTTCCAGTGAAAGGACCACAATT[C/T]TTATCAGAACTAGAGACCAACTCATTAAAATCACC
3,186	6	6009	44.70	89810497	F1Dsnp	PHR	T	C	6	21,772,848	+	ATGCTCTGTGCCGATCCAAAAAATACGGTTTTCAT[C/T]GTCACTGGTAGAGGGAGGGAGAGCTTAAGCAAGTG
3,187	6	6009	44.70	TP4879	GBS				6	21,863,953	21,864,016	TGCAGCTACTTGTTTCCGATTTCCGACCAAGAGCTTTCTTGTTTAGAACGTTTCATGTTTCTAA
3,188	6	6009	44.70	89810498	F1Dsnp	PHR	T	C	6	21,931,357	+	TTCCCAGTTACAGTCTCCTTGTCAGCCTGTATATT[C/T]GATACTGAAGGGGGAGAACATCAGTGAAGACAAAG
3,189	6	6009	44.70	89866449	F1Dsnp	PHR	A	G	6	21,983,988	+	ATTGATTTCATTGTTGGAGACTTCTTCCAACTTGC[A/G]CCATCATTGAAGGTACTGCTTTCCTATCTGTACTA
3,190	6	6009	44.70	89810499	F1Dsnp	PHR	T	C	6	21,987,814	+	TCGAAGATATGCAATATCTGCAGTTTCCATTACCG[C/T]CTGTGCCGTTCATGAATCCTTATTTGGGTACAATG
3,191	6	6009	44.70	89810500	F1Dsnp	PHR	T	C	6	22,025,532	+	GAGTTCAATTTCAGCGACTTTGATATCGAAACTGA[C/T]GATCACAACGACGCCTCAATTGAGCTTCTCAAGAC
3,192	6	6009	44.70	89866450	F1Dsnp	PHR	T	C	6	22,037,296	+	TCCCAAAATTATGATGCTACACCTAATCTTGGAGG[C/T]GGAGGAGTATCCACTAGGTCCAAGTCCAACACCAA
3,193	6	6009	44.70	TP5147	GBS				6	22,077,012	22,076,972	TGCAGCTCGTCGACGACTTCAGAGCCAAAAATGCCGCGCCGAGATCGGAAGAGCGGTTCAGCAG
3,194	6	6009	44.70	89810501	F1Dsnp	PHR	T	C	6	22,093,229	+	GTAACATGGAAACAAAACAGGAAAGTGTGCCCACT[C/T]TATTTTTGTTCTGTTCGTGAGCTGCAATAATTGCA
3,195	6	6009	44.70	89866451	F1Dsnp	PHR	T	C	6	22,161,567	+	ATTCCCTGGCCTGTGCGAATGAGTATTACCAATTG[C/T]AAAATTCCGTTGCGCAATCCTGAGGAGGCATTCAA
3,196	6	6009	44.70	89866452	F1Dsnp	PHR	T	G	6	22,220,957	+	CTGCATGATCATAAGCTTGTAGGGAAGCTTTCACC[G/T]ATCATTTCAAATCTAACCGGCCTTCGTTACTTGGA
3,197	6	6009	44.70	89810502	F1Dsnp	PHR	A	G	6	22,287,075	+	GACATTCGATGGACAGATCATATGACCTCTCGCCC[A/G]ATATTGATATATCAATTGTGAGTAGTGAAAGACCA
3,198	6	6009	44.70	89810504	F1Dsnp	PHR	T	G	6	22,328,532	+	AAGAATGGAAACATGGAGGAAGCTGAAGAATTCAT[G/T]CTTGTAAGTAAAAAGTTCTTCCCACTGGAGGTCGA
3,199	6	6009	44.70	89866454	F1Dsnp	PHR	A	C	6	22,347,508	+	TTCCAAACCCAAATTGTTGTACTTGAGGTCCATTT[A/C]CATTTTCAAGTTTATCAACTGGAGATGCAATATCT
3,200	6	6009	44.70	89810505	F1Dsnp	PHR	T	C	6	22,347,926	+	ATTATAATTTACGGAATTCAAGTTCAAAGCTTTAA[C/T]ATTACAGCACTTCCTACTATTTTTCGATGATGAAG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,201	6	6009	44.70	89810506	F1Dsnp	PHR	T	C	6	22,356,785	+	CTTTTGTAGGTTGGATGATTTGGATACAATGTCAA[C/T]AAGTTCAGATACCGGGAAAGTGAAGAAATGTGGAT
3,202	6	6009	44.70	89866456	F1Dsnp	PHR	T	C	6	22,711,616	+	GTAAGCCGGCCAACGCCGCGAGATCTAAGGTCTGT[C/T]GTCTTTGTCCACTTTGGTTCTCTTCTCGCTTTCTT
3,203	6	6009	44.70	360_116973	GBS				6	22,780,236		CGCGTGGAGGAGGAGGAGCGCGTCAAGAATTSGGAAGAGGAGGCGGAGAAAGTGGATGAGGTGG
3,204	6	6009	44.70	89810510	F1Dsnp	PHR	T	C	6	22,847,156	+	TGCAGGTTAATCTCCCTGTTAACATATTGCCAGTG[C/T]CATTTCCGGGTCACAGTCATAGTCAGGCTTTGAAT
3,205	6	6009	44.70	89866457	F1Dsnp	PHR	A	G	6	22,857,226	+	GCATCCAAATTAAGTGATTTAAGAGATGATAGCCC[A/G]GACAGCTTTCTTAATCCACTATCACAAACCTCAGT
3,206	6	6009	44.70	TP6572	GBS				6	22,885,026	22,884,966	TGCAGGCCTAGTTGTGACCACTCTTTTGACAATTCCTTGGCTAAATCCAACTGAACAACCGAGA
3,207	6	6009	44.70	89810511	F1Dsnp	PHR	T	C	6	22,926,009	+	AGGTTGGAAACCCCCATTGCAGATTAGAAGGATGC[C/T]GAAGAAGCAGTGTGATTTGATTCGAAAGCAATGGC
3,208	6	6009	44.70	215_106220	GBS				6	22,970,863		TCACCAATGTTGAGAAGAATAAAAGCACCAGYTCCATAAGTGCTTTTGGCTTCACCTTTCCTGC
3,209	6	6009	44.70	89810512	F1Dsnp	PHR	T	C	6	22,971,871	+	GTGGCTTTGTTCACAGCCGTAGCCATACAAAGTTT[C/T]ACGCCCTCAAATATCTCCATTGGATCATGCTCCAC
3,210	6	6009	44.70	89810513	F1Dsnp	PHR	A	G	6	23,036,180	+	GGCTCCAATAATGTTGATATCACGAACCCAGTTCA[A/G]TGGTTTGATCATTTGTATAGAAGAGCAATGCAAGT
3,211	6	6009	44.70	89866458	F1Dsnp	PHR	T	G	6	23,069,459	+	AAGATAAGGCTGTTCCGAACGGTGATTGTTGATTC[G/T]GAGGGTCACAGAAGCATAGATGTTGACGAAGGAGA
3,212	6	6009	44.70	89866459	F1Dsnp	PHR	T	C	6	23,138,061	+	GAGTTGCCTTGTTGTGCCTGCTTCAGATGCATTGT[C/T]AAGGCATAGTTGTTGAGCTGCCACCAAACAAGAAA
3,213	6	6009	44.70	89866460	F1Dsnp	PHR	A	G	6	23,141,970	+	GCTTTTGTGATCACTCTTTCAATCTTCTTGAACTC[A/G]GAGTGAACACAAGCCAAGGCAGATCCACCTGATTG
3,214	6	6009	44.70	89866461	F1Dsnp	PHR	A	G	6	23,185,019	+	TTCTTCTGAGCCTTGGGTGGCCTATGATGCAACTC[A/G]TTCAACACAAAACATTTTAACAACTTCTGATAGCT
3,215	6	6009	44.70	89810515	F1Dsnp	PHR	A	G	6	23,208,248	+	TGAGTGCTGACCATGAAGATGAGAAAGCAAGCTCA[A/G]ATTTGGCATGTAATCATATACAATTAAACGCTCTT
3,216	6	6009	44.70	89810516	F1Dsnp	PHR	A	C	6	23,210,473	+	TCAAGGAAAAGATCCTCCATGTTGGTTGCTTCTTT[A/C]CTTTTTGTTTCCTGTACATCAGATTCCATTCAAAT
3,217	6	6009	44.70	89810517	F1Dsnp	PHR	T	C	6	23,457,439	+	TCCACTTCTTCCCCTTCAATAAGTTGTTCAACAGG[C/T]ACATACGCTCTTCCAATTAATGATGCTCCAATAGG
3,218	6	6009	44.70	89810518	F1Dsnp	PHR	T	C	6	23,504,381	+	CAAGTTTATTCCATCATACCATGAGGTCCAACCTA[C/T]ACGAAGGCACAACTTCTGTCAATATTTCCTAGCGG
3,219	6	6009	44.70	366_42777	GBS				6	23,513,849		TAACCCTGCTTATTACATCTCTACAATCCTCATACTTCTTGACAAAAATAGTTTGAATTGATGC
3,220	6	6009	44.70	TP2236	GBS				6	23,532,417	23,532,461	TGCAGATCTATGTATCTTGCCTCTCCCACCGTCGGCAATCCTCCGAGATCGGAAGAGCGGTTCA
3,221	6	6009	44.70	89866462	F1Dsnp	PHR	A	C	6	23,679,409	+	ACACATGATTCTCATGTTCTCTGATTCTACTATGC[A/C]CAAGTTTAATCTTTTTGAAGTGAAAAAGTTGGTCT
3,222	6	6009	44.70	89866463	F1Dsnp	PHR	T	C	6	23,697,213	+	GCACAGAGAAGACAAAGGGTTTTCCCAGTCCCAGT[C/T]GGACTCTCCAGCAGTGCATTAGATCTCTGCATAAT
3,223	6	6009	44.70	89810519	F1Dsnp	PHR	A	C	6	23,713,997	+	AGAGGAAGAAGTTGAGGTTCCTGTCACAAAAGAGC[A/C]ACCAAAGGAGGCAACAAAGATGGAGACTGATGAGG
3,224	6	6009	44.70	TP5910	GBS				6	23,782,880	23,782,936	TGCAGGAAGCTCTCCTAAAAGCTACCAGGAAGATCTCTTCGTATTGGGTATGCATAGGCAGGAG
3,225	6	6009	44.70	89810520	F1Dsnp	PHR	A	G	6	23,800,145	+	CTAGGTGAATACCTCTGCATGAGACGTGAACTGCA[A/G]GAGATCAAGATCCCTACAACACGATATCGCTCAAG
3,226	6	6009	44.70	89810521	F1Dsnp	PHR	T	G	6	23,807,106	+	GCTGCGGCCATAATAATGTTTGAAACAACTGTTTT[G/T]GCTCCAGCATTGTAGTTGACTGCAGATCTAGAGAA
3,227	6	6009	44.70	TP6460	GBS				6	23,837,747	23,837,812	TGCAGGCATGAACTCCTAAAAGCCCTCGCGACTAGACAAAGGATCAAATCGTTTTAAACCCGAG
3,228	6	6009	44.70	89810522	F1Dsnp	PHR	T	G	6	23,957,908	+	TATCCTTGAGTTGGAGTATTCAGTTCGTGTGACTG[G/T]TGCATATCCTGGGAGGTAACATATTATCATAATAA
3,229	6	6009	44.70	89866464	F1Dsnp	PHR	A	G	6	24,005,321	+	ATTTAAGCTTCTTTGCAATGAAGTCTTAATGTGTT[A/G]ATGAACATGCACACAAGGAGACTCTCAAAAGTCGA
3,230	6	6009	44.70	237_164087	GBS				6	24,367,728		CAGAATTTGTTGACCTTGGAATTTGTCGTCTSGTGGACGCGCCGCCGGACGGGGCATGAAAAAC
3,231	6	6009	44.70	89866465	F1Dsnp	PHR	T	G	6	24,381,312	+	GGCTGGTATGAGTTTGAGATTTTCATGAAAAAGCT[G/T]GGTATATTAACTATTAAGCAAATGTTCTCTCTCTC
3,232	6	6009	44.70	89866466	F1Dsnp	PHR	A	G	6	24,452,523	+	TGGACTCACCTATATCCCTCTGCCATCATAGACTT[A/G]ACCAAGTCCAGTATGCGAAAGTAATGATAGAAAAG
3,233	6	6009	44.70	89810525	F1Dsnp	PHR	T	C	6	24,660,441	+	CCTCAGATTCTCCACAACTGAAGTAGGATCTCGTG[C/T]AGTTCGTTCATATTTATTGTTAAGCAAAGGAGCTG
3,234	6	6009	44.70	89866468	F1Dsnp	PHR	A	G	6	24,733,310	+	ACTTAAATCTCTTGCCCCAAAATCCAAAACCCTCC[A/G]CTCTTTCTTCAACTCTCTTCTCCGACCCACCAAAC
3,235	6	6009	44.70	89839419	snp	PHR	T	C	6	24,740,476	+	AAGCATGTTACAGTGCTTTACGCCTCACAAAATCC[C/T]TGGAGAAGAAAGCCTCTGAGCTTCTTGATGCCATA
3,236	6	6009	44.70	89839420	snp	PHR	T	C	6	24,740,613	+	TATCCCAACCTAGCTCCTGCTTCTATTGAAGCCAT[C/T]AAGGCAGCACAGGGAGATAGAAAGCCGTGGACTGG
3,237	6	6009	44.70	89796837	snp	PHR	A	G	6	24,740,704	+	GGAAGCGAGGAAAATGTCCTCTTACGCCTAATGAG[A/G]CAGCCTTCATACTACAAGTGCTTTCCATCCCAACA
3,238	6	6009	44.70	89796838	snp	PHR	T	G	6	24,740,855	+	CAAATCTAGCCTACTTAGTGGTGAGGATTTCAAAA[G/T]CATGCATGGAAACACAAAAGCAGCATTGGACTACT
3,239	6	6009	44.70	89810526	F1Dsnp	PHR	A	G	6	24,817,815	+	ACTCTAAAATTCTTCTAGATGTCCTCACTGGTAAA[A/G]CACAATGCCCTTGGAGGATCAAATTTTTAGTCCAA
3,240	6	6009	44.70	89866469	F1Dsnp	PHR	T	G	6	24,919,068	+	ATTCAGAAAATAAAAAAAATAACCATGGGTGCAGA[G/T]ATCAAATTAGTTGGATTGCATGAGGCCCTCGACCC
3,241	6	6009	44.70	89866470	F1Dsnp	PHR	T	C	6	25,021,718	+	CATTGGTGAAATTGGACTATGTGGTGAACTTCGCC[C/T]GGTAAGCTTATTATTTCAGCATTTTAATCTTATGT
3,242	6	6009	44.70	TP6043	GBS				6	25,032,497	25,032,432	TGCAGGACTCTGATTCACAAAACAGATATAACAATTAAAAACCAACGAGGAAATAAATATATAA
3,243	6	6009	44.70	89810527	F1Dsnp	PHR	A	G	6	25,107,507	+	AGATTGAATCAGGGACTCTTTATAAACTTGTCATT[A/G]GAGTCAAGGATGAGAATGTTCATTTCCCCACAGCC
3,244	6	6009	44.70	89866471	F1Dsnp	PHR	T	C	6	25,214,018	+	ACTGCCTCAAGATGATTTTGATGTGCCTTTCCCTC[C/T]AAAACTGGAAGCAGTATTTGAGATTGGTGCAAGTA
3,245	6	6009	44.70	TP2786	GBS				6	25,363,631	25,363,568	TGCAGCAACACCCCCAACTACCCCTTCCATCTCATGGGTGGAAAGCGCCGCAGCCACCACAGCA
3,246	6	6009	44.70	89866473	F1Dsnp	PHR	A	C	6	25,434,464	+	TGTATGATATCCCAGTTCTACAAAACTCTCAGCAT[A/C]GGAGTTTGTGGATACTGACGAGCTATATTCTGGTG
3,247	6	6009	44.70	89810529	F1Dsnp	PHR	A	C	6	25,491,284	+	ATTACATTCAATGCCTTGATAACAGGGTACTCGAA[A/C]GATGGCTTGAATGAAGTTGCTATTAAGCTCTTTGC
3,248	6	6009	44.70	89810532	F1Dsnp	PHR	A	G	6	25,701,357	+	TAGATCTCCTTGTCACTCTTCCCAGCATGAAACTC[A/G]TCAGGAATTAACTGCACAATTATCAAATGCATTAC
3,249	6	6009	44.70	89866478	F1Dsnp	PHR	T	C	6	25,998,626	+	ATACAGGGGGTGAGGCTGCTGCTGGGAGTGAGAAG[C/T]TGAAGCTTGAGATGGTTAGTCAATTTATTCACTTT
3,250	6	6009	44.70	89866479	F1Dsnp	PHR	T	C	6	26,021,149	+	ACAATAATATAGCAGCATTCCATAATATGTGGAAG[C/T]TGAAGGTTTCAGAAGGTGAGAAAGATTCCTCGGGT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,251	6	6009	44.70	TP4676	GBS				6	26,028,220	26,028,279	TGCAGCGGTATCTGCTAGGCAGAGTATGGTGTCGTTGGGAAGTGATACTGGTGGAAGTGTAAGG
3,252	6	6009	44.70	89810535	F1Dsnp	PHR	T	C	6	26,028,445	+	GCTGGGATTCTTCTTCATGCAATTTCTGGTCATGA[C/T]AGGCTTGATGCCACCAGCAGCAAGCGTGTAAGTGT
3,253	6	6009	44.70	89866481	F1Dsnp	PHR	A	G	6	26,388,931	+	AATGAAACATTCCGAGCAGCATTGCTCAGTACATT[A/G]ACCTTAAACATCCTATGGGATTTCATAATGAAACG
3,254	6	6009	44.70	89866482	F1Dsnp	PHR	T	C	6	26,399,761	+	CTGGGAGCTGCTAATGATGTAAATGACTTGCATAG[C/T]GTTTGTGAGCAGTTCTTGTGTAGTATAAGCAGTGT
3,255	6	6009	44.70	89810537	F1Dsnp	PHR	A	G	6	26,400,297	+	GATTTGATAGGGAATATTGGGAACTCGAGGGTCTT[A/G]AGTTTGTTTCTAAGCTAGAGGAGGTAACCATAGAG
3,256	6	6009	44.70	89866483	F1Dsnp	PHR	T	C	6	26,400,421	+	TCGTAAGTTGAAGATGATGTTTGTTATTATTACAC[C/T]TGATCAATCAAGTTTAGTACCGGAAATAAGGATGA
3,257	6	6009	44.70	89866484	F1Dsnp	PHR	T	C	6	26,401,472	+	TTTCCCCTCCTCCATAACTTTCAAAACTTGGACAC[C/T]ACTGCTTCTAAAATCGCCAGTAAGAGAATGAATTG
3,258	6	6009	44.70	89866485	F1Dsnp	PHR	A	G	6	26,403,642	+	ATGAAGCCTGTTGTATAATGCATTAGGATCTGAAA[A/G]CTTCAAGACCATGTTGTTTGGGCTCAAAACACTTT
3,259	6	6009	44.70	89810540	F1Dsnp	PHR	T	C	6	26,516,486	+	GCAGTGCAGACAGACAATGGACTATTTGTTCCTGT[C/T]GTCAGGGTGAGTAATGGGCTTGGCCTTATCCGTTT
3,260	6	6009	44.70	89871546	codon	PHR	T	G	6	26,619,680	+	GGAGCATGTTCCCAACTTGCCTAATTGTCCTGACC[G/T]ACCTGAGAATCTCAAGTATGTTCTAAGATTTTATC
3,261	6	6009	44.70	89810543	F1Dsnp	PHR	T	C	6	26,669,417	+	CCGGAAGATGGAAACATGCTGCTGGTTTCCACCAC[C/T]ATGAAAATCAACTAGCGGGACTTGCAGTGTCCCAC
3,262	6	6009	44.70	89866493	F1Dsnp	PHR	A	G	6	26,680,838	+	GGGGAAGGAGGCCTAACAGGGGATTGAGATGGAAC[A/G]AAACTCTTTGCATGTGGGTTGAATTTGAATTCCTG
3,263	6	6009	44.70	89866494	F1Dsnp	PHR	T	C	6	26,717,942	+	TCGAACGAAGATTCTTGTCGGAGATGCACAGAAGG[C/T]CATTGCATGAACCATATATTCTGAATTGTTTTCCA
3,264	6	6009	44.70	89866495	F1Dsnp	PHR	A	G	6	26,799,595	+	GAGAGTAGAGCCACATGTCTATACAAGGCGCATGG[A/G]ATGTGTGCTTGCATTTTGGAAGCTGCCTCACAAAT
3,265	6	6009	44.70	89866496	F1Dsnp	PHR	T	C	6	26,935,007	+	CAATGACATGTACAAGTCTTGGTTAGGCCAAACTG[C/T]AGTGGTTCCATATGCTGAAGTGAAATCACCATCTG
3,266	6	6009	44.70	89866497	F1Dsnp	PHR	A	G	6	27,073,340	+	CCGCAGCCTAAGCTCAAACAGTATATTGCTTGATC[A/G]TTATTTTGAACCCAACATATCCAACTTTGGAGATG
3,267	6	6009	44.70	255_183108	GBS				6	27,175,990		GCCAGCGTAGAGAAACTACTTGCAAGTTTCGRCTAACAAGTCTGCAGTCTGTGATATCAAAAAT
3,268	6	6009	44.70	89866498	F1Dsnp	PHR	T	C	6	27,203,067	+	TGAAGTCAATCTCTTGCAGGATCTCCCAGTAGATG[C/T]TTTCAAGATGCGGCAGTTGAAGAAGTATCAGGGTT
3,269	6	6009	44.70	TP9308	GBS				6	27,223,066	27,223,129	TGCAGTTCCAGTTTAACAGTTGATTAATTTTCTGAAACTTCATTCAAAATAGAAAAGTGAAAAC
3,270	6	6009	44.70	89866499	F1Dsnp	PHR	T	C	6	27,233,935	+	TACAGGCTCCCTCCCCTATAATACTACCTCTCCAA[C/T]TGAAGCTGCTTCTTTCTCAAATTCTTTTATCAGCT
3,271	6	6009	44.70	89810547	F1Dsnp	PHR	T	C	6	27,262,195	+	AGATTCTCTGCAATCAGCTCAACGAGAGATTGCAT[C/T]CTTCTTTGAGGAGAAGTCTTCAGGTAAAATCGCTT
3,272	6	6009	44.70	TP2568	GBS				6	27,310,012	27,310,075	TGCAGATTGGGAGTTTCCGCAAGAGATGCAGGAATTTCCCCACTGAAATTATTGCGGTCCAGCC
3,273	6	6009	44.70	TP7794	GBS				6	27,645,554	27,645,617	TGCAGTAATAATTTGATCAACCAGCTGTTAACTTACAATACTAGATGGTAAGGAAATTAAAACA
3,274	6	6009	44.70	89810549	F1Dsnp	PHR	T	G	6	27,757,046	+	ACAACCCAACGATGCATCAAGATGGTCAAACCCAT[G/T]CTGCAGATTCAGGAACTATGAATGAAGAGTTCCCT
3,275	6	6009	44.70	89810550	F1Dsnp	PHR	A	G	6	27,806,254	+	ACAATAACCTGTCTTACACTCAAGAGATCTAGCCC[A/G]CGGCCTAAAACACCGGTGGCAACAATAACAGGAAC
3,276	6	6009	44.70	89810551	F1Dsnp	PHR	A	G	6	27,812,724	+	GTTGAAAAGTGTTTTACTACTGGTAACATCTCACA[A/G]AGGGAAGCCATAGTATCTGAGTTGGTAGCTGTGCA
3,277	6	6009	44.70	89810552	F1Dsnp	PHR	T	C	6	28,216,736	+	GGCCAGATTTTGTAACAGAGTACAAAGATGCTAAG[C/T]TCTTTATCATCAAATCTTACAGTGAAGATAATGTT
3,278	6	6009	44.70	89810553	F1Dsnp	PHR	T	C	6	28,240,463	+	AGCGCAGCTATGCGCAAAGGGGTTAGTTTTCTACT[C/T]AAGGCGCAGAGAGAGAACGGTGGTTGGGGAGAGAG
3,279	6	6009	44.70	89810554	F1Dsnp	PHR	A	G	6	28,274,233	+	GAAAGAGTTTGACTTTGACCACAACTCGATCATAT[A/G]GCGATCGGTCGGAAAATCGTGGGAAGCAAGAAGTG
3,280	6	6009	44.70	25_639380	GBS				6	28,287,097		TTCGGTAAGAGGAGCCAAGAAGAGGACAACAYGAGTAACTAGAGTTTGGGACTGATTTTCCTAG
3,281	6	6009	44.70	89810555	F1Dsnp	PHR	T	C	6	28,317,990	+	CACATGACCCTTGTGGTTGAATATCTTGAAAATAT[C/T]GGAGTCCGCAGAGAAAGCATGAGAACCATATTTTC
3,282	6	6009	44.70	89810556	F1Dsnp	PHR	T	G	6	28,328,440	+	AATTATGTTCTCATCTTCCAATCCGCCTCTCTTCA[G/T]TATTTGGTATGCATGGCATACATCAGCCTGCACAA
3,283	6	6009	44.70	89866503	F1Dsnp	PHR	T	G	6	28,431,416	+	AAACGAGAACGCAGAAGTGACAGTTGAGACTTATA[G/T]GGAGTTATGATGCCAATTCTTCCACCATGAAATTC
3,284	6	6009	44.70	89866505	F1Dsnp	PHR	A	G	6	28,460,270	+	ACCTGACTTGAACACTTGAGCTTGACTTACCAATA[A/G]GTTATCATTTTCCTCCAACTGTCCAATGATTTCGT
3,285	6	6009	44.70	89866506	F1Dsnp	PHR	A	C	6	28,530,320	+	ATATTTGGAAAATGTTGAAGACTTCTGTATCCATT[A/C]TTTTCTCAAAGTCAATCCTCCAGGTATTGTTGAAG
3,286	6	6009	44.70	89810558	F1Dsnp	PHR	T	C	6	28,573,105	+	TATGTTCATAGATCATGTCTTGATAACTGGAGGTC[C/T]ACAAAGGTGAGCATTTCTTTCCTCATCGCTGGCTC
3,287	6	6009	44.70	TP1728	GBS				6	28,596,125	28,596,093	TGCAGAGGATAGATTTGATAGTTGTGGACTTGTGGTTTTGGGTACAATCCCATCAGTAATGTGT
3,288	6	6009	44.70	89866510	F1Dsnp	PHR	A	G	6	28,649,867	+	GAAGTGGAAAATGTTACCTCCTATGCCTAAGCCAG[A/G]TTCCCATATTGAATTTGCCTGGGCTATTGTTAACA
3,289	6	6009	44.70	89810559	F1Dsnp	PHR	A	G	6	28,685,372	+	AAGAAAATCCACACAAACCTGCAACGGGGAACATG[A/G]CACTGATCTCGTTTGCAAGGCAGAGCATGGTGATA
3,290	6	6009	44.70	89897320	snp	PHR	A	G	6	28,739,395	+	TTTTCTATTGATATGTCCTTGACATTGGCATCTGC[A/G]TCTTCACCTTCAAGTACTGAAGCCCTGCTTCCAAT
3,291	6	6009	44.70	89866511	F1Dsnp	PHR	T	C	6	28,783,754	+	ATGGAGCAACGGAGATTGCTTTCCTTCGACGAAAC[C/T]GATGACCGGATCAAGAAAGGATCGGTAATTCGGCC
3,292	6	6009	44.70	89810560	F1Dsnp	PHR	T	G	6	28,837,659	+	TGGATAACTGAAATTACCAAAAGTTTGTTAACATG[G/T]CTCCGGAAGTCTGTACACCTGTCAACTTCTGCACC
3,293	6	6009	44.70	TP3947	GBS				6	28,862,334	28,862,294	TGCAGCCATGCATATAGAAACTTTAATCTCTTCGGTATATGGTGGTGGACTAAACATCCCAAAA
3,294	6	6009	44.70	89866512	F1Dsnp	PHR	A	G	6	28,923,457	+	TCCCAATGATATATCTATCATTTAGATCCTCTGTA[A/G]CCTCCATGACTTTGGTGAGTAAGGAAGATGGTCCC
3,295	6	6009	44.70	89797420	snp	PHR	T	C	6	28,990,383	+	GATACAATGTTGCATGAGCTCTGCCACAATGAGTA[C/T]GGTCCTCATAACGCTGACTTTTACAACCTTTTGGA
3,296	6	6009	44.70	89866515	F1Dsnp	PHR	T	C	6	29,003,252	+	TTCAACGTGCAGCGGGCTCAGGGAGATTGGGCAAG[C/T]TTAATGTGGGCTATTTGTATGTCTCAGCCGCCTGA
3,297	6	6009	44.70	89866516	F1Dsnp	PHR	T	C	6	29,014,161	+	CGTCCACAGAGTTGAGGGATTTTATTGCTTGCTGT[C/T]TGCAGAGAGAGCCCCAGAAGAGAAAGTCGGCCGCA
3,298	6	6009	44.70	89866517	F1Dsnp	PHR	T	C	6	29,048,068	+	TTCCCAAGGTTGCTTCTTGCATGTCTCATCTTCAC[C/T]TTCACTGCATTTTTCTTGCCTGCAAGTTTTGGACA
3,299	6	6009	44.70	89866518	F1Dsnp	PHR	A	G	6	29,087,519	+	AAAGGGCAACTCACCACCGTGAACCCAAGTGAGGA[A/G]AAATGTATATTCCCTTGAAGAAACCTTATCTGTGT
3,300	6	6009	44.70	89866519	F1Dsnp	PHR	A	G	6	29,126,403	+	AAGTCTTACCAAAGTGTTTCGCCAATCAGATCCTC[A/G]GCTTATCAAGTTACTTAATGGGATAAGAAGAGGAG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,301	6	6009	44.70	TP2197	GBS				6	29,130,511	29,130,574	TGCAGATCCTATATTGTAAGTCACTGCAATCTATCAGAGACATGCAAACAACCGTAAACGGTGG
3,302	6	6009	44.70	89810563	F1Dsnp	PHR	A	G	6	29,168,572	+	TTCCTTACTCCTGAAGAACTAATCCTGATCCTGGA[A/G]CGTGCTTCTATTTCGGTAAGCCAAACCAACCCCTT
3,303	6	6009	44.70	89810564	F1Dsnp	PHR	A	G	6	29,171,217	+	TATAAACTCATATTAAAGTGAAGTTATTTGCAGGC[A/G]CCAACTATTGCAGCAGCAGCTTATTTGAGATTGGC
3,304	6	6009	44.70	89897476	snp	PHR	T	C	6	29,799,487	+	ATTACACTTCCTGATGATGAAGATGAGCTGTTAGC[C/T]GGCTTAACAGATGATTTTGATCTAAGTCGGTTGCC
3,305	6	6009	44.70	89810565	F1Dsnp	PHR	A	G	6	29,967,763	+	TGTTGGATCCATTTTATGCGCCTTTTCAAATCCAT[A/G]GAAGCGGCCTGTTTGAACAAAATATATTAATATCT
3,306	6	6009	44.70	89810566	F1Dsnp	PHR	A	G	6	30,016,590	+	ACGTCTCAGGAAGGGGAGCCTATGATAACAGATAG[A/G]GTGTGGGAGGCCCTTGTGAAGGCTTTTGCCAACCA
3,307	6	6009	44.70	89866523	F1Dsnp	PHR	T	C	6	30,022,107	+	AGATTGATCAAGAGGTCAGCATATTTGACTATGAG[C/T]TGTCAGGGCTACTATGATCAGATTGTTTGTTCTTC
3,308	6	6009	44.70	TP4681	GBS				6	30,066,823	30,066,760	TGCAGCGGTCCACGTAGGACGTCGACGCCTAACTGCTGCACGCCGTCTTCCTCCACCGCCAAAA
3,309	6	6009	44.70	89866525	F1Dsnp	PHR	T	C	6	30,067,597	+	TCACGTCAACAAACACTGCTAAGAGCTGCAAGCTA[C/T]GGTCAAGCTTTTTGCAGGTTAGTTTTGGGTTATAT
3,310	6	6009	44.70	89810567	F1Dsnp	PHR	T	G	6	30,070,772	+	CAGGTTTCTGAGAAGAGATGGTATTGGCTGAAAGC[G/T]TTTGCTCTGGCTACAGTCAGAGATTGGGATACCCT
3,311	6	6009	44.70	89866527	F1Dsnp	PHR	T	C	6	30,072,847	+	CAAGCCCTTAAGAACGGGACCTATCCATCCATTGC[C/T]TTCTTTCTTTGCCTCAGCTTCCTGTAAAACAATAA
3,312	6	6009	44.70	TP3948	GBS				6	30,125,646	30,125,709	TGCAGCCATGCCCAAATTATATATTAGATCTTTACATATCTTAATTAGCTAGCAAGGCGTGGAT
3,313	6	6009	44.70	2_1657269	GBS				6	30,129,814		ACTGACATCGTAGGAATGTAAATAAGGATCGTTTTGCAGCAAAAATGTTACTTTGCAGTATTCG
3,314	6	6009	44.70	TP580	GBS				6	30,130,741	30,130,679	TGCAGAAGCAAAGCAAACTCCGACAGAAAAATCTGAAATGTTATACATTGGATCTAAGTATGCG
3,315	6	6009	44.70	89810569	F1Dsnp	PHR	T	C	6	30,130,825	+	ATCAAGATGTATTTGATAAATCCTGCACTTGCTGT[C/T]GGAGTTTGCTTTTCTTTGTTGATAAAATCTCCACC
3,316	6	6009	44.70	89810570	F1Dsnp	PHR	T	C	6	30,140,679	+	TGTCAAAAATTAGTGGGCAGGTTACTCAAATGCCT[C/T]CTTCATCTTTGAGGACCTCAAGGGTTAATCTTGAA
3,317	6	6009	44.70	89810571	F1Dsnp	PHR	A	G	6	30,142,592	+	CTGCATTGATGAGATCATTAATTTTCTCAACAGAA[A/G]GAGTAGCAGTCACAATAGTAGTACCAGGAACAGTT
3,318	6	6009	44.70	89866528	F1Dsnp	PHR	A	G	6	30,142,711	+	ACGGATGGTATCCTGATAGGAACATGTCCTATGAA[A/G]AAGGATATATTTTCCGAGGCTGTACTACTGGGGAC
3,319	6	6009	44.70	89866529	F1Dsnp	PHR	A	G	6	30,143,027	+	CAAGAAGACAAGGATCTCTATCTGGTTTGCCAAAG[A/G]ATTTTTGGGCTTGATGAGACTGCCCAGACCTAGTG
3,320	6	6009	44.70	89866530	F1Dsnp	PHR	T	C	6	30,180,828	+	ATGCTTGGTTGATGTGGCTTCTTCCTGCTTCCAAT[C/T]TGGTATGTATTTCTTGTAAGATGGGATTCTTTTGA
3,321	6	6009	44.70	89866531	F1Dsnp	PHR	A	G	6	30,182,149	+	GTGGCACTTTTCCCATTTGGTGGAAGGCGAAACTC[A/G]TTCATCATCCAGTCAGTTTTGGTGCCTTTGCCTGC
3,322	6	6009	44.70	TP4337	GBS				6	30,243,067	30,243,004	TGCAGCCTTCTACCATTTCAGCCAAGGAAATGAAGATTATCACTCATATTCAGCACCAGAATCA
3,323	6	6009	44.70	2_1540953	GBS				6	30,270,309		ATCGGCATAAATAGTCTCATATAATCACATAACATATATCTGACCAGGTACAGTATATAAGTTT
3,324	6	6009	44.70	TP2825	GBS				6	30,270,354	30,270,291	TGCAGCAACGACAATCGTTAATTCATGGATGAACTTCTATCTACGATCGGAATAAATAGTCTCA
3,325	6	6009	44.70	TP352	GBS				6	30,293,732	30,293,795	TGCAGAACAAGGGGTCTTTCTTCCGAAGGGCTTTCTGAATCTTTTGACAACCTTCACCCATCCT
3,326	6	6009	44.70	89810574	F1Dsnp	PHR	A	G	6	30,300,961	+	GAAGAAGCTTTCATTGCTAGTGGTAGTGAGGACTC[A/G]CAGGTAAAGAATTTAGTTGCATCCTTCTAAGATCT
3,327	6	6009	44.70	89810575	F1Dsnp	PHR	T	C	6	30,309,917	+	TTTGAAGTGTAGGAACGATGCCTGAGAAAATAACT[C/T]CTGAGGATCTTTTGAACAACATTGTGGGCTTAGCT
3,328	6	6009	44.70	89810576	F1Dsnp	PHR	A	C	6	30,310,355	+	ATCTGGGTGCTCTTTGAATGGCTCAATTATCATTT[A/C]TTGACTCTTGTGGGTTTTGCTTTGGTTCTTGGTAT
3,329	6	6009	44.70	89866537	F1Dsnp	PHR	T	C	6	30,411,825	+	GTATGGTTTCGTGGTCCATCTCACCAAGGTCTTCA[C/T]ATCCCGCCAAAAGATTTGCACCAGGAAGGGGAAGG
3,330	6	6009	44.70	89866538	F1Dsnp	PHR	A	G	6	30,417,676	+	ACTGCATTTTCATCTGCAGATCATGTCCGGAGAGC[A/G]CAGTTGCAGGCCATATTTAGAAGGTGCACTTATTT
3,331	6	6009	44.70	89866539	F1Dsnp	PHR	T	C	6	30,427,749	+	CTCATGGCTAAGAAAGGCTCTGTTCCAATTGGTAT[C/T]GGAAAGAATTCTCACATTAAGAGAGCTATAATTGA
3,332	6	6009	44.70	2_625535	GBS				6	30,440,229		TGTGTGTTTTTGTGTATATGACTTCGTTTGTTGAAATTCAAGGCAACCATAGCAGCCTAGTTTC
3,333	6	6009	44.70	89810580	F1Dsnp	PHR	T	C	6	30,502,794	+	ATTCGTGTTCTTTTGATCAGATCGGTTTTCGATGT[C/T]ACCAAAGGGAAGTCTCATTATGGTGAGGGTGGGGG
3,334	6	6009	44.70	89866540	F1Dsnp	PHR	T	G	6	30,562,834	+	ACTTGATTTTGATTGTAAAGGCTGCTTTATGTTAT[G/T]GAACCCTTGTACTGGAGAATATCATGTGCTACCAA
3,335	6	6009	44.70	89810581	F1Dsnp	PHR	A	G	6	30,563,531	+	AAGACGTTTAAGATTTTGTTTGGACTTGATGATAC[A/G]GCTACTTATGTAGAGAGTTTAGTTTCACCATTAAT
3,336	6	6009	44.70	TP4464	GBS				6	30,566,362	30,566,420	TGCAGCGATCTTCAATCGGAGTTCGAAAGATGCAGAAGATTGGGTTTCCGAGCATGAGGAGCTC
3,337	6	6009	44.70	89866541	F1Dsnp	PHR	T	G	6	30,582,415	+	CTTTGATCTCCGATCCCTATTTTGTGAAGAAACAC[G/T]TTTCATGGCGTGCTGAGACCTACAAGGTCAATTTC
3,338	6	6009	44.70	89866542	F1Dsnp	PHR	T	C	6	30,652,559	+	TCATCAATTCACTGATTTTAGACTATGAAGGTCTA[C/T]GAGATTTTCAGCCGTCTGGCCCTTTTGGCTCGGTC
3,339	6	6009	44.70	89866543	F1Dsnp	PHR	T	G	6	30,712,156	+	TAGTTCTTGGAAAGGAGCCAGTAACTGATCTTTCA[G/T]CAAGGCTTCAGTGACCACATTGACGTCTTGGGTGG
3,340	6	6009	44.70	89866544	F1Dsnp	PHR	A	G	6	30,748,447	+	ACTTGAAAATTCGTCGGGAGATCCCTTAGCCGGAT[A/G]TCTTTCATTGCTGGAATCCAATCTATGACCTTGTC
3,341	6	6009	44.70	89840433	snp	PHR	A	C	6	30,770,299	+	CGACTATGGCAATGGAGAAATGCAGCTCGGAGGAG[A/C]TGGAACTCGGCCTTCCTCCGACGACAATCGATTCT
3,342	6	6009	44.70	89866545	F1Dsnp	PHR	A	C	6	30,770,321	+	CAGCTCGGAGGAGCTGGAACTCGGCCTTCCTCCGA[A/C]GACAATCGATTCTATATCACAGATGATTTACCGGA
3,343	6	6009	44.70	89868821	SNPinIns	PHR	A	G	6	30,802,600	+	TAAAAGAAATAGAGAACATCATCTCATCATCACAC[A/G]TTGTAAAATATCAAAATAAAACTGATGCAACCCGA
3,344	6	6009	44.70	89866547	F1Dsnp	PHR	A	G	6	30,929,941	+	GAACTCATACGGAAGATTCTTCGGGCAGATGATGC[A/G]GCTTACGGCCTGACATTCCGTCTTCTCTTAAAGAG
3,345	6	6009	44.70	2_1082711	GBS				6	30,930,399		TGTTTGACAGCAAATCAGCTGCCCGACGTCTRTTGAAGCAAGGGGGGCTTTACTTGAACAACTC
3,346	6	6009	44.70	TP274	GBS				6	30,932,403	30,932,339	TGCAGAAATAGCCGATGATGATGGTGAAAAGTATGTGGACTTCATGTCTTCATGTAAAGCAATA
3,347	6	6009	44.70	89866548	F1Dsnp	PHR	T	C	6	31,039,681	+	GTCGTTATAAGAACCTACGACAACTGGCTCTTCTT[C/T]CAAATGGTGGAAATTCATGAGTCTTTTGAACAAAG
3,348	6	6009	44.70	89810584	F1Dsnp	PHR	A	G	6	31,220,228	+	ACCATATTATTCCCCATATTTTTATCAATCTCAAC[A/G]TCAGGGTTGGAGTCGGCAGGCGCCTGCGCTGCAGG
3,349	6	6009	44.70	89866550	F1Dsnp	PHR	A	G	6	31,225,252	+	AGCTCTTCCAAGTTATGTAAATTTTTAGCTGATGC[A/G]CACAGAAGTCTGGTAACCTTTTCAGCAGCAACAAT
3,350	6	6009	44.70	89810585	F1Dsnp	PHR	T	C	6	31,287,201	+	TGTTACTTCGGCAGTATATGATTGAGCAGAAATTC[C/T]TCCCAACAATGTGGACATCTGACCCAGATAAGCAA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,351	6	6009	44.70	89810586	F1Dsnp	PHR	T	C	6	31,334,923	+	AAATCAATAACAGGTCCAGGCGTCACAATCATTGT[C/T]GTAGATACATCTGCGCAAAGAAATGGAAACAGCAT
3,352	6	6009	44.70	89810587	F1Dsnp	PHR	A	G	6	31,413,836	+	CAGCAGCAGCTTGAAACAAATGAAGTTCCAAAATG[A/G]CAAGCTTTGAAAGACTAAGATCACCATGGGATGGA
3,353	6	6009	44.70	89810588	F1Dsnp	PHR	A	G	6	31,463,184	+	AGGGGTGATACCTGAAGCTCATTCAAGTAATTTAT[A/G]CCTCGAACGTTACTCCATGCAACTTCAAACACAAT
3,354	6	6009	44.70	89866551	F1Dsnp	PHR	A	G	6	31,516,405	+	AATGATGAAAAGTAAAGAACACCATTTATACCCGC[A/G]AACTGTTGAAGTGCAAAAAGGGCACCTCCTATCCA
3,355	6	6009	44.70	89866552	F1Dsnp	PHR	T	C	6	31,516,855	+	TTTCCAAATCACTACCATCATTCTTGATTACTGCC[C/T]GAATATCTTCAATTGCCTTTTCAACTTCTGATGCT
3,356	6	6009	44.70	89866553	F1Dsnp	PHR	T	C	6	31,524,856	+	GCTTCATTCCTTCTAACCATGTATTCAGATTTCCT[C/T]AAAAGCTCGAACCAAAAGCTCAGCTGCCATGGAGG
3,357	6	6009	44.70	89866554	F1Dsnp	PHR	A	G	6	31,525,160	+	TAGGGGCTTTAGTTGGAGGGCCTGATTCTCATGAC[A/G]ATTTTTTGGATCAGAGGGACAATTATATGCAGACA
3,358	6	6009	44.70	89866555	F1Dsnp	PHR	A	G	6	31,530,744	+	TGCCAATCTGGTCAACATGTATTCTCTTTTGGACG[A/G]TCTATTCTCAAATGACTACCTTCACCATTGAAGAA
3,359	6	6009	44.70	89866556	F1Dsnp	PHR	T	C	6	31,532,097	+	GCATCCTTTTGTTTTCGGGCTTTATACATCTCTTC[C/T]GTCTCAACCACAACCAATCTCTTGACCTGTATAGA
3,360	6	6009	44.70	TP1501	GBS				7	148,667	148,631	TGCAGAGAGTTAAATGTGATGATAACTAAACAAACAGGGTAAAACAAAATTTGCATATCTATTA
3,361	6	6009	44.70	157_375557	GBS				NGH			GCCCCATGGCGGCTTCCAGGCAGTGTGACGGSGGGCGGGACCGCTCCAGAAATGGAGAGGAGGT
3,362	6	6009	44.70	2_952854	GBS				NGH			TTCCCCTCCATCTGCTGTTTTACGGTATAACAATGACAGTAGGGATCGGTTAGTCCATCGCCTC
3,363	6	6009	44.70	TP6082	GBS				NGH			TGCAGGAGACGCAGGGGGGCATTTTTGGAGGTTTTGGGGGTTTCGGGTTCTTTGTTTTCGATAT
3,364	6	6020	47.19	89866549	F1Dsnp	PHR	T	C	6	31,120,382	+	TGGTATTACCCTCGTCTACAGACCCAGATATCACG[C/T]GCAAGGCTGATTATCTTTTCAAACTTTTGTTAAAG
3,365	6	6020	47.19	89866557	F1Dsnp	PHR	T	C	6	31,546,174	+	ATTAGATGCTGTCAAAAGTTGCAAATGATATTTAG[C/T]CTTCTCAAACGCATCAGGGTACTCTTTGGTTGCTT
3,366	6	6020	47.19	89810637	F1Dsnp	PHR	T	G	6	34,560,442	+	TGCGATCCAGTAACCCTCATCAGAACTCCACCTGG[G/T]CATCCCTGAAAACAAGGACAGCCTTCTGATCCTAT
3,367	6	6020	47.19	13_555560	GBS				6	34,592,694		CAGCCTACAGTATGATTATGTTAGACATCATCAGCAAAACCACCGGTATGAGTCTTAAGACTAA
3,368	6	6020	47.19	89866608	F1Dsnp	PHR	T	C	6	34,594,949	+	AGTTAGAGCTCCTTTTAGATATTTCACCAAGAATT[C/T]CACGCTTTCTGGAAATAGTAATAACTCAATGGAAT
3,369	6	6020	47.19	89810639	F1Dsnp	PHR	T	C	6	34,628,962	+	TCTCACAAACAGACTAATAACCATCCTACAGTGAT[C/T]AAGGTACGTAGCAATCTAATTGTAATAACTCATAG
3,370	6	6020	47.19	89810640	F1Dsnp	PHR	T	C	6	34,629,367	+	GTGGACTGCGATATGTATGCCAGCAACTCGAAAAT[C/T]GTTCTTCACGCAATGTGCTTGTTGCTGGGTTTCAA
3,371	6	6020	47.19	89866610	F1Dsnp	PHR	A	G	6	34,633,717	+	TTGCCATTGTATCTCTACCCTTTCATTAGCACTGA[A/G]AGCAGAGACAAGCCTCATGAATATCTCAGACTATC
3,372	6	6020	47.19	89810641	F1Dsnp	PHR	T	C	6	34,635,306	+	GTACATCTCGCTTGGGAGGTATTGAAAGGTTGCTC[C/T]CAAGCATAAAAGAGAGATCATGCATCTGTGACATT
3,373	6	6020	47.19	89798340	snp	PHR	T	C	6	34,636,068	+	TTATTTTCATTTTCAGCTATTATGCCATCCTTCAC[C/T]GTAGCAAGTGATTCTAATGGTTGAGGCTGCCCTGC
3,374	6	6020	47.19	89866611	F1Dsnp	PHR	A	C	6	34,636,161	+	AATAGATCATCTGAAAACCAATCATTACTAGTGGA[A/C]GCACTATGATTTGATTTTACTTTAGTTGAGTCCCC
3,375	6	6020	47.19	89898496	snp	PHR	A	G	6	34,675,506	+	ATGTGCCGAGTGAATCTTACTGTGAACTGATCAGG[A/G]CGCCGTTGTTCTGATGCAAGAAAATGCAATCTCAT
3,376	6	6014	49.68	TP2673	GBS				3	18,591,606	18,591,548	TGCAGCAAAACCAAATCTCTCTAATACCTCACGCAAAAATAGTCATTCCATTATGTCGTATGCT
3,377	6	6014	49.68	89810207	F1Dsnp	PHR	T	C	5	1,945,312	+	GGACGAGTGTACGGCTCTGGTAAGCTAGGAGTTGA[C/T]TGGCCGGGACTCGCACGACGTACCATGGCGGCGAC
3,378	6	6014	49.68	TP332	GBS				5	4,398,165	4,398,118	TGCAGAAATTTACAAGAGTAACATGTCAGATAATGGTAAGAAAGGCATATCCGAGATCGGAAGA
3,379	6	6014	49.68	13_310635	GBS				5	14,537,122		TGGCGTTTGGTCATCATGATGTTTTGGAACCWCAGTATGCAAAACCTTAAAGTCATTGGTACGT
3,380	6	6014	49.68	85_201269	GBS				6	31,595,589		GGACACACCCGACCCAGAAGAAGGCCGGAGATCGGAAGGCGCGGCGTCCCCGCCGGATCGCCTC
3,381	6	6014	49.68	85_181584	GBS				6	31,612,827		TTTCTCCCATAAGATCACTCTTCTTCGCTTGTGCTGAACGAAGGGACAAACAGTTCCCAAAGTA
3,382	6	6014	49.68	TP8445	GBS				6	31,657,367	31,657,304	TGCAGTCGGATTCGAAAGACCAGGAGGGTTTGAAGGCGGAGAATCCAGAACCTTCGTTGTCGTC
3,383	6	6014	49.68	TP6720	GBS				6	31,780,112	31,780,174	TGCAGGCTGCAATATGTAACTTCATTTAATGATCAAATTTGAAAATGTAGGAGTGAAAGACTTA
3,384	6	6014	49.68	89866558	F1Dsnp	PHR	T	C	6	31,796,076	+	AACGATCCAGAGAAGGTCGTCTTCCATCTTGTAAC[C/T]GATGAAATCAACCATGCTGCAATGAAGGCCTGGTT
3,385	6	6014	49.68	89810591	F1Dsnp	PHR	T	C	6	31,821,054	+	TTGCTCTTTACCATATTGTCAAAGTCCTTCATTGA[C/T]AAAGATTTTGGATGCTGCTTCGGAGGGCTGTCCCA
3,386	6	6014	49.68	89866560	F1Dsnp	PHR	A	G	6	31,874,670	+	ATGAAGGTTGAACCTTAATCTGTAAGCTGCGGCCA[A/G]CCTGAAAATTTGAAGAGTAGTCTGTGCGCTATGAC
3,387	6	6014	49.68	89810592	F1Dsnp	PHR	A	G	6	31,966,060	+	ATCAAGAATGGCTACGAAGACAAAGCCTTCAATAG[A/G]GTATGTTATCTAGGACAAACTAACATCTCCTCTGT
3,388	6	6014	49.68	89810593	F1Dsnp	PHR	T	C	6	31,971,024	+	AAACATGGTCTGATGCTACAATTCTCGCTGCACCC[C/T]TTGCGTAGTATACGGCATCCATTACAGCTCATCCG
3,389	6	6014	49.68	89897876	snp	PHR	A	C	6	31,982,341	+	GAAGATATCTTTCCTTTTATCCGGGGCATCGACAC[A/C]GCTAAAGCTGCCTGGAATACTTTGGAAAAGAAATT
3,390	6	6014	49.68	89866561	F1Dsnp	PHR	A	G	6	32,007,581	+	TCTTTTAAGATATCTGGGAACTTTGCTGTTGCTAA[A/G]GATGCTTTGGCTGAGATTACATCAAGACTGAGAAT
3,391	6	6014	49.68	94_559276	GBS				6	32,010,833		ATACGAGGGAAAGGCTGGAAATATCATGTTTGGAATTTGTTGCTTTATTGGATACTCGCAAAGG
3,392	6	6014	49.68	89866562	F1Dsnp	PHR	T	C	6	32,049,046	+	CTCCATGCCTCAACGTGGTACTTGCCAGCCTTTTC[C/T]AGAGCCCTAAGCCATCTGACTGCAGATTCCTTTGG
3,393	6	6014	49.68	89810594	F1Dsnp	PHR	T	C	6	32,084,007	+	TTGTGGGAGAGCAACAAATTGTGTAGTGTATGGAT[C/T]GCAGATGTGGTAATCATATTTTTCTATGCTAATTC
3,394	6	6014	49.68	89810595	F1Dsnp	PHR	T	C	6	32,085,858	+	GACGAGAAGATTTCCACCTTCAAATTGGAGGAAGT[C/T]ACAGCATGTATATCTCCAAATGTTCCAGGAATTCT
3,395	6	6014	49.68	89866563	F1Dsnp	PHR	T	C	6	32,107,390	+	AACAAATACAGAGGATACGTACGCGGGTGATTTTG[C/T]TCGCCGTCGATGTACTTATCAAGTGACCAACCAGC
3,396	6	6014	49.68	89810596	F1Dsnp	PHR	T	C	6	32,109,344	+	TCAAACAGAAAAACTGCAATGTTGATAGATCCCAA[C/T]ATGCTTCTGCAAACAAAGATTAAAAAAAAAAAATC
3,397	6	6014	49.68	89866564	F1Dsnp	PHR	T	G	6	32,173,360	+	AGAAAGCTGAAGGCGCCGTCAGGTTCAAATTATCC[G/T]GATCGGAGCCTTGAATTGAACCCCCAGAGGATGGA
3,398	6	6014	49.68	89810597	F1Dsnp	PHR	T	C	6	32,219,110	+	CACCTTTAGGTTTCATTGCTGACACAAAAGTATAT[C/T]CACCTACCGTGTGGCTGATCTTCCCCTCCATTTTG
3,399	6	6014	49.68	89810598	F1Dsnp	PHR	T	C	6	32,219,220	+	AATGGAGTGACTTGGATAACTGAATCCACTGCAGC[C/T]GCTTTTGAGAATTTCTTAAGAACCCCAGTTGGCGA
3,400	6	6014	49.68	94_324052	GBS				6	32,234,897		AAATATTGTATGACTAGTCCCACATTTGTTCTATACTGCAGAGAGGTTATAAGTTTTATCCCCT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,401	6	6014	49.68	89866565	F1Dsnp	PHR	A	G	6	32,236,146	+	AAATTGCCATCTAGAAGAATGTTTGATGACTTGAT[A/G]TCTCTATGAATAATGCGAGGATGGCCTGACAAAGA
3,402	6	6014	49.68	89810599	F1Dsnp	PHR	T	C	6	32,237,319	+	TTTGTGGCTTGGATCAGTTCTTCATATGTGAACCA[C/T]GATCTTGAATTGCTTGCTCCAGACTCTGATTGTGC
3,403	6	6014	49.68	TP3975	GBS				6	32,250,917	32,250,979	TGCAGCCATTCTACAATGCAACCCTCATGGTAAAGATGAGCACAAGGCATTTTAGTTGCTCCGA
3,404	6	6014	49.68	89866566	F1Dsnp	PHR	A	C	6	32,251,281	+	GCTGGGTCGTTAGAGTCGTCAAGTTCGATCGAGGT[A/C]CTCTTCGTGATCACCTGGTCGGAACTGACACGTCT
3,405	6	6014	49.68	94_281686	GBS				6	32,256,660		ACGAGAGTCCAAGTGCCATCAACAGTGTGTTYGGTTTGTATGGAGGAGATGATGCTTGGGTTCG
3,406	6	6014	49.68	89866567	F1Dsnp	PHR	T	G	6	32,262,475	+	AAAGCATCTCAAACGTGGATAATTCGAGTTTCCCC[G/T]CCTGCCTAAGTTCATAAAATCCGCAGCAATTGAAT
3,407	6	6014	49.68	89810600	F1Dsnp	PHR	A	G	6	32,262,802	+	ATCAAGATAACCCACCTCCTCAGCAATCAAAGCCA[A/G]CCTAGCAGCTCTAGCAATCAACTTCCCATAAAAAT
3,408	6	6014	49.68	89866568	F1Dsnp	PHR	A	C	6	32,263,093	+	TTCACCATCAATAAGCTCCAAATGCAGAGGGTGAG[A/C]TAACATAAGCAAGTCTCCCCATCCTTTCTTCTCCC
3,409	6	6014	49.68	89866569	F1Dsnp	PHR	T	C	6	32,279,247	+	AGGCACAAGCAGAAGGCCTAGTTGGTGAAATTCAT[C/T]TGAAAGAGATGGAACTAGAAAGATTAAATGGGTTA
3,410	6	6014	49.68	89810601	F1Dsnp	PHR	A	G	6	32,281,272	+	CAAGTCTCATTTGTGTAGTAAGCAGGTCCATCAGG[A/G]TAAGGAATCCAGTTCCCACTAAATAGCTGGCATTG
3,411	6	6014	49.68	89897962	snp	PHR	A	G	6	32,302,231	+	GCCCAATTTTCAATACAAGGATAACAGTATCGATG[A/G]CCACATGGCAAAATTCCTCGGGTTGTACTAAACTC
3,412	6	6014	49.68	89866570	F1Dsnp	PHR	T	C	6	32,353,752	+	TGAGATCTCAAAGCAATTGTGGGTGGTAACAGGAT[C/T]GACATTATCTAAATCAAATCAAGTGGTGAACAGGG
3,413	6	6014	49.68	89866571	F1Dsnp	PHR	T	C	6	32,397,064	+	CCTCAGGAAATTGGGAAGCTCTCAAAACTTAAGAC[C/T]CTTGATGTTTCCAGCAACTTCTTGACCGGGGGAAT
3,414	6	6014	49.68	89866572	F1Dsnp	PHR	A	G	6	32,482,897	+	GAGGTCACGAACCACGACCCCGGACGCCCCTTGTC[A/G]GTGGATGTAAAGGTCGGCTGCAACGAATTTGAAAA
3,415	6	6014	49.68	89810604	F1Dsnp	PHR	T	C	6	32,509,974	+	AAAGCCATGATTCCAGCACCAACAATTGTGGTTGA[C/T]AAGTTGAAAACTGCCCCAGTAAAGGAGGCTCCATT
3,416	6	6014	49.68	317_148255	GBS				6	32,567,923		CTCTAGGAATTCCAATGTTACTGCTAGTACTGCTGGCAGCAGTTGTTATTATTTTGATCTCACC
3,417	6	6014	49.68	89810605	F1Dsnp	PHR	T	C	6	32,579,374	+	ACAGGTTGCAACTGCCATCTGGTAATGTACAAGTT[C/T]ATCCACCTCAGGAGACATGAAATGAAGCGTAGAAC
3,418	6	6014	49.68	TP3249	GBS				6	32,579,442	32,579,488	TGCAGCAGAGAGCTTCTCTCTCAAGCAGACGCCAATCTCAAATGCCGAGATCGGAAGAGCGGTT
3,419	6	6014	49.68	89810606	F1Dsnp	PHR	T	C	6	32,585,124	+	ATGTTTGAAAATGTTGTTGATAGGACCTCCCTCAG[C/T]ATTCTCTGGGAGCTCAGCAGGATTTATGGTCGTGA
3,420	6	6014	49.68	89898047	snp	PHR	A	G	6	32,633,005	+	CCTTCCAGCCTTCTATCTCCACCGTATATTTCTCC[A/G]GCAGCAATGTAAATCTGAACATTGTGATCTATACC
3,421	6	6014	49.68	89810607	F1Dsnp	PHR	A	C	6	32,653,357	+	TCATACCAAGACCGCATGCCTTCATCTAATTTAAT[A/C]ACCCTATGGAATATAGTAATATCAGAAGGTATATG
3,422	6	6014	49.68	89810608	F1Dsnp	PHR	T	C	6	32,691,505	+	AGGTTGTATCATTTTGTGGCTGCTTCGAAAGCTCT[C/T]AAAAACACTTCCATCGGCTGAGCACCGACGCAGTT
3,423	6	6014	49.68	TP655	GBS				6	32,712,277	32,712,336	TGCAGAAGGAGCTGGAAAGATTCATGTCGTTAAATACTACATGCATGCATTTTAGTTATGAGCG
3,424	6	6014	49.68	67_665269	GBS				6	32,737,791		AAGAAGAAGAAAACTGAACCAAACCTGTTGAGGTGAAGAAGCTGCAGAAACCAATCCCAAACAG
3,425	6	6014	49.68	89810609	F1Dsnp	PHR	T	G	6	32,739,027	+	GCTGGACAGTAGGATGGACATGGGCAAAGAAGGAG[G/T]TAATTTGGAACATGGTGGGAGGACAAGCCACCGAG
3,426	6	6014	49.68	89840851	snp	PHR	T	C	6	32,741,768	+	AGTGTGTAGTTCATCCGATAGTTAAAGTTTGTAAC[C/T]GTAACCTTCACACGCCAGTACTCCTTGTAATTCAC
3,427	6	6014	49.68	89866573	F1Dsnp	PHR	T	C	6	32,778,768	+	AAAGTCCTCCTATCTCTTTCTCTCGCATTTTTAAT[C/T]GCCTGAAACAAATTCAAATCCATCCACATCAATCC
3,428	6	6014	49.68	89866574	F1Dsnp	PHR	A	G	6	32,809,089	+	CTTAGAATGGCCGTACCAAGGAGTGCGGCTTTCTC[A/G]CTCAGAATTTACTTACAGATTCAATCTCACCGCCG
3,429	6	6014	49.68	89866577	F1Dsnp	PHR	T	C	6	32,871,662	+	CTGATTCCGTACTTGAAAATCTCAAAACCTCCCTC[C/T]CTCTAGTTCTCCAACACTTCCTACCTCTTGCCGGA
3,430	6	6014	49.68	TP8072	GBS				6	32,924,868	32,924,925	TGCAGTATAAGCCTCACACACGAAAGCAAGATCATGTAATGAATCGAAGAATCATTATCGAGTT
3,431	6	6014	49.68	89866579	F1Dsnp	PHR	A	G	6	32,939,950	+	CCCTCCTCATGATGATGATTATTTTATCCCTCCTC[A/G]TGATGATGATGAAGACAATGAAGGCAACAAAGACG
3,432	6	6014	49.68	89866580	F1Dsnp	PHR	T	G	6	32,985,041	+	ACAGAAGACAGGCAAGTCCAGGTGCGCTTCGTGAC[G/T]AAGCTTCAGGACATCCCCTTCAAAGTTCCCAACAC
3,433	6	6014	49.68	67_401755	GBS				6	33,017,105		CCAAGTCATATATAGAAAGGAGCTAGGGGCAGTACTGCAGTATTCAAGGCTAGGAGGCATTTCT
3,434	6	6014	49.68	89866581	F1Dsnp	PHR	A	G	6	33,018,541	+	GGTGTCAGCAATGGGGTTCCTTTCTTGTGCTGGCC[A/G]TACTTTGCTGACCAGTTCATCAATGAGAGCTACAT
3,435	6	6014	49.68	89810612	F1Dsnp	PHR	T	G	6	33,022,797	+	CCCGAGGCCAGTTCGTAATGAAATTTTCGAAGATA[G/T]CATTCCTCCTCCGGGGGATAATGGAGTACCGGAGT
3,436	6	6014	49.68	89866583	F1Dsnp	PHR	T	C	6	33,067,722	+	ATGGTGCAACTCACAATAATCAGCTCAGTCATACT[C/T]CTTCCAATGTATGTGTACATCTAGTTGAAATTTGA
3,437	6	6014	49.68	89810613	F1Dsnp	PHR	T	G	6	33,182,642	+	AGCATGGAGATGATCCTGATGCTCAAAAGGATTTG[G/T]ATGTAATCAAACAAGGTATGACAATCAGGGAGGAT
3,438	6	6014	49.68	89810614	F1Dsnp	PHR	A	G	6	33,182,709	+	GGATTTGATAGAAGCTTCCGAAGGCCCTAAGGATC[A/G]CAACACCCCACCATTTAATGCTTCTGCCACCACTC
3,439	6	6014	49.68	89810615	F1Dsnp	PHR	A	G	6	33,225,444	+	GATGAAGCTGCTGCCAAATTGAAAATGGAAATTAC[A/G]TCAAAGCCCACAGCGCTAGATGAGATTAATCGTTC
3,440	6	6014	49.68	89866585	F1Dsnp	PHR	A	G	6	33,245,603	+	AGCTATTCCATGATCTTTGAGCCAATTGAACATGC[A/G]AACCCTAAGCTTGACCCTTTCCATTTTATAGGAAA
3,441	6	6014	49.68	89866586	F1Dsnp	PHR	A	G	6	33,255,084	+	GGGTTTTTTTGATGCTGGAGATTCTGAATTTCCAG[A/G]ATGTCTTTCTGAGCTGCTGAAAGCACCAAGGGTCA
3,442	6	6014	49.68	89810616	F1Dsnp	PHR	T	G	6	33,255,977	+	TTCAGAGGATGGCTATCCACATCTTCAGAACAAAC[G/T]ATCCCAGACTTTCTGGGCCTCCCTTTGTAATCCTC
3,443	6	6014	49.68	89798241	snp	PHR	A	G	6	34,077,443	+	TGCAAAGAATAGAAAAGGATGAATCCACATTTGAG[A/G]ATCTCATTGGTAATGCTTCTTTCGTCAGAGAAGAC
3,444	6	6014	49.68	89866603	F1Dsnp	PHR	T	G	6	34,093,453	+	GATAATTACCTCGTTCTTAATATAAGGGAGGGTGT[G/T]TAAACCAGTGTTTTTGAATATGTTGTCAGCCAAAT
3,445	6	6014	49.68	89866604	F1Dsnp	PHR	A	G	6	34,219,325	+	CACCAGTATTCTCCCTTGAAATTTATGGACATATA[A/G]TTGGCATGTTTGAGTTGAATAATCTGTAAGTCTCA
3,446	6	6014	49.68	89810631	F1Dsnp	PHR	A	C	6	34,251,009	+	CATCCAACAGTCCAGTTTCATGTCTGAACTCGAAA[A/C]CCAGGTCCCATCTACTTTTGGTGAGGCTCTCTTCC
3,447	6	6014	49.68	89810632	F1Dsnp	PHR	A	G	6	34,307,923	+	TTAGTGAGTTGTGTATCTCAAGCCTTCTTTTTCCT[A/G]CCCAACATAGGTCTCTTGCCGATCATTGAACTAGT
3,448	6	6014	49.68	89866605	F1Dsnp	PHR	A	G	6	34,342,178	+	CAATAACCAATTTTACGAAATCCAGTTCCACCAAT[A/G]TTCAGAATGTCATAAGCTGGATGAATTAAATTCTT
3,449	6	6014	49.68	89810633	F1Dsnp	PHR	T	C	6	34,392,403	+	ATACCTGATAATGTTGGAATGCTATCATTTGTGAA[C/T]GGTGTCAATGGTGAAGGCGCTAATAAAGGCAGAAA
3,450	6	6014	49.68	89866606	F1Dsnp	PHR	A	G	6	34,398,860	+	CCAGCTTTGAAACAAAGTGGAATAATACCCATACC[A/G]ACCAAATTACTGCGATGGATTCTCTCAAAACTTTT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,451	6	6014	49.68	89810634	F1Dsnp	PHR	A	G	6	34,400,175	+	TCCTTGCCTGTTCCAATTGGCTCCTTATCGAAATC[A/G]ATGTCAACCTGCAACATGATTGATGGTGAATCATG
3,452	6	6014	49.68	89810635	F1Dsnp	PHR	A	G	6	34,402,825	+	TTCCTCAGCATTTGTGTGACAGTCAAGACCAAGTC[A/G]GTAGCAGTAACACCATTGTTCAACTTTCCAGATAA
3,453	6	6014	49.68	89810636	F1Dsnp	PHR	A	G	6	34,403,131	+	ATGGTTGTATGGGAATCAGTTCCAACCACACTATC[A/G]GGGTAGAGTAAGCCGTTAGTGTTGAACACAACCCG
3,454	6	6014	49.68	13_432728	GBS				6	34,484,612		ATGATAGAGACTAGGGCATGTTTCTACGGCCGCATACGTTTAGCCTTTAGGCGATCCATTTTCC
3,455	6	6014	49.68	13_491850	GBS				6	34,548,387		GTCGCAGGAAAGCTTTGGAGCTTCAGTCAATTTGGAACAGTTTATGTAACTGACAACCCTCTCA
3,456	6	6014	49.68	TP3190	GBS				6	34,548,509	34,548,571	TGCAGCACTGGACGGCCTTAATGCCCTTATTGTGTTTTCAGTCAGGTTCACAAACAAGGAGTAC
3,457	6	6014	49.68	13_494448	GBS				6	34,549,732		GCTGCAGTCACCTATACTCTGAGAGGCTACATCCAGAATCCCTTAAACCCTCGCCCCAATGGAT
3,458	6	6014	49.68	13_508817	GBS				6	34,551,504		TTCGGTTATGGTGAAAAAGTAGGATATTAGGKTTAAGAGAGAAGAGAAATGAGAGAGGCGAGAG
3,459	6	6014	49.68	TP1971	GBS				6	36,058,401	36,058,461	TGCAGATAACTTTGCTATAATTGGCTTGCGAGATGCGAGGATGGAGTATTTGGCTCTTTGATCT
3,460	6	6014	49.68	89866627	F1Dsnp	PHR	T	G	6	36,275,275	+	TTGAACCTCTATCGACCTTCTAGGATACTAATGGT[G/T]AGTTGATTGGCCGAAAAAACTGTAGGTGTTTGAGA
3,461	6	6014	49.68	TP7381	GBS				6	36,297,496	36,297,433	TGCAGGTCTTTTCACATGAAAGCTCCACAACTATCCAGAATTTTTTTCGCCAACAGCAGGGTAC
3,462	6	6014	49.68	85_458164	GBS				6	36,297,562		CGTGACAATGTAACACTTTCAGATGAGTTAGRCGATCACCAGCAACTAAAGGACACGCATCACG
3,463	6	6014	49.68	89866628	F1Dsnp	PHR	A	C	6	36,331,744	+	AGATTGTTGAGCGTAAAATCTTTTGGGAAAGGATC[A/C]TTTGATATCAGAAACTGAGACCATATGCAGTTGGT
3,464	6	6014	49.68	89810662	F1Dsnp	PHR	T	C	6	36,335,364	+	CAGTTCATTGGATAAGAGATATAAATAGAGCAGGA[C/T]TCCCTAAAAATAGATTATTTTTCTGCAAGAAAGCT
3,465	6	6014	49.68	89810663	F1Dsnp	PHR	T	C	6	36,353,706	+	AGCCCACCAATAATGACACCTCCACCAGCAACAGA[C/T]TTATCTTGGTGATGCTTTGATGACCCCAACTTTCT
3,466	6	6014	49.68	89810664	F1Dsnp	PHR	T	G	6	36,360,792	+	TGAGACCCAACTCCTCTCTTTGATGCTGGTTCAAT[G/T]TTACTGCTCCAGTATAAGATTCCTTCAACCTCTCC
3,467	6	6014	49.68	89810665	F1Dsnp	PHR	T	C	6	36,379,836	+	GGCCAAAACCTGCACAGCACTTAAGGTATATAGTA[C/T]GTGCGGGTCATGTCCAATGTTACCACCAAAACCAC
3,468	6	6014	49.68	13_96134	GBS				7	9,306,997		CGAAAAMCTCCTGGAAGACCAAAGACAAGGASGATCAGGTCTTTTGGTGAAGAGGCAACACCAA
3,469	6	6014	49.68	13_492040	GBS				7	20,697,514		GCAGCACACTAGAGATACAAGGAAACAGTATCTTACGGGAGCCGGTTAGAGAGCTTTCGGTGGT
3,470	6	6014	49.68	13_29309	GBS				NGH			TACATGATTATAGAGAACCTGTGAAGATGGACGATTGAAGGGGGAAGTCGAAAATGTCATTTTT
3,471	6	6016	52.17	89866588	F1Dsnp	PHR	T	C	6	33,264,114	+	ATGGTTTTGCAAAATGGTGGATTTTGGTGAAGAAA[C/T]AGTAATGGCTGCCATTGCTTCTTGAAATCAAGTCA
3,472	6	6016	52.17	TP7165	GBS				6	33,279,867	33,279,914	TGCAGGTAACACATGTACATTACACACACCATCCTTACAGAATCCCTCTATTCATATTAAGTGG
3,473	6	6021	54.66	TP4851	GBS				6	33,420,021	33,420,084	TGCAGCTACCAGTTTTGCTCTGAATGATCGCCAATCGGTATTAATGGAAGGTTTGTAGTCATCA
3,474	6	6021	54.66	TP19	GBS				6	33,420,024	33,419,961	TGCAGAAAAAGTATCACTGCCCAAATTGCCTACTTCCATAGTTGGTGATCTAGACACTGTTGTA
3,475	6	6021	54.66	67_15897	GBS				6	33,489,889		TCCACCGGATTTTGATGGTTTATTTAGAACARTAGAATCAAAAGTATTCAATTCAATTACTATG
3,476	6	6021	54.66	89866589	F1Dsnp	PHR	A	G	6	33,500,768	+	TTTGCTTGTTCGGTGGGTGTGCTCGGTTGGGGGAG[A/G]TTGAGATTGGTGTGCAAGGACATGGGTTGATGGTG
3,477	6	6021	54.66	TP2296	GBS				6	33,513,276	33,513,215	TGCAGATGAGGACCCACTAACCAAAGCATTTATGGTTCTGGGTTTTAAGCCATTAGCTGTGACA
3,478	6	658	57.20	89866591	F1Dsnp	PHR	T	C	6	33,557,745	+	TGTGTGAAAGGTAGACGCAACAATTCTCCAGTTCG[C/T]TTATCATACTTCTTTAGAATTTTGACTAGCCCTAT
3,479	6	6022	59.67	89810617	F1Dsnp	PHR	T	C	6	33,626,189	+	ATAATCATTTGAGAAGAATAAAGATGCAGGGGTTC[C/T]AAGGTAAGTGGTTTGAAATAGAGTTTGCCATCTCC
3,480	6	6022	59.67	89898287	snp	PHR	A	G	6	33,633,579	+	TAAGCTCCATAAGCTCCATAGGGGCTGCCGCTACC[A/G]CCCACCTATGATATCATATAACAAAAGAGATTTAA
3,481	6	6022	59.67	89866595	F1Dsnp	PHR	A	G	6	33,647,275	+	TCTTCCTTAAGATTGCTCAGTACAGAGCTGGAGTT[A/G]TCCCTGTATCATACAGAAGGTGAATAGATTTTCTC
3,482	6	6022	59.67	107_396030	GBS				6	33,678,879		CAGCCTCAACACAAAGCAAGGTTCAAGAATAATCTGCAGCTGTTCTGATTTCAAACTCATTAGT
3,483	6	6022	59.67	107_395974	GBS				6	33,678,935		CGTATTCTAATCCTACCGACCATGCCATTCAWAAGTTAAATTCAAGGGAGATGCATCAGCCTCA
3,484	6	6022	59.67	89866598	F1Dsnp	PHR	A	G	6	33,699,138	+	TTTCAATACAGTCGGAGTGGAACCTGTGCGTACAA[A/G]CCATCTCCTTGGCTTCACCAGAGACTTTGAAGCTT
3,485	6	6022	59.67	89866599	F1Dsnp	PHR	T	C	6	33,725,034	+	TTGCACATCTTGATTAATCATCCATGGAATCGCTT[C/T]TGCTATAAGATCAACACCTTTCTGGTGATCAAGTC
3,486	6	6022	59.67	89866600	F1Dsnp	PHR	A	C	6	33,747,872	+	CAGCTTCTTACTGAAATGGATGGATTTAGTGGGAA[A/C]AGTGGAGTAATTGTTATTGCTGCTACTAACCGCCC
3,487	6	6022	59.67	89810621	F1Dsnp	PHR	T	C	6	33,790,258	+	AGAAAATCACAAATACAAACCTGCTGATATTTTGC[C/T]AAGACTGAAGATGAAGACTGAAGAAGAGCATGTGT
3,488	6	6010	62.18	89865791	F1Dsnp	PHR	A	G	4	10,027,284	+	TCCGAAGATGATGACCTGAATTCCTCAGGGGACTT[A/G]TATCTTCAAGACCCTCCATCAACTCCCAAGCATCG
3,489	6	6010	62.18	TP318	GBS				4	10,030,476	10,030,539	TGCAGAAATTAACGATTAAACCAAGTCGAGCTGACCACGTTTTGTGGGTTTCAGAAATGGGTGG
3,490	6	6010	62.18	89865792	F1Dsnp	PHR	A	C	4	10,079,082	+	ATTCCCCATTGCCATTATCACTTTCTCTGTCTGGG[A/C]TGCCAATTCCCTCGTTGGAGAAAGTATCAATGCCT
3,491	6	6010	62.18	89885611	snp	PHR	A	G	4	10,083,843	+	GGTTCCGGTCAGGTTGGAGGTTTTCCTTCTCTTTC[A/G]GGTGACTTCTTCACTTATGCTGATAGGCAGCAGGA
3,492	6	6010	62.18	89865793	F1Dsnp	PHR	A	G	4	10,084,335	+	GGAACCCGCCAAACAGTAGTCCTTTTCAATCCCTC[A/G]GAGCAGATAAGAGAAGAGGTTGTGATGGTTATTGT
3,493	6	6010	62.18	89885616	snp	PHR	A	G	4	10,104,555	+	AGACGGTGAACAGTTGGTGCGGATTCACATCCATG[A/G]TTCCACTCTTGATTGCACCCTTTGCTGATTCTTAC
3,494	6	6010	62.18	89809830	F1Dsnp	PHR	A	G	4	10,105,512	+	ATCAGTCGTAGTTTTCTCGTGTGGAAGCCGAATTT[A/G]TACATATAAACAGAGGAATGATGATTACAAGCCTG
3,495	6	6010	62.18	89809831	F1Dsnp	PHR	A	G	4	10,106,013	+	CACTTTCTATAGTCCTATTGATGCCTCTTTATGAC[A/G]AAGTTTTGATCCCAATTACTAAGGTCCTGACTTGT
3,496	6	6010	62.18	89809832	F1Dsnp	PHR	T	C	4	10,121,007	+	TTTTTCAAAGAATTTTTGGAGTGCACTAATGGTTT[C/T]GACCTCACCGTTGTGACGGGATGATGTTTCGTTGC
3,497	6	6010	62.18	TP3079	GBS				4	10,123,088	10,123,151	TGCAGCACCAGCCCCACTCCTCGAACCAAGTTGGGGATTGCCGAACTCGAGTTGTCGCGCAATT
3,498	6	6010	62.18	89809833	F1Dsnp	PHR	A	G	4	10,126,704	+	GGTATCCCATACTTCTACTTGACAACTCTTGATCC[A/G]ACTGCAAGAAATGCAGGGAAAGACCAAAGGGCTTC
3,499	6	6010	62.18	89809834	F1Dsnp	PHR	T	G	4	10,129,838	+	AAACTCAGCCAGCCTTAATACAAGGGGTTGGTTTG[G/T]CAAATAGGTTTCGGTTTCAGCTTCCAGGCGAGGCA
3,500	6	6010	62.18	89865794	F1Dsnp	PHR	T	G	4	10,139,484	+	TCCGGGACATACTTCTGTGTTGATAAGGGAGTCAC[G/T]TCTGTTGTTATCAAGGTAATGTGTTGTCCATAAGC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,501	6	6010	62.18	TP4072	GBS				4	10,150,396	10,150,459	TGCAGCCCTCGACTCCTCTCCGCCTTGAAAACCCTCGTTGTTTCCAGGTACATTAATATTCAGG
3,502	6	6010	62.18	89809835	F1Dsnp	PHR	A	G	4	10,159,913	+	TCCTTAAAAAACTCCGTCTTCAATTCCTTCAGTGG[A/G]ATATCCAATCCAACTATAAGTGACGGTAGTTCAGG
3,503	6	6010	62.18	89865795	F1Dsnp	PHR	T	C	4	10,170,511	+	GATCTGAAACTGATTCAGGCAGTTTTCTCAATGCA[C/T]AACAACCAACCATTTGCAGCTTCATTAAACTCTTC
3,504	6	6010	62.18	89885647	snp	PHR	T	G	4	10,172,688	+	AGAAACAGTGACGAAGAAGATGTTGTCCTTGAACT[G/T]ATCTAAACAAATTCAGTAAAAACACATTAGTTTGT
3,505	6	6010	62.18	89809836	F1Dsnp	PHR	T	C	4	10,173,143	+	GATTTGTTTTGATTCGCAATATCTAAGAGCTCATG[C/T]AGTATACCATTGTTCTCGTCTGTGACAACTGCTAC
3,506	6	6010	62.18	89865796	F1Dsnp	PHR	A	G	4	10,201,289	+	TTGAGTTTGAGCACTAAGAGAATTGGCTGTCACGA[A/G]TTGTTCTGAAATGAAATCCGGGTCCTCAGAGGTAG
3,507	6	6010	62.18	89809837	F1Dsnp	PHR	A	G	4	10,229,344	+	GAGTATCATACCCTTGTGGCAACAAAGAGAATGGT[A/G]ACCAAGAGAAGGAGGAAGGCTTTGAAAGCCATAGT
3,508	6	6010	62.18	14_878196	GBS				4	10,232,397		TTCATTCTTTATGATTAAACATCATTGTATTTTGTTATGTGTGTGATTTATGGTTTTGGTTATT
3,509	6	6010	62.18	14_878153	GBS				4	10,232,468		ACCATGTTTTTTCAGGTACCCGGTTTGTAGAYTTGTACAAAGTTTCATTCTTTATGATTAAACA
3,510	6	6010	62.18	89809838	F1Dsnp	Other	A	G	4	10,237,865	+	ATTAACTTGCTGCTCCACTTCAAAATGGAAGCATA[A/G]GTTAATGTTTTGCAGCCTTGTAAGTAAATTCTCAT
3,511	6	6010	62.18	TP8729	GBS				4	10,240,665	10,240,720	TGCAGTGATGCAGCAGAGGATGGTTTTCGAGCTCAAGACTACTAACATGGAATGTTGTCCGAGA
3,512	6	6010	62.18	89809937	F1Dsnp	PHR	A	C	4	17,410,708	+	CATTAAAATCTACCATTAACCCACCAAGGTTGCTT[A/C]TTGCAACTCAACACAATCTCAATCAAGCTTAACAC
3,513	6	6010	62.18	TP2362	GBS				6	1,593,583	1,593,520	TGCAGATGCTTTAGAGTTGCTTATGCGACACAGAAGGCGAACAGCGAGGTTCCAGCAGTATAGG
3,514	6	6010	62.18	89866419	F1Dsnp	PHR	T	C	6	1,594,220	+	GTGGGAGGTGACATAACTGTAACACCAGCCATTGC[C/T]GATGGCATTCTCTACTTCCCAAGCTGGAATGGATA
3,515	6	6010	62.18	89810444	F1Dsnp	PHR	T	G	6	1,604,577	+	CGTGTCAAAGCTCAACTTAAATCAATGTTTGATCT[G/T]GACGCAAGTGATGCTCTTTTAACATCTGCGAAAAC
3,516	6	6010	62.18	89810448	F1Dsnp	PHR	T	C	6	1,639,861	+	GACTTGCTTGCTTTTGAGGCTGACAGAAGGGCTGT[C/T]AATATAACCATAAACAGGTATAGTTTTGTCGAGTT
3,517	6	6010	62.18	89866422	F1Dsnp	PHR	T	G	6	1,649,212	+	GATATTGTGCTGTCCACTTTCGGCTTCAACCATCT[G/T]ATGTAAGAGCTCAAGTCGAAGTTGGTCACAGCATT
3,518	6	6010	62.18	89849685	SnpSnp	PHR	T	C	6	1,650,825	+	AGAAATATCACTGGTTGAGTGGTAAAAGTACAAAA[C/T]GCATTGATGCATCACTACATTTACTCTGGATAATG
3,519	6	6010	62.18	89810450	F1Dsnp	PHR	T	C	6	1,683,064	+	CCTTCTTCGAGATCCAAAGTTGATAGCACCATGAC[C/T]GGGACTACTATGTCTTTTGGTAATTTGCTACAGAC
3,520	6	6010	62.18	89810456	F1Dsnp	PHR	T	G	6	1,711,361	+	ACATTCTAGATGATCCAGGATCTGCTGATCTCAGT[G/T]CATACGTTGATTTTGCTTCTATCAGGCACTCAGCC
3,521	6	6010	62.18	89866427	F1Dsnp	PHR	A	G	6	1,776,245	+	ACTCTGATATCAACAAGGCTGAAGGTTCTGCATCA[A/G]TCACTGGTGGCTGCTTTTACCGATCCATGACAGAT
3,522	6	6010	62.18	14_1131487	GBS				6	1,851,057		TCGACGGGCAAATTCGCCGGAATGTTACCTCGTCCGTCTCGGCTGCCGTGGATTCTTCCGACCC
3,523	6	6010	62.18	TP6982	GBS				6	1,859,461	1,859,523	TGCAGGGCTTGTCGGTACAAGGGTTTTCTCTCTGTGGAGGAGTGTAATCATCTGATTAATCTGC
3,524	6	6010	62.18	89810469	F1Dsnp	PHR	A	G	6	1,860,232	+	TGTTTTTTCTTTTGTTCTCTAATCAGAGAATGGGG[A/G]GGGATTGCAGATAATATTGCACTATGATCATGGTC
3,525	6	6010	62.18	89810471	F1Dsnp	PHR	T	C	6	1,865,780	+	TGGACTAATTACCTCAGGCCTGACCTCAAGCATGA[C/T]ACCTTCACTCCTGAAGAGGAAGAGCATATTATCAA
3,526	6	6010	62.18	TP2552	GBS				6	1,919,721	1,919,777	TGCAGATTGCACAAGCACAACTTACGAAGTTGGAACTAGCTAGTAGATTACCACTACGTACTAT
3,527	6	6010	62.18	89810476	F1Dsnp	PHR	T	C	6	1,928,041	+	GAGATCAAGGAGAAGACGAGGATTTATTCACTTTG[C/T]TTTCTAGGGTTGGCTATTTTCTCTTTGCTGGTTAA
3,528	6	6010	62.18	89810478	F1Dsnp	PHR	A	G	6	1,947,889	+	ACAGGTGTCATTGCAAGAGTAAAGGAATTGTTTAA[A/G]GGGCATACCAAGTTAATTTTGGGGTTTAATACCTT
3,529	6	6010	62.18	TP4962	GBS				6	1,960,567	1,960,504	TGCAGCTATGGTGCCCCTCAAGTACTCAGAATCAATAGTCATTGCAACATGAACAAGAGAAGGA
3,530	6	6010	62.18	89898323	snp	PHR	T	C	6	33,886,470	+	GCAAACGCGATGCCTTCTTATATTCTTACTTTCTC[C/T]ATCGTAATGTTTTGCCCTATGGTCAAGTCTCAAGT
3,531	6	6010	62.18	89810622	F1Dsnp	PHR	A	C	6	33,898,869	+	CCGGGAAAGACAATGAGTCCCCTTCAGAATTGAAG[A/C]AACGTGAAAGAAAGGGAGTGCATGGCAAGAATGAC
3,532	6	6010	62.18	TP2840	GBS				6	33,918,361	33,918,424	TGCAGCAACTAGCTTAATGCTAAACAATGTCAGTCCATCTTCTTGATCATCATCAGCTAGCTAG
3,533	6	6010	62.18	89866602	F1Dsnp	PHR	A	C	6	33,977,817	+	ATCTGCTCCACCAAGTTTCTCCATGCGATCCTTGG[A/C]AAACGACATCAATTGGCAGGAAAATCTCAGTCTCC
3,534	6	6010	62.18	89810625	F1Dsnp	PHR	A	G	6	33,978,820	+	AGAATGTAATATGAACATCTATAATACTTCTCCAC[A/G]TCTAAAAGATCAACCAATGAGGTCTGGAGTTTAGT
3,535	6	6010	62.18	89810626	F1Dsnp	PHR	A	G	6	33,980,953	+	TAATCATAGCCTCAGCAGAAAACCCTGATGTATCA[A/G]TAGCCAGGTTGGTGTCATTGAAAGCAGCTCTAAGG
3,536	6	6010	62.18	89810627	F1Dsnp	PHR	A	G	6	33,983,361	+	TTCCTTTAACAACATGAGCTCTAAATGGGAAGGCA[A/G]ACTAGCTGTCTTGGGGTTCAAGAAAAGAGTCTCTG
3,537	6	6010	62.18	89810628	F1Dsnp	PHR	T	C	6	33,984,307	+	GATTTTATTTGCTGCAAGCAAATCTGCAACACAGT[C/T]AACGCATGAAAGTTAAAATGGCTATCTGTAGGGTT
3,538	6	6018	64.64	89810666	F1Dsnp	PHR	T	C	6	36,451,640	+	TAGTAACTCAACCCTTTTGATGTTGCTGACTTGAA[C/T]AAGATGTTTAAACCAACGTTGGTGCTCTCCACTGT
3,539	6	6018	64.64	TP7267	GBS				6	36,458,277	36,458,214	TGCAGGTATTTTGAACAACCTCACCACATGTTGCAAGTTCGTTGAAAAAATTAGCATTGGATTC
3,540	6	6018	64.64	89810667	F1Dsnp	PHR	A	G	6	36,469,275	+	GATTGAACTGACATATGACCAAGATCACCTTCATC[A/G]AAGAAGCCAGAGAAATCAGACAGGCCATCATTCCC
3,541	6	6018	64.64	89866629	F1Dsnp	PHR	A	G	6	36,469,708	+	CCATGTCATTGAATCTGTAATTCACAGGCTTTCGC[A/G]ACCGCCCAGACTGCAAATGAGAATGCCAAGAAAAG
3,542	6	6018	64.64	89866630	F1Dsnp	PHR	A	G	6	36,470,403	+	CCATCATTACAGGTGTTTTCAGACTCTGGAGAGCT[A/G]GAATCTACTTTTCTCTTTCCTCTTCCAAGTACCCT
3,543	6	6018	64.64	89810669	F1Dsnp	PHR	T	C	6	36,470,476	+	TTGTTCCTCTTCCTCTTCCTTTTCCTCTGCCTCTT[C/T]CATTTGCATCTGTTTTTCTATTGGTTTGTCCACCC
3,544	6	6018	64.64	89810670	F1Dsnp	PHR	A	G	6	36,474,809	+	TCTATAATCACCAGATTCTTCTGTCATCTTGTTTG[A/G]CATTGACTCACCTATGGAAGAAGGTTTCACCATTT
3,545	6	6018	64.64	89810671	F1Dsnp	PHR	T	C	6	36,475,190	+	AAGTCCATCAACAACAGATTTATTTTGTTGGGTAG[C/T]TGGGTCAACCATCTTGGTTTCTCTATCAATACATT
3,546	6	6018	64.64	89906421	SnpSnp	PHR	A	G	6	36,475,914	+	CCAATGTTATTGCTAGTGAGCATGTTCCCAGCATC[A/G]ATTATCTTGTTTCCATTGGTTTTCTCCTGTTCCAT
3,547	6	6018	64.64	89810672	F1Dsnp	PHR	A	C	6	36,476,300	+	CAATAACAGAGAACTAATACTCACTGTTTATCACC[A/C]GTAAATGATGAGGAAAAGATAAACTCTCTGTGGCT
3,548	6	6018	64.64	89866631	F1Dsnp	PHR	A	G	6	36,478,702	+	CTAAATCACTACTCCCCGAAACACCAGCTTTCTCC[A/G]AAACTTCCTGCCTCTGGTTCTTAATATCCTCAGCC
3,549	6	6018	64.64	89810673	F1Dsnp	PHR	T	C	6	36,525,966	+	GAAGAGATCGATTTTAAGATTGGAATCTTTGGGGA[C/T]GCTTTCAAGAGTAAAGCCGCAATGTCAGGCTTTGT
3,550	6	6018	64.64	89866632	F1Dsnp	PHR	A	C	6	36,526,959	+	AAGGTGACCCAGTAAATGAGATGCTGTTTATTATT[A/C]GAGGGAAACTTGAGAGCTCCACAACCAATGGAGGG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,551	6	6018	64.64	89866633	F1Dsnp	PHR	T	G	6	36,529,983	+	GAACAATAACTTAAGACCCCAAAAATTACCTTGAT[G/T]GATGTTGAACTCTTCAAACTCGTCATCGTCCTCGA
3,552	6	6018	64.64	TP4627	GBS				6	36,563,285	36,563,320	TGCAGCGGCGGCAAACACGTCGGAGAAGTTATTCCGAGATCGGAAGAGCGGTTCAGCAGGAATG
3,553	6	6018	64.64	89810674	F1Dsnp	PHR	T	C	6	36,585,390	+	ACTTCCACGAGTCAAATCAATCTTGATGTTGGTAA[C/T]AGCAACATCCTCCTCTTTCAATATAACACCTCCAT
3,554	6	6018	64.64	TP3827	GBS				6	36,590,301	36,590,275	TGCAGCCACCACATTTCAACACTCAAAAGTTCCTCACATTTTCATTTTCATACAAGCATAACAA
3,555	6	6018	64.64	89810675	F1Dsnp	PHR	A	G	6	36,641,237	+	TACCTATAGTTTGTGACTGGCATGGGTGGCTTTAC[A/G]TAAGTGTGGAAGATGATGTTATCATATTCATCAGT
3,556	6	6018	64.64	89810676	F1Dsnp	PHR	T	G	6	36,652,065	+	CAAAGGCAAGTCTTGGGAGAAACAGACCCTCGATT[G/T]GGTGAGACATGTCGATATGTAGCTGAGGCACATGT
3,557	6	6018	64.64	89866635	F1Dsnp	PHR	A	C	6	36,652,101	+	GGTGAGACATGTCGATATGTAGCTGAGGCACATGT[A/C]CAAGCATTGCAGTTTGATGAGGCTGAGAAGCTGTG
3,558	6	6018	64.64	89810677	F1Dsnp	PHR	T	C	6	36,653,992	+	ATTGATTCATTGCATGGTGCTCACCCATGACAAGC[C/T]TCTGTGATTGAAACCGGTGGATCAGATAGTAAGCC
3,559	6	6018	64.64	89810678	F1Dsnp	PHR	A	C	6	36,654,370	+	AATACACATCAACATAAGTGAATACTGCAAGAGGG[A/C]GCTGCTTCCTCAAGTGTGATACGCTGTTCTTAAGC
3,560	6	6018	64.64	89866636	F1Dsnp	PHR	T	C	6	36,658,447	+	GCAATATTTGGGAAGTGTGATAGAATTTTATCCCT[C/T]GGCTTGTGACTTATATCAAGCAGCACATACTTCTC
3,561	6	6018	64.64	14_488778	GBS				6	36,702,916		CATAGTTACTACTGCTAGATTCATTTCAAAGGTCTGTCCCTTGAACCTTCGAATTTCAAAACGC
3,562	6	6018	64.64	89866637	F1Dsnp	PHR	T	C	6	36,717,231	+	TCTGCACCTTTGCAAAGAAGCAACAGTTTGTTTTC[C/T]GGACTCCTGACAATTACTGACATTCTTTTGCGAGA
3,563	6	6018	64.64	89810679	F1Dsnp	PHR	A	G	6	36,741,205	+	CTGGGTTGAAGCTCACTACAATCTGCCCAGGTCTC[A/G]TTACTGGTCCTGAATTTTGCTCAAGAAACTCAACA
3,564	6	6018	64.64	89798700	snp	PHR	T	C	6	36,753,028	+	ATCTCAAGTTTATGCCTAATGAAACCAACCTGCGA[C/T]GGCTTACCAGCAGGCGTTTCTGAAGCTACTGATGC
3,565	6	6018	64.64	89866638	F1Dsnp	PHR	A	C	6	36,755,110	+	ATACATTGAGCTCAAGAGCACTAGTCAAGGAAGCA[A/C]CTTGTGCAATATGTTTCAATTCAGCAAGAAGGTCA
3,566	6	654	67.11	89862145	del	PHR	-	GTA	6	36,770,204	+	GTTAGTTCATTTCTCCAAATGTGAAAAAGAAAACC[-/GTA]CGTAGAACATTTCTTTAGCTTCAACAGACAAGTTA
3,567	6	6013	69.57	14_399472	GBS				6	36,787,324		TTTGCAGAACAATGAACCAGAAATTGTTCCTRGCCTGCATGTGAATAATTATAAAGGATGTGAC
3,568	6	6013	69.57	TP1098	GBS				6	36,787,368	36,787,304	TGCAGACCAGTGGTACGAATAAGGATACATAGCAGCCAAATTTGCAGAACAATGAACCAGAAAT
3,569	6	6013	69.57	89866641	F1Dsnp	PHR	A	C	6	36,800,377	+	GTCAATATGGGGTACACAGAATTCGAGGCTTCAAT[A/C]GCAATAGAAAGATGCGGTAAAACTTTTGTGTCAAG
3,570	6	6013	69.57	89866642	F1Dsnp	PHR	A	G	6	36,820,603	+	ACCTCATGGTAACTACAAGCCAAACACACTCTACA[A/G]CAACCATTTTCACTTTCAGAACCAAGACAGGGGGA
3,571	6	6013	69.57	TP7960	GBS				6	36,822,900	36,822,840	TGCAGTAGACTTCTCCTTCTTCCTTTCAAACCTGCGACGATAGACCTTGGACTCAGCTGGATTT
3,572	6	6013	69.57	89810683	F1Dsnp	PHR	T	C	6	36,872,868	+	GAAGAGCAGCAAGTAAATATATGCATTACATGAAA[C/T]TTCCTCAGCACGGCATATAACATGAAGAGCATCTT
3,573	6	6012	74.71	TP9640	GBS				6	36,966,261	36,966,324	TGCAGTTGTTCCGAAACTTGATTCTGACAGCCTTGATGAACATGTGAAAGAGGAGATCATTGCT
3,574	6	6012	74.71	89866643	F1Dsnp	PHR	A	G	6	36,987,248	+	AGGGATATGTGGACAGATATACGAAAAGTGGCAGC[A/G]CTGTAAATATGTTGACTTCTACACACCCAGAAAAT
3,575	6	6012	74.71	89866644	F1Dsnp	PHR	T	C	6	37,001,963	+	TATCAGGAGCCACCTGAGTGATCTCACTTATCATA[C/T]GTAATAAGGCCTTGACTATGTCACCAAGCAATTCC
3,576	6	6012	74.71	89810684	F1Dsnp	PHR	A	G	6	37,003,174	+	ATCCAAGATGACAGATGACACTTTAGCATCAAAGA[A/G]CAAGATGTCTGCCCTCAGCCAACGGCGCATGAAAG
3,577	6	6012	74.71	89866645	F1Dsnp	PHR	A	G	6	37,005,067	+	GTAGAGATGCTAACACTCCATATGATCTGTAAGAT[A/G]TCTTTTGAGGCTTCAGGATGTGCTTCAGCGTCCAT
3,578	6	6012	74.71	89810685	F1Dsnp	PHR	A	G	6	37,009,666	+	AGAAGTACACTCACTTCTGAACTCTTGTGCGGAAC[A/G]TATTGAAGACATTCTGTCAACAATCTAAGCACAGG
3,579	6	6012	74.71	89868896	SNPinIns	PHR	A	G	6	37,018,075	+	TACATCATTTAAACTGCGAAGTATCAGAAGATGTT[A/G]AAGGTCTCAGAATAGGTTTTACGTTTAGCCAAAGA
3,580	6	6012	74.71	89866646	F1Dsnp	PHR	T	C	6	37,069,534	+	TGGCAGCTATTATCTGAAACCAATGTACATCACCT[C/T]GTTCATGTTCCTCTTAAGGACTCTCCCCTGAGTGA
3,581	6	6012	74.71	89810686	F1Dsnp	PHR	T	G	6	37,070,875	+	TTGCAGAATGATGATCTAAAGCTGTCCAAAACCCA[G/T]TCAGATTATTGGCAAATTTTTCCTGTATCAGATGA
3,582	6	6012	74.71	89866647	F1Dsnp	PHR	A	G	6	37,071,218	+	TATGTGATCAAGTGAAGTTCAGTTTGAACAAAACT[A/G]TTGCTTCTCCAACCATTCTCCTTCCTTGGGTCCCT
3,583	6	6012	74.71	89866648	F1Dsnp	PHR	A	G	6	37,071,450	+	CAGACATGGGTATTGTGTCTGTATCTGCTTCTGGT[A/G]TTGTCCAGGCTAAGAAGCCTGGTAAAGCTACCATT
3,584	6	6012	74.71	89866649	F1Dsnp	PHR	A	C	6	37,115,604	+	TCCGACGACCTCTCCTCCTTGCCTCCCGCCGACGA[A/C]GAGAAGTACGGCTTCCAGAGGCCGGAGATGTTCAC
3,585	6	6012	74.71	14_94110	GBS				6	37,119,039		TGGCAGAAGAATTGCTGTTGCTTTTGAGGGACTGCTCGAGTTATGGTCCGAGAAATCAGCAGTC
3,586	6	6012	74.71	TP1351	GBS				6	37,119,133	37,119,087	TGCAGAGAAAACTACAGAGGATTGATTTTGAGGGAAGGGGTAATGCCCGAGATCGGAAGAGCGG
3,587	6	6012	74.71	89866650	F1Dsnp	PHR	A	C	6	37,120,239	+	TAGTCTGATTAGGAAATACAAAAACGATTCCTGAG[A/C]ATGAATCTTTAACATCCTTTTGGGGAAGGCAAACG
3,588	6	6012	74.71	89866651	F1Dsnp	PHR	A	G	6	37,129,174	+	TTCAGCTTCTCGAAAATTGTTCAATGGCTGATCTC[A/G]TTTGCCCTATTTGTGATTATCTACGAGAACATAGG
3,589	6	6012	74.71	89810687	F1Dsnp	PHR	T	C	6	37,129,723	+	ATTGTGGACAATATGAGGCATTATCTGACTAGTAA[C/T]GATTCTTCTCCTTTTGACATTAGGAGTAATGGCAG
3,590	6	6012	74.71	89866652	F1Dsnp	CRBT	T	C	6	37,129,975	+	AAAATCAAAACAGTTTTGTTACATGGATTGAACCT[C/T]TCAAGAAGGTTACTTACTAGTAGTATTACGGTTTT
3,591	6	6012	74.71	89866654	F1Dsnp	PHR	T	C	6	37,212,042	+	CTCATTCATAATAAGCTGCCATTTGAAGGCATGTC[C/T]AATCTGCAAGCAGCATATGCAGCTGCTTTTAAGGT
3,592	6	6012	74.71	89866655	F1Dsnp	PHR	A	G	6	37,238,467	+	ACAATTGGATTTGATCCATTAATGTCAATTTTGAA[A/G]TTACGAGGAAGTACTTACAGTTTCACTCAACAAAA
3,593	6	6012	74.71	89810688	F1Dsnp	PHR	A	G	6	37,240,397	+	CAACCAATTCTCTTGAAAATGCTGGTGACTTGGCT[A/G]GCTGATTTCCCTAGTGCTGTGCATTGCTTCCTAGA
3,594	6	6012	74.71	89810689	F1Dsnp	PHR	A	G	6	37,241,394	+	GCTGGCAAGATGGAATCCGACCTGAAGAGTCTATC[A/G]GATGCTTACAACAGTCTTGAGCAGGCCAATTTCCA
3,595	6	6012	74.71	89798813	snp	PHR	T	C	6	37,267,296	+	AGAACTTCACAATTGTTTTATTTCACTATGATGGT[C/T]GAACAAGTGAATGGGACGAGTTTGAGTGGTCAAAG
3,596	6	6012	74.71	89810690	F1Dsnp	PHR	A	G	6	37,296,695	+	CAGACTATGGTTTGCTCTGATACTTGCTTGTACCA[A/G]ATGCCTATGTAGAATTTTGAAGCATTACCTGGTTT
3,597	6	6012	74.71	TP5879	GBS				6	37,348,653	37,348,716	TGCAGGAACTGAGCCATCTGCATATCAAGCGAGAAGGGACTTATACCATTCTCGAAAATGGTCT
3,598	6	6012	74.71	89866656	F1Dsnp	PHR	A	G	6	37,349,040	+	GCAGCTGAGATCCCGCCGGTGTCGGAGTTCGAGTC[A/G]CCGAAGTTGTAGATTGCCGGAAAAGAACAAGATGG
3,599	6	6012	74.71	89866657	F1Dsnp	PHR	T	C	6	37,357,430	+	GAGGACGGTGATGATGAGATTATCTCTGAAACACC[C/T]AAGTCTCATAGTGAGGAAAGTGATTCTGAAGAAGC
3,600	6	6012	74.71	89810691	F1Dsnp	PHR	A	G	6	37,362,562	+	AGTATAGGAGGAATGTAACTAACTTGTTCGAGTAC[A/G]TTCTGTATATTTCTGCCTCTTTCGACTGTATCACG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,601	6	6012	74.71	89810692	F1Dsnp	PHR	A	G	6	37,382,912	+	ACTGAATTTGCTCTAGCAGCCTTGATGGAAATTCC[A/G]CCTCAGTATAAAGCGACAATAGAGCTTAATCTCCT
3,602	6	6012	74.71	89866659	F1Dsnp	PHR	T	G	6	37,408,790	+	TGCCTATCCGCGCTTCGTGACCCATGTCGACGATG[G/T]CTTCATTTCCACACTGACCAATCTGTATAGAGAAA
3,603	6	6012	74.71	TP2766	GBS				6	37,417,596	37,417,661	TGCAGCAAATTTTGGTACTACCTCTGAAGATGAAGATGAAGCTTGAAGATGATGGAGCAGTTGT
3,604	6	6012	74.71	89866660	F1Dsnp	PHR	A	G	6	37,445,014	+	AGCGGGAAAAACTGTAACCACCCACGGTGGCTTAA[A/G]ACTTCATATACCTCTTTTGCTGTTGACACACCCTT
3,605	6	6012	74.71	89866661	F1Dsnp	PHR	A	G	6	37,445,667	+	TCCTTACAGCATGTTGTGATGAGATCAGCAACACC[A/G]CAGCTTTCAAAGAAGGTGCTGTCCTTGACAGATGA
3,606	6	6012	74.71	89866662	F1Dsnp	PHR	T	G	6	37,446,472	+	GGGAAATAGCCTCCACATCCCCGCTTATCTTCCCT[G/T]CTAGTCTTTTGCATATACCCTCCATAAATTGATGT
3,607	6	523	79.85	89866665	F1Dsnp	PHR	T	C	6	37,647,325	+	CCATCGGCGACCAGCAACTAAAGCAGCAGCAGCAA[C/T]AGAGATTTGGCTTTTAGAGGATTTTATGGTATGTG
3,608	6	523	79.85	89810727	F1Dsnp	PHR	T	C	6	38,699,736	+	TGCTTTACAGTAGCCATTCTTTCTGCAATTGCAAC[C/T]AAGTCTGCAGAAACATAGACAAAAGTCGGAGGACA
3,609	6	524	82.31	89866694	F1Dsnp	PHR	T	C	6	38,585,948	+	CTTTGTAGGCGTTACCAAATACAAATATATTCGTC[C/T]GAGACTCGAAGTTGGAGGCATCTCAATTCTTCTAT
3,610	6	524	82.31	89866695	F1Dsnp	PHR	A	C	6	38,595,920	+	GACGAGGAAGAAGAAGCTGCTGATCTCGTTGCCCC[A/C]AAACCTGTAGATGATATAGAGGAGGGAGAAATCGA
3,611	6	524	82.31	89866696	F1Dsnp	PHR	A	G	6	38,598,339	+	GTTGCCTTTGTCTATGCATTGGACTTCAGGTTGAC[A/G]ATCTGTGCTTGTACCATGTATCTTTAATTGTAGAA
3,612	6	524	82.31	89866697	F1Dsnp	PHR	T	C	6	38,601,602	+	ACCCAGTTAACGATCCAAGATAAGCTAAACTTTCG[C/T]GGTTTCTTGATGGCAAGCCACATGATGCAAGGGAG
3,613	6	524	82.31	89866698	F1Dsnp	PHR	A	G	6	38,611,068	+	TTCTTATAAGTTTCATAAGACTCTGGTAACTCACA[A/G]AGGGCTTCTACATCATTGAGGAAGATGAATTTCCA
3,614	6	524	82.31	89866699	F1Dsnp	PHR	T	C	6	38,611,332	+	GTAAGTAAATTCTCATCCTTGTTCACAAATGACCA[C/T]CTTGCCTGGACTAGTCCTAATTCTGGATTTCCCTG
3,615	6	524	82.31	89866700	F1Dsnp	PHR	T	C	6	38,636,222	+	CCAGCAGGCATCCTGGCCATCCCGTCTGGCATTGC[C/T]ATGGAAGTTGCAGATGCAAGGAAATTCAAAGCGAC
3,616	6	524	82.31	89866701	F1Dsnp	PHR	A	C	6	38,638,374	+	ACTTGCTGCTCAAGGTATTTACTCCATAATTTCTT[A/C]CTCATCTTCATCAGAGAAACGACTCGATGTTTTTT
3,617	6	6008	87.60	89810717	F1Dsnp	PHR	A	C	6	38,283,015	+	AATGATTACAACTTACAGGAGGAAAATGGAGGCCC[A/C]TACAAAGCATCAATTCCACTGATTCAGGCCACAAG
3,618	6	6008	87.60	89866683	F1Dsnp	PHR	T	C	6	38,284,406	+	CATCAGCAACCTGGCATCCCATATATTGCTGAGTC[C/T]ACATGCAGTGACAAATGGGCATGGGTACTTTTCGA
3,619	6	6008	87.60	89866686	F1Dsnp	PHR	T	C	6	38,357,804	+	CAATTATGTTATGGGCGTGGTGGATATAACCCTTA[C/T]GGCTATGCTAATGGTTATTATCCTCATCAGCAATA
3,620	6	6008	87.60	89866687	F1Dsnp	PHR	T	C	6	38,362,790	+	TCACCTTTGCCTTCTACATGTTGCATCTTCAAAGT[C/T]CCCGAGGTGCTACGAAGACAAAAGGTAGATGCATT
3,621	6	6008	87.60	89866688	F1Dsnp	PHR	A	G	6	38,377,181	+	ATCTAAACGGAGTTGATACCCCCAACATGTTTGGT[A/G]CCACCACATTGATCGTCAAGGTGAGTTGGCTATCA
3,622	6	6008	87.60	425_56770	GBS				6	38,447,874		ATATTCTCTGTTATAGTTGCTTGATGATTTCGACTTTTTTTACGTTTACATAAGACTCTGGCTA
3,623	6	6008	87.60	425_56868	GBS				6	38,447,971		TGGAGGATTACTACAGAAAACAGAACAAACTMATCGATTTTCACATCAAAGGTGCCCCCGGAGA
3,624	6	6008	87.60	89810720	F1Dsnp	PHR	T	C	6	38,483,560	+	ATCTCCTTCTCCTTTGCTTTGCACAAGTCCTCTGC[C/T]TTCTTGATATACTTTTTAGTTAGCTCCTCAACCTG
3,625	6	6008	87.60	89810721	F1Dsnp	PHR	A	C	6	38,485,733	+	GTGATTCTGAGCTGAAAGATGGAAGCTTTATGTGA[A/C]TTTCCTTCTCCTCTGCAAGTTTTGTTCAGAACTGG
3,626	6	6008	87.60	89810722	F1Dsnp	PHR	A	G	6	38,487,540	+	GAAGAGATCATAGGTAAGGTCTTAACAAGGTGCCC[A/G]AACATAATTAGTTACAGTGTCGAGGACAAGTTACG
3,627	6	6008	87.60	89866691	F1Dsnp	PHR	A	G	6	38,487,610	+	GGCCCACAGCTGAGTACTTTCGCTCACTAGGGGTG[A/G]ATGTTGGTGTTCTTCTGCATCGATCTCCCACAGTG
3,628	6	6008	87.60	89866692	F1Dsnp	PHR	T	G	6	38,493,498	+	AGACACATTTGAACTTGATGCTTTTGATATGGGGA[G/T]CCTTGAAGATGTCAGTAGGTTAGTTGCATATCTCA
3,629	6	6008	87.60	89866693	F1Dsnp	PHR	A	G	6	38,495,578	+	TCTTTCATAACCCTATTTCTGTGATACTATCAGAC[A/G]TTTCGCAAGAGCTGAGGTCCCTTTTATGCAAAAGG
3,630	6	6008	87.60	89810724	F1Dsnp	PHR	A	G	6	38,530,429	+	AAAGGCTGAAAGCCAGGATGATAAAGATTCACGAA[A/G]GGGCAGGAAGAAGGATAGAGTCGAAGTGAATGTAT
3,631	6	6008	87.60	89810725	F1Dsnp	PHR	T	C	6	38,532,894	+	AAAGGTGCTATTCCTAAGATTATAAGAGATCACTT[C/T]ACCCGGAACATGCAGCAAAAGAGAAGAAGAACTTTCCT
3,632	6	527	90.07	89866682	F1Dsnp	PHR	T	G	6	38,258,072	+	GAAACTATGGCAAAAAGTCCGCGTGTTTTGTCGCC[G/T]GGAGACATAATGCAGTTTCAAAATGTCACGGTACT
3,633	6	527	90.07	89810716	F1Dsnp	PHR	T	C	6	38,264,527	+	ACATGTACAAGGTCATCCACAGTAACATTGTTCCT[C/T]CCTTTTTTCTTTATGAATGACCTACCATTATCAAT
3,634	6	6015	98.17	89810481	F1Dsnp	PHR	A	G	6	19,841,862	+	CATCAAAAATTTGCATCTACCAAGCACACTGTATA[A/G]AGGATGCAAATCATCAACCCCTTTCTTCAACATTT
3,635	6	6015	98.17	89866667	F1Dsnp	PHR	A	G	6	37,693,906	+	AAGAAGAAGCATACCACACCATGACACTTTGGTGC[A/G]TCCTGTCCAAGTATTCCTTGGAAAATTGATCCTGG
3,636	6	6015	98.17	89810694	F1Dsnp	PHR	A	G	6	37,694,388	+	GTAATCATCGTATACCTCACAACAATCTCAGAGAA[A/G]TAACCACCGCCGACACGACCAAGAAAGTTCCAAAT
3,637	6	6015	98.17	89866668	F1Dsnp	PHR	A	G	6	37,724,672	+	GCTGGTGACGATTATAAAGCATCGGTTGATGATCT[A/G]CAGTATTTTTGGCCTCAAAAGGCCACAGACTTCTG
3,638	6	6015	98.17	125_359089	GBS				6	37,777,008		CGGCCGGCCTTGTGGTTGAACTTATTCTTCACCTACTGTGCTTGATTCATGTTCAAGAAGGAGA
3,639	6	6015	98.17	89866669	F1Dsnp	PHR	T	G	6	37,787,320	+	CTCTCTCTTTTTCCCGCCAATTTAACACCATTGAT[G/T]CTCTGCTCAAGCAGGTCAGGACCCACAAAATCTGG
3,640	6	6015	98.17	125_344814	GBS				6	37,791,209		GGGCATCACCGGGCTCACATGTTGGGACATAATTCTTCAGAAAATTACCAGAAACAGCAGAGGT
3,641	6	6015	98.17	89866670	F1Dsnp	PHR	T	C	6	37,805,365	+	GTGACAAAATTCAAATGTGGAGGGTTTTCTCTTGG[C/T]CTGTGCATGAACCACTGTATGTTTGATGGCATTGG
3,642	6	6015	98.17	89866671	F1Dsnp	PHR	T	C	6	37,826,183	+	TTGGGGAGATTATTGTTCATGTTTGCCACCGGGGA[C/T]AAGACCATGAAATCCGTATCAAATTGTTCGGAAAA
3,643	6	6015	98.17	89810695	F1Dsnp	PHR	T	C	6	37,837,080	+	GGCAAAGATCATCTTCTTGGCTATTTTATTCAGAT[C/T]GGACACAGCCTCCTGAGGATAACCAGGATATTCGA
3,644	6	6015	98.17	89810696	F1Dsnp	PHR	T	C	6	37,837,466	+	TACCCCACCTGCATCTTCCTTCGCAACAGATATCA[C/T]CTACCCAATTCAAGAACTTTTCAATAAGCTTAATG
3,645	6	6015	98.17	89810697	F1Dsnp	PHR	T	C	6	37,851,618	+	TTACATTTATGTGCATTGATTTGACAGACTACATA[C/T]GAGAATTTTCGATATCGATATGATAGGCGAGCCAA
3,646	6	6015	98.17	89866672	F1Dsnp	PHR	T	C	6	37,873,891	+	TCATCTCCGAAAATATCTCCAACTGCTTCACCTCC[C/T]CTTGCCTCTTCACCCAAGATAAGTGAGCTTCACGA
3,647	6	6015	98.17	89810698	F1Dsnp	PHR	T	G	6	37,880,040	+	CTTGCCTGCAGAACTGATCAAACAAATACTCCTTC[G/T]GTCAGTGATAGTAACAGTACGTCACATGATCATAA
3,648	6	6015	98.17	89866673	F1Dsnp	PHR	A	G	6	37,888,427	+	TTTAACTTCTTTAATATTTCAAAGTTGTGTCTTAC[A/G]GAGAGGTTAGATATTGATGGTGCAACAATATCCCG
3,649	6	6015	98.17	125_249064	GBS				6	37,888,796		TCATGTACTAAGTACAATTACAGGTCAGTCTGCTTTTGTGTTTCATTTACTAGTAGCTTGATCT
3,650	6	6015	98.17	89810699	F1Dsnp	PHR	A	G	6	37,888,824	+	GTACATGAGGAAGGCTAAGATAGGGAGTGTCAGGC[A/G]TGAACTGTAGTAAAGGTAATACAGCTTGAAGTGGT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,651	6	6015	98.17	125_249005	GBS				6	37,888,855		CTTCAAGCTGCATTACCTTTACTGCAGTTCATGCCTGACACTCCCTATCTTAGCCTTCCTCATG
3,652	6	6015	98.17	89810700	F1Dsnp	PHR	T	C	6	37,889,242	+	CCAACAGATTCTCCAACAAGATATATGGGACGATC[C/T]GGCGAGGCATGATGCTCTGACCGAATTGTTCTCTC
3,653	6	6015	98.17	89810701	F1Dsnp	PHR	T	C	6	37,913,039	+	GTTAATGCTTTGGCTTGCAGGTTCATCTTCGCCCA[C/T]GCTGCTCCCGACACTGATGTCCCAGTTTTAACTGC
3,654	6	6015	98.17	89810702	F1Dsnp	PHR	T	C	6	37,930,813	+	GCAGAACAAATTATATCATCCATAAAGGTCTTACT[C/T]GGAGAGGATGGTTCCAACAGAGGTGAGGATAGATT
3,655	6	6015	98.17	89810703	F1Dsnp	PHR	T	C	6	37,937,126	+	TATTCCAGATCAAACGGACGTGTGCAGGAGAATTT[C/T]GGGTCTGTTGAGAACCTGTCTCTTGACGAGTTCTA
3,656	6	6015	98.17	89810704	F1Dsnp	PHR	T	C	6	37,937,861	+	TGCCTGTTCAAAACTCGGCGTCGTCTTTATGGAAC[C/T]GCCTCCAGGATCAAATCTCCAAGCATTCCTTCGAC
3,657	6	6015	98.17	89810705	F1Dsnp	PHR	A	G	6	38,038,373	+	ATTGAATGAGTGGAGGGTAGAATTACAATTTCAAC[A/G]TAGACAAATTTGCGACTCTTGTCAGCCAGCAGAGC
3,658	6	6015	98.17	89862162	del	PHR	-	CAA	6	38,039,728	+	GCTATACAAAAAGCATTGATTACTACAATCTACAG[-/CAA]CAACAAGTACGTGGTGGTCGACGCCCAAATCTTGC
3,659	6	6015	98.17	89866674	F1Dsnp	PHR	A	G	6	38,040,139	+	TCAACATTTGCCAACACAGAATAGTCCTTGTCCTC[A/G]CCAGTCTTCAAACATATCAAACAGCCACAAGACCA
3,660	6	6015	98.17	89810707	F1Dsnp	PHR	A	G	6	38,040,558	+	CTTCGATCATTGTCTCACCTGTTCGGCAAAGGCCA[A/G]TAGAAGTGGGACACTTATCTCTTGGCCAGCTGTGC
3,661	6	6015	98.17	89810708	F1Dsnp	PHR	T	C	6	38,041,660	+	TTGGTTCACTTGTAGGTCCCAATCTGTCCTGAAAT[C/T]ACGAACCTGTCAATCATTCAATAGTAATGAATTCA
3,662	6	6015	98.17	89810709	F1Dsnp	PHR	T	C	6	38,043,085	+	AGTTGCATTTGAGAGAGGTAAAAGCTGAGCTTCAA[C/T]TTTTCTTTGGGTAGAGTCTTGAACAGTGACACTTT
3,663	6	6015	98.17	89810710	F1Dsnp	PHR	T	C	6	38,044,323	+	AGTATTTGACTGATGATAAATTACCTGTTCAAATT[C/T]GGTGGCTGTGCGCTTCTGTCCAGAACTTGGTTCTG
3,664	6	6015	98.17	89810711	F1Dsnp	PHR	A	G	6	38,044,821	+	TAACCTTTAAAGGCCGGACGACTTGTAAAATAACC[A/G]GTCCAATATGCATTTGGATGATCCGCATAACTGAA
3,665	6	6015	98.17	89810712	F1Dsnp	PHR	T	C	6	38,045,614	+	TGAGTAAAGGTGAATAGACTTACCTGAATAGGAGG[C/T]GACACATCATTTATTTCAAATACGAAACCATCAGG
3,666	6	6015	98.17	89866676	F1Dsnp	PHR	A	G	6	38,060,181	+	CCAGCATTTGGCAAGGGAATGCAACCCAGATGTGT[A/G]CAGACCCCAACAACAATAAGCCATTCTGGGTCTTT
3,667	6	6015	98.17	89810713	F1Dsnp	PHR	T	C	6	38,060,439	+	CTGGCTGACATGCTCAGTACAAACTTGAGGACAAG[C/T]AGACGAATTAGAGAAGCATAGACAAACCTACCGCC
3,668	6	6015	98.17	89866678	F1Dsnp	PHR	A	G	6	38,060,594	+	TGAAGATGGATTTTTGACAGCTGCAACAGTTGGAG[A/G]AACATCTGGTACTATGCTGTTGTCCCCTGATGGGG
3,669	6	6015	98.17	89810714	F1Dsnp	PHR	A	G	6	38,064,497	+	GGAATGATATGAGGCCGTACATTGATTCTACTTTC[A/G]CTAGCTATGATATTCCGGCTGATGTTTTTGTTGTT
3,670	6	6015	98.17	89810715	F1Dsnp	PHR	T	C	6	38,080,200	+	AACTTAGCTGCGTATCAGAGTTTGATAACAGAGTC[C/T]ATGTACGAAAAACAACTAGATAGTGGAAGGGGAAC
3,671	6	6015	98.17	1035_10278	GBS				6	38,086,071		CTTGAGATGCTCTTTACAAAGAGGCAACATCATCATCATCATCATCTTTGATGGAAGATTT
3,672	6	6015	98.17	89866679	F1Dsnp	PHR	A	C	6	38,099,470	+	TTTACATCTTGTTGCTTTGCAGCTTTCATGGGTCA[A/C]TCTCTCCAGAAATCTGTTACTTGCATATCAGAGCC
3,673	6	6015	98.17	125_435302	GBS				6	38,181,468		TCAGCAGACTTGTTATGTCTTCTTGAAGAACACATCGAGTATTGTGAGGATCACTCCTCCTCCT
3,674	6	6015	98.17	89866680	F1Dsnp	PHR	T	C	6	38,216,145	+	CAGTGTCGTACGCGCCATGGCCTCCATTTTGGACA[C/T]CTTCAACAGTCCAGGTGCCTTTTTCTCTTCTTTGG
3,675	6	6015	98.17	89866681	F1Dsnp	PHR	A	G	6	38,243,023	+	GATACCATATGCTCAGTGATTGCTAGTACATTCAG[A/G]GAGTACAGAGCTCTTGAAAGTTCCCTAAACCTGCA
3,676	6	6015	98.17	125_215033	GBS				7	22,125,309		CCATCTCTCTCTCTCTCTCTCTCTCTCTCTCGCTCTCTCTCTCTCTCATTGCCATTCCATGT
3,677	7	7001	0.00	TP8412	GBS				3	10,009,626	10,009,594	TGCAGTCGATGAGGAAGCTCCTGCACAAATTGGTGCCGTTGGAACCTGTTCTCGTGCCTCACCG
3,678	7	7001	0.00	89809500	F1Dsnp	PHR	T	C	3	10,021,669	+	GGCGTGTCCGGGTGTTGGGTGCAGGTTTACAGCAA[C/T]GGGGATGTGTATGAGGGTGAGTTTCATAAGGGGAA
3,679	7	7001	0.00	89865463	F1Dsnp	PHR	T	C	3	10,144,981	+	GATGAGTAGTTGAGGCCGTTGTGGAGGTGGACAAT[C/T]TGTGGGTCGATGAGATTAGCGAAGAGGGAGAGGAG
3,680	7	7001	0.00	89865464	F1Dsnp	PHR	T	G	3	10,175,706	+	ATCACAATGAAGTCAGGCGTCATTTTGATTGTTTT[G/T]CTTGGGTGTGTATATCTCAGAGATGCCAAGGAAGA
3,681	7	7001	0.00	89865465	F1Dsnp	PHR	A	C	3	10,275,347	+	AAGCAATCCCATCCAAAAATGAAATTGTGATGGAC[A/C]CAACACTATTGATTAAACTTGGCCGCTGGCAATGG
3,682	7	7001	0.00	TP304	GBS				3	10,330,445	10,330,508	TGCAGAAATGCATATGATACTTGTCATTTGAAATTGTGCATACCTCAGGCTTCCCTGTGGAGAG
3,683	7	7001	0.00	89865466	F1Dsnp	PHR	T	C	3	10,360,393	+	GAAATTCACCGTCAAGGATTGAGGGAAGGTGCAAG[C/T]CTTGTGGAAGTGGTATGTGATTAGCATAAGTAATT
3,684	7	7001	0.00	89865467	F1Dsnp	PHR	A	G	3	10,490,437	+	TAACAGGTATCTCTCGGACCTTTGATGTTTGCTTC[A/G]TTATTTGTCCTGGTTGGTGATCATTATCAATTACC
3,685	7	7001	0.00	89865468	F1Dsnp	PHR	A	G	3	10,563,829	+	CAAATATGTTTGTGGGATATCAATGCAAATTCTAA[A/G]AACAAAACCCTGGAGGCTACTCAGATATTTAAGGT
3,686	7	7001	0.00	89865469	F1Dsnp	PHR	A	G	3	10,575,217	+	TAGATATTAATCTATTAATTTCAGCTTCCTCTCCC[A/G]AGTCACAGAGCCCCTCCATTAACATAGCATAAGTA
3,687	7	7001	0.00	89809504	F1Dsnp	PHR	T	C	3	10,575,285	+	GTAGACTTGTTTGGCAAACAGCCTTTTTCTAACAT[C/T]TCATCCAAAATCCTAATCCCCTCAGTCGCTTTCTT
3,688	7	7001	0.00	89809505	F1Dsnp	PHR	A	G	3	10,593,873	+	AAGGAGAAACAATTTATACAACTAATTGTCAAAAG[A/G]CGATTCGTATAGAGCCTCGTGACGTAGCCATGGAA
3,689	7	7001	0.00	89865470	F1Dsnp	PHR	A	G	3	10,692,056	+	CTCCATCCGGAATTTCCAATTTCATTCCAGGTTTT[A/G]CATGGATAGCCACTTTCCCCTTAAGAAGCAAATCA
3,690	7	7001	0.00	89809996	F1Dsnp	PHR	A	C	4	22,026,496	+	AACTTTGACAAATCTTCATTGTTCTTCTCCAAAAA[A/C]ACCCCCACTGATGCTCAAGACAGTATTGCGAGGGT
3,691	7	7001	0.00	89795305	snp	Other	T	C	6	11,279,383	+	ACCCAATTTTGACTTGCTTAAGAGGAAGATTGTTA[C/T]GAATTGCAATGGATTGCCGTTGGCTGCAAAAACTC
3,692	7	7001	0.00	89810406	F1Dsnp	PHR	A	G	6	11,294,876	+	TTGACTTCCTTGTTGGACAGAAGCCAACTACCCAG[A/G]GCACTTGAACGTCTTTACTTATGGGATTGTGAACA
3,693	7	7001	0.00	89810408	F1Dsnp	PHR	T	G	6	11,342,172	+	CCTCAAGACGTTCTTTGCAGTGGTTTGGGTTACCA[G/T]AACAAAATCACTGTCTTTGCTTAGTGCCACCCCGT
3,694	7	7001	0.00	89866807	F1Dsnp	PHR	A	G	7	1,428,237	+	TTGGATTGCTTCGACTCATTGGATTGCTGTGAAGT[A/G]GGTTTTGGAGGATTAGGGACTTGAATAGATGGTGA
3,695	7	7001	0.00	89866808	F1Dsnp	PHR	A	G	7	1,431,615	+	TTAAGAGAGTCTAAATCCTACTGTGAGAATGCCTT[A/G]AGGATATATGCAAAGCCTTTGCCTGGAATTGTCTC
3,696	7	7001	0.00	89866820	F1Dsnp	PHR	T	C	7	1,508,628	+	GGTTCTAGGAAATCCATTCAGAAGGTGTAAAAATC[C/T]CTGCCCATTTCTGGCTTTTATTTTAACCTCACCTG
3,697	7	7001	0.00	89866821	F1Dsnp	PHR	A	G	7	1,509,914	+	ATAATGTATGCACAGGCCTTCAGGGCTCTCAGGGT[A/G]CTGATGTAGAACATTTAATTCCACAAGATGAAAGG
3,698	7	7001	0.00	89866827	F1Dsnp	PHR	T	C	7	1,527,281	+	CAATGTTAGATTCCTTTGAAGCTTCTAAGCAAGTC[C/T]CTCAGCCAGCTTTAAGTGATGTGAGTAGCAATGCA
3,699	7	7001	0.00	89866884	F1Dsnp	PHR	A	G	7	1,868,960	+	GCAAGACTTTCTTCTAACAGTTTCTCAACAAAAGC[A/G]CAGGAAGCAGAAAGCTCTTCATGTTCCAGACCTTG
3,700	7	7001	0.00	TP5933	GBS				7	1,940,103	1,940,040	TGCAGGAATATAATATAGTGCATCAGCTTGGAATGTATTAGAAAAAGATAAGCTCAAACAAATA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,701	7	7001	0.00	TP1739	GBS				7	2,015,002	2,015,065	TGCAGAGGCAAGTCCAGCGCCCACTGCTGCTGATACTGTAGTGAAAGCAGAAGCTTCACCAGAA
3,702	7	7001	0.00	89866933	F1Dsnp	PHR	T	C	7	2,116,336	+	CACACGGTCTGGTATGGGGTGCCCATTGATTGAAA[C/T]ATTGCTCCTACCATTCTCATTTGTCTGATTTGACT
3,703	7	7001	0.00	TP1899	GBS				7	2,130,149	2,130,207	TGCAGAGTGTACAAAACAAACGATCAGAAAACAAAGATTTCATATACACACATAACTCAATTCA
3,704	7	7001	0.00	150_248013	GBS				7	2,131,711		TATTATCATCAATCTAACTATAATGTGTGTTGAGAGAGAGAGAGACACACACACACACATACTG
3,705	7	7001	0.00	TP3034	GBS				7	2,205,383	2,205,438	TGCAGCACACCTCCAAGTGGTTAGGTGGTAGAATGAATACTACTCCAAAATAAGAACAAAGTGT
3,706	7	7001	0.00	89810991	F1Dsnp	PHR	T	G	7	2,222,409	+	TGCTTCGGATTCTCCAAGGCCATTTTCCGAGTCCT[G/T]GCAGTGTTGGCACTCCTCTTCATTGCTTCAGCCTC
3,707	7	7001	0.00	89810994	F1Dsnp	PHR	A	G	7	2,231,758	+	GAGACAGTTAATATCATTGGCCAACCAAGAATAAA[A/G]TACGACATCAATTTACGATTTCAGAATTCAGATAC
3,708	7	7001	0.00	89866950	F1Dsnp	PHR	T	C	7	2,399,710	+	AGTGGTGTCATGTGACTCATGTCGTCTGTTTAGGG[C/T]CAACTTGTAGTGAGGTTTAGGACGAGTTTGGAATG
3,709	7	7001	0.00	TP4780	GBS				7	2,479,970	2,480,033	TGCAGCGTTTTGTAGCCAAAAACTATAGGAGAGCATATCTTGGCATATCTCTTTCTCCATCCTC
3,710	7	7001	0.00	89866951	F1Dsnp	PHR	T	G	7	2,498,426	+	AACTTTGGTTGAGTGGAGATGGTTGCAGACAAAAC[G/T]TTAGGTGATACACCAACTTGAATCTTCTCTGTATT
3,711	7	7001	0.00	89810996	F1Dsnp	PHR	A	C	7	2,501,122	+	TCACAATTATAAAGTAAGAATCCATAATCTGAACA[A/C]TGATCACAATTGTGAAGTAAACAAGCTGGTGTCAA
3,712	7	7001	0.00	89810997	F1Dsnp	PHR	T	C	7	2,544,260	+	ACGAATTAATGCACCAGAGACTAAGAATATCATAT[C/T]TTACTATCATCTAAGTATACTGAAGATGTGTTCGA
3,713	7	7001	0.00	TP1202	GBS				7	2,548,605	2,548,544	TGCAGACGCTGCCTTGTCCAAAACCATCCCCTTTGTAACTCACTAACAAAGCCATCAACATCAG
3,714	7	7001	0.00	66_573476	GBS				7	2,553,059		GGTCAAGCATTTCGTCGAGCACCTTCAGTGCRTCATCAACTCGCCCCATACTCACCAACATCTT
3,715	7	7001	0.00	89810998	F1Dsnp	PHR	T	C	7	2,883,588	+	CGAATCATATATAGGGTGTTCTACATATGTTCATA[C/T]AATTGATCGAGTCGTCAAATGCCTTTATCACAATA
3,716	7	7001	0.00	TP8582	GBS				7	2,889,881	2,889,926	TGCAGTCTTTATCTGCAAATTGAACCACTTGATTACTAACGAAATTCATCCACACAGGCAACCT
3,717	7	7001	0.00	47_159479	GBS				7	3,047,567		ATCAAGATGAGCACTCTTTATAGACGACGACGGACTCATTTTGATCACTCTATTTCCATCAGGG
3,718	7	7001	0.00	TP1595	GBS				7	3,102,428	3,102,365	TGCAGAGCCATATCTTCAGTAACTGTAGAACGATAGCGAGTTGAGCCCTCCAGTGGGCAGCTTC
3,719	7	7001	0.00	89866954	F1Dsnp	PHR	T	G	7	3,156,534	+	CTTTAAGAAACTGTCATATTGGAATCCTAAACATC[G/T]CAGCTGAAAATGTCAATGTCAACCTCAATGTAAAC
3,720	7	7001	0.00	89866955	F1Dsnp	PHR	T	G	7	3,157,786	+	CCATGAGCAATAATTAAGTCGGCCAAATTGGTGCA[G/T]GAATTATCAAGTTATCCAATTAAACCGTCATCCAT
3,721	7	7001	0.00	89802255	snp	PHR	T	G	7	3,217,552	+	CATTTTTTGTGTTCTTGTCACATATCTTGTTGTAA[G/T]GAAAAATATAAAAAGAAACATAAGGTTTTGTTAGT
3,722	7	7001	0.00	89866958	F1Dsnp	PHR	A	C	7	3,296,849	+	CGTTCTGGAGCATGAACCCTCGCAGCAGGTAACTT[A/C]ATGGTTTCATTCACTGTGCATAATTAGTATGAAGA
3,723	7	7001	0.00	47_385165	GBS				7	3,309,934		AATCAGTTTGGTTTTGGCCCAAAACCGAGAATTTGACGGAACCTGACTTTCCGGTTGGTTTGGT
3,724	7	7001	0.00	89811001	F1Dsnp	PHR	T	C	7	3,340,012	+	TTGTTGCAGTGATTGAGTTCCTGGGCTGCGTTCCT[C/T]TGCTGCAGCGCCTACCCAGCTCTTCCCTCAAGAAA
3,725	7	7001	0.00	89811002	F1Dsnp	PHR	T	C	7	3,524,002	+	ACTAAGCATTTTCATGTACCCAAATGAAGCAGACA[C/T]TCTATACAAATTATCCACAACACGTTTAATTAATA
3,726	7	7001	0.00	89866959	F1Dsnp	PHR	A	G	7	3,547,195	+	CTAAGATAATTTGTCCACCTGAGTCGGCAACTCTT[A/G]CCACATCGAAGAAGGCCTATTCAAGCAGAAAATCA
3,727	7	7001	0.00	89866960	F1Dsnp	PHR	A	G	7	3,560,864	+	CCTATATTTGAGAGGGAAATCTCATGAGCCACAGC[A/G]ACAGAAACACTAAGCCCCAAGCTGGTGGCTATTTC
3,728	7	7001	0.00	89866961	F1Dsnp	PHR	T	C	7	3,626,728	+	ATTTTTTGGAGAATTATTTGGAGACTCAAGCCATT[C/T]TCTAAGAAATTTTAGAAGTTTGGAAATATAGAAAA
3,729	7	7001	0.00	89869158	SNPinIns	PHR	T	C	7	3,644,478	+	ATGGGATTTTCATTTCCTTTTCTTGGCGCAGAAGG[C/T]ATATATACTTATTGATTTAGTGTACCCAAACCAAA
3,730	7	7001	0.00	89906840	SnpSnp	PHR	A	G	7	3,645,124	+	AACTTGCCAACTTGCAGAAAATTAACCCTCTGCCC[A/G]TTCTAGCTAGCAGAACAAATAGAAGGTTGCTTCAA
3,731	7	7001	0.00	89811003	F1Dsnp	PHR	A	G	7	3,669,927	+	ACATAATGAAAAATCCCATTTTTGCGGGCTTGATC[A/G]CCCACATGTTTTACCATGGTTGTCTTCCCAACCCC
3,732	7	7001	0.00	47_716937	GBS				7	3,771,610		GCGACCATTCATTGTCCCAGCACCTTCAATTTATCGAGGCAGGACTGTGGGCCGTAGGGATCAA
3,733	7	7001	0.00	89811004	F1Dsnp	PHR	T	C	7	3,784,295	+	CACCCCTCCTAGAGTCTTCATCATCAGAGCTCTCC[C/T]CCCTAGAGTCGCCATGTCTCCTCCTTGAGCCACCA
3,734	7	7001	0.00	89811005	F1Dsnp	PHR	T	C	7	3,809,459	+	GATGAATGTGCAGGACTGAAAATTCAATAAAAAAC[C/T]ACTGGAACTGCTCAGTTAAGAAAAAACTAGAACTA
3,735	7	7001	0.00	47_757717	GBS				7	3,809,752		TGCAGCTACATTTGGTCCTAAAGTTGAACAACGGAAAGAGTTATATAATAACTATGGCAGGTTG
3,736	7	7001	0.00	89866964	F1Dsnp	PHR	T	C	7	3,815,489	+	GTTTAGTTTACGGATTCTGTCATAGTTTATGGATT[C/T]TGTCAATAACATATGATGCTTTCTAAACTTCGATG
3,737	7	7001	0.00	89802336	snp	PHR	A	C	7	3,815,520	+	GATTTTGTCAATAACATATGATGCTTTCTAAACTT[A/C]GATGAAGAAGACAAAGTATTATTTCAAATTGGTAG
3,738	7	7001	0.00	89845711	snp	PHR	A	G	7	3,890,200	+	CATCAGAAACTACCTCTCATTCTAATATGAACCAT[A/G]TTTCAGTTCACTAATGATCATATAATCTCCTCCAA
3,739	7	7001	0.00	89811007	F1Dsnp	PHR	A	G	7	3,955,463	+	CAATAATTACTTGAGGCAGAAAATAAATCAACTCC[A/G]TGCATACATAGTGATCAAACTGAAAGCCAGAGAAT
3,740	7	7001	0.00	150_248012	GBS				7	4,058,989		ATATTATCATCAATCTAACTATAATGTGTGTTGAGAGAGAGAGAGACACACACACACACATACT
3,741	7	7001	0.00	TP6773	GBS				7	4,145,726	4,145,789	TGCAGGCTTGGCCTTTGTCAACATTCGTCGATATAATACGAACCATCGTTTCTTAGGTGGTAAC
3,742	7	7001	0.00	89866966	F1Dsnp	PHR	A	G	7	4,478,787	+	AAGCTGCCCTGTATAGCTTTAGTTTGATCTAGAGT[A/G]TACCTTTCGAGAATTCTTTCTCTCTGAATGGTCAC
3,743	7	7001	0.00	TP5404	GBS				7	4,672,159	4,672,216	TGCAGCTGGAATTCATGCATCTTCAGATAGTGTCATAATTGTTGATATGCATGCACCGAGATCG
3,744	7	7001	0.00	89811011	F1Dsnp	PHR	T	C	7	4,847,315	+	AGCCTTGATTTTGTATTGGTTGAAGGTGGCTAGGA[C/T]GTAATCTAGCAAATAGTCGCAGCTATGTGTTTGAA
3,745	7	7001	0.00	89811015	F1Dsnp	PHR	T	G	7	5,769,812	+	ACCATCTTGTTGAATTCTTCAATTGCTGCCATGGT[G/T]CAATGCTTTGATTGGAAGGTTGGAGAAGGGGGCAA
3,746	7	7001	0.00	89811016	F1Dsnp	PHR	T	G	7	6,003,329	+	TTTCAGATGTACTGAATTCTGTAAAGCCTGATTCT[G/T]TTGGTTCAGAGTTTCTTGTTAGTAGTATTTTTGGT
3,747	7	7001	0.00	89866976	F1Dsnp	PHR	A	G	7	6,750,357	+	CATCAGAAAACTGATTAAGCAACTCAACAAGTCTA[A/G]CTGTGCCATGCATGTTCTTGTCTTCTGGAAACTCA
3,748	7	7001	0.00	89866977	F1Dsnp	PHR	A	G	7	7,472,823	+	GCACTTTGAGCTAACCGCAACATGCTATCCCGTAT[A/G]CAAAGTCTTGTTCTGATGTCCAACTGTAGTAATTA
3,749	7	7001	0.00	89811019	F1Dsnp	PHR	T	C	7	7,612,665	+	AGGAACACAAACCATAGCATGCAACTCTGAAGTTC[C/T]GTTAAGACATTGGACAGCAAGAGCCTCCGCATAAT
3,750	7	7001	0.00	89811020	F1Dsnp	PHR	T	C	7	7,613,186	+	GTATATCATTTCCTTGAGTAGTTGCAGGAACACAA[C/T]CCGTAGAATGCAACTTGGATGATTCATTTGGAAAA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,751	7	7001	0.00	89811021	F1Dsnp	PHR	T	C	7	7,619,112	+	TGAGTTGGAGCAGCAGTAATGACAACCAGAATATG[C/T]GTTGCGATTCGATCTTTTGATAAACACCCCTTGGG
3,752	7	7001	0.00	89866981	F1Dsnp	PHR	A	G	7	7,703,414	+	TTTTCCTGCAGCTTGGATGAATGGGTTGGAAGTTT[A/G]TGCGATTGAAGTTGATTTTGCACGGGCGTGCTTGA
3,753	7	7001	0.00	89811024	F1Dsnp	PHR	A	G	7	8,928,759	+	TTTTGTTGCAAGCAGAAAATAGTCTTCACTCCAAT[A/G]CTGCGAAGCTTGTCAACATCTTTAGGAGTCTGTTG
3,754	7	7001	0.00	89866984	F1Dsnp	PHR	T	G	7	9,108,663	+	GAGATCAAGACACAACGCAAAAGAATTGCGAGGGC[G/T]ATCTTGCAAGAGGACAGTGATGTTGCTAGGGTTGA
3,755	7	7001	0.00	89866985	F1Dsnp	PHR	A	G	7	9,193,404	+	CGGAAAGCAATACAAATCTTTGATTAGACAAGTCA[A/G]GCAGTGCATTCGCTAATAGTCGTCGCTCTGCATCC
3,756	7	7001	0.00	89811026	F1Dsnp	PHR	T	C	7	9,196,205	+	CTTAAACTCTTGAAAGTTAATGAAGCCATCACCAT[C/T]GACGTCAAAATTGGTAATCATGGCGGCACATTCCA
3,757	7	7001	0.00	89811028	F1Dsnp	PHR	T	C	7	9,410,160	+	GGTTGAGCCTTTCCTTTCCTCTGAAGGATTCTTCT[C/T]GGGTCTTTCATTCTTATCCTTACCCTTGGCTCTTC
3,758	7	7001	0.00	89811029	F1Dsnp	PHR	T	C	7	9,574,239	+	GTACCTTCAAAAGCATTTTGTACGCCTCCAACAAG[C/T]GATTAGCAGCTGGCCCAAAACCATGGAGCTGGGGT
3,759	7	7001	0.00	89866989	F1Dsnp	PHR	A	G	7	9,602,134	+	TTCCATAAATAGTCGGGCTTTCTCTCAGCTTCTCC[A/G]TTTTCTAGGTCATCGTTACCCTAAGGTTTGTGGTT
3,760	7	7001	0.00	89811033	F1Dsnp	PHR	T	C	7	9,980,866	+	CTTGAGAAGCTATTGGATATAAATGATTCAATGAG[C/T]CGATGTGCTGCTTCTGCTACACCAGCTACTTCTGT
3,761	7	7001	0.00	TP4795	GBS				7	9,994,384	9,994,447	TGCAGCTAACCTCGGACATTCTTTCTTCACTCCTCAGAATCTACTGGTAAGTTTTCTGTCTTTC
3,762	7	7001	0.00	89811034	F1Dsnp	PHR	A	C	7	9,994,426	+	AACCTCGGACATTCTTTCTTCACTCCTCAGAATCT[A/C]CTGGTAAGTTTTCTGTCTTTCGTTTGTTCTATAAT
3,763	7	7001	0.00	89806299	del	PHR	-	TAAT	7	9,995,687	+	GAATTCATCAATCAACTTCACCCTCCTTCCATCCG[-/TAAT]TAACTTCATGTTGTAATTACGTACTCAGGTCCTAT
3,764	7	7001	0.00	89866763	F1Dsnp	PHR	T	C	7	10,013,942	+	AGGGGGCGCATCTCAAGAACCAAGAAGAAGAGAGA[C/T]GATGAGCTTCTTAAGGTCAAGAAAGCAGAACATAA
3,765	7	7001	0.00	89866764	F1Dsnp	PHR	A	G	7	10,080,593	+	TACCACCGGCGTGGCAGCGGCTCCGGTAGAGAACA[A/G]GGCATCTGAAGCAGTTGGTGTAGAGGAAGCGAAAT
3,766	7	7001	0.00	89866765	F1Dsnp	PHR	A	G	7	10,102,555	+	CGAACCGGAGATGGGGGCCTAGGAGGGTCAACATA[A/G]TTAACCTTCAACTTACACTCTTCAACATTATGCCC
3,767	7	7001	0.00	89866766	F1Dsnp	PHR	T	G	7	10,189,811	+	GATAACATCATGAGACAAAATGCTACATCTTCCTC[G/T]GTTGTGGCATCAGAAATTGAACTCACCGGTTCGGG
3,768	7	7001	0.00	89866767	F1Dsnp	PHR	A	G	7	10,339,697	+	TCAAGATCTCCCCAAATGTTGTTCTCATCATGAGC[A/G]TTGGTTTCATTGGCTTTGTTGCTGTTCTTCATGTC
3,769	7	7001	0.00	89810804	F1Dsnp	PHR	A	G	7	10,533,362	+	TTGTAGATAATGAGAGATCCTGACACTGGAAACTC[A/G]CGGGGATTTGGCTTCATTAGCTATGATTCCTTTGA
3,770	7	7001	0.00	89866768	F1Dsnp	PHR	A	G	7	10,560,841	+	CCAGAACGAACACCTTCGGAGTCCGCATAGACAGA[A/G]AAAAAGTTGAAGCCTCGAATCCTGAGGTTAGGAGG
3,771	7	7001	0.00	89866769	F1Dsnp	PHR	A	C	7	10,560,942	+	GGCACCACTACTTCTACGGTTGAACTCCCCCGGAA[A/C]CTCATTTCCAAGAAGAAATGTGTTGAATATACCAT
3,772	7	7001	0.00	89866770	F1Dsnp	PHR	A	G	7	10,560,986	+	CAAGAAGAAATGTGTTGAATATACCATATTCAGAC[A/G]CTCCCTGTAATATCAATGTATCCCAAGTCATATAG
3,773	7	7001	0.00	89866771	F1Dsnp	PHR	T	C	7	10,561,199	+	TTTGTTTGATAGATAAAGACAGGCATTGTACATGT[C/T]AATAAGTTCCCTAGGATTCAAGTTGTGCAAGCCTA
3,774	7	7001	0.00	89866772	F1Dsnp	PHR	T	C	7	10,561,483	+	ACTTTTGAAACTTAAGGAGATCAATCCCTCTGAGG[C/T]CTCTGATGCAATCCGGTAAGCCAGCAATTGGATTC
3,775	7	7001	0.00	89810807	F1Dsnp	PHR	A	G	7	10,562,349	+	TTGTACATTACAAAGGTCGAGTAATCTTAATTTGC[A/G]CATACTTGTAAATGAAATTGTTTCCAAGACTACCT
3,776	7	7001	0.00	89866773	F1Dsnp	PHR	A	C	7	10,562,354	+	CATTACAAAGGTCGAGTAATCTTAATTTGCGCATA[A/C]TTGTAAATGAAATTGTTTCCAAGACTACCTCCTTT
3,777	7	7001	0.00	89866774	F1Dsnp	PHR	T	C	7	10,638,827	+	TGAAGATGATGACTCTAACTATTACCTTTCACCAA[C/T]TTTCAAATTTGAACAGGTAAAGATTGGCATGCCAT
3,778	7	7001	0.00	89866775	F1Dsnp	PHR	A	G	7	10,655,275	+	TACTTGAATAGCACTGCCTCCTCCCTAGCCCATAC[A/G]CGCAATCAAAGTTCCCAACACAAGTGGAACCCCAA
3,779	7	7001	0.00	89810808	F1Dsnp	PHR	T	C	7	10,718,917	+	CAGAAGATCGCTAGGAAGCTCTAAGAAAGACCTTT[C/T]AAACTCCCCAAGGACTGGAACAGGTGCCTCAACAA
3,780	7	7001	0.00	89866777	F1Dsnp	PHR	T	C	7	11,116,301	+	CACCACCATGAACTGCCTCTAAACCTTCGATCCGT[C/T]CCACCAACGATGCTTGTGAAGAACGAACCGAACCA
3,781	7	7001	0.00	89866778	F1Dsnp	PHR	T	C	7	11,133,256	+	GCCTGATGTTGGCTCACCAAGCTTTTCAGCTCAGC[C/T]TCATTCTTTGAACACCGTCTGAGAAATTTCTCATA
3,782	7	7001	0.00	89866780	F1Dsnp	PHR	T	C	7	11,234,006	+	GATATGGTGAAGATGGTCTTAAAGATGGACCAGGA[C/T]CAGGAGATGGTCGTCCCTCACATAATCCATTTGAT
3,783	7	7001	0.00	89810812	F1Dsnp	PHR	T	C	7	11,237,428	+	GTGCACATTTTATGATGAGGAGAGGTAGAAAGCGT[C/T]CGAGGAAATCCGCACAAATTGGGGATGAGGGCAAT
3,784	7	7001	0.00	89810813	F1Dsnp	PHR	A	C	7	11,356,444	+	ACCTGCAACCTCTAGGGAAGATTTTAGATGATGTA[A/C]GCATGGCAACTGCCCATGGTCACCATTCTCGATCA
3,785	7	7001	0.00	89843282	snp	PHR	A	G	7	11,390,689	+	TTTGATGAAGAAGATCCTCAAATCCGAAAGTTATC[A/G]GTTCGTGAAACTGGCAGAGTTGGTAGAGTTGGCGT
3,786	7	7001	0.00	89866781	F1Dsnp	PHR	A	C	7	11,551,696	+	CAACCAATAGAGATGCTCAAAGTTACTGCAGTGGG[A/C]AATGGAACTTCATCAAGACAAAAGCTTGAGGACAC
3,787	7	7001	0.00	89866782	F1Dsnp	PHR	A	G	7	11,556,214	+	AGAGAGCTCTAGTTTCTCCGCCGTTTCAAACCCCA[A/G]ACCCACAATCACAAATCTCCCTTGTCTTCCACAAC
3,788	7	7001	0.00	89810814	F1Dsnp	PHR	T	C	7	11,558,932	+	CTCAATATGGTAGAATTACTGGTCTACTACCATTG[C/T]ACAAATGCTACTCCCGAGAACAGATGCCAAGACTG
3,789	7	7001	0.00	TP6187	GBS				7	11,696,086	11,696,031	TGCAGGAGGCCTCAGTTTCTAACCTCGGTCCACGAAGCTGTTTGGGTTTGTTTGGGTTTTGAGG
3,790	7	7001	0.00	89810815	F1Dsnp	PHR	A	C	7	11,959,757	+	CCAACAGGAATATCCAATCTGTTTCCAGTTGTTAC[A/C]GCAGGAATGGGCGGTTCAATAGATTCCTGAACAGA
3,791	7	7001	0.00	89866783	F1Dsnp	PHR	A	G	7	11,959,794	+	CAGGAATGGGCGGTTCAATAGATTCCTGAACAGAT[A/G]TATCATCTACTAGAGGCAATCTAATAATTTTTTGC
3,792	7	7001	0.00	89810816	F1Dsnp	PHR	T	C	7	11,976,438	+	ACCTGGAAGACCCTAAGCAATGAAGACTTTTTCTG[C/T]TTCCTTTTATTCATCCAATAACTATATACAACTTC
3,793	7	7001	0.00	89866784	F1Dsnp	PHR	A	G	7	12,061,309	+	GGTTTAATTTCTCAGAGGAACGCGCGCTTATTCTC[A/G]TCAGCCAATATGCAGGTACGGAGTTGAACATGAGA
3,794	7	7001	0.00	TP972	GBS				7	12,217,459	12,217,415	TGCAGACAAGTAATCATTACCAAATAGATTTAGAAACTGCAACCGAGATCGGAAGAGCGGTTCA
3,795	7	7001	0.00	89866785	F1Dsnp	PHR	T	C	7	12,456,788	+	ATTTCCGCACAAAATCTCTAGCAGTGCACAGCTTC[C/T]TCTCCTTCCATCTTCTGAAATTTTCTTATATCTAC
3,796	7	7001	0.00	89810819	F1Dsnp	PHR	A	G	7	12,464,320	+	TGCTGAGTGCGTCCTATAAGATCACTTTTAAGAGC[A/G]AGAGCACCAGCCTCCAAATCAGCTGCACTTGTTAC
3,797	7	7001	0.00	89810821	F1Dsnp	PHR	T	C	7	12,479,811	+	GGGGGGACAATCAGGGGCATCAATGAGAACAACAC[C/T]ATTACTGACCGACATGATTTGCTTAGCATCCACAT
3,798	7	7001	0.00	TP7288	GBS				7	12,513,556	12,513,619	TGCAGGTCATAAAGTACGACACTATTTTCAACCACCTTAGAGATGCAGTAACTACACGCTTCAC
3,799	7	7001	0.00	89866786	F1Dsnp	PHR	A	G	7	12,521,697	+	ATTTTCCTATTGGCTTCAAGGATAATGAGGAGAGC[A/G]GTAATATCAGCAGGATTCACCCCACCAACTCTACT
3,800	7	7001	0.00	89850456	SnpSnp	Other	A	G	7	12,561,261	+	ATGGTTTTGGTTTGTGTGTTCTTAGTGGCGACAAC[A/G]TTGTCTAGATGTTGTTGACGGCTAGCTAGTGGATT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,801	7	7001	0.00	89810822	F1Dsnp	PHR	A	G	7	12,586,905	+	GCCTGAAATCCATAAATGTTCCTGTTGGGTTTCTC[A/G]CACTTGATCAACCCGGTGATCCTGTCCTTTTCAGG
3,802	7	7001	0.00	89810823	F1Dsnp	PHR	A	G	7	12,590,501	+	AGCACAGCAAAACCTGAAAAGTATCCAAATCTCAC[A/G]TAGGATGGTCTGTCCAATGACCCCAACAGAAAGAC
3,803	7	7001	0.00	89810826	F1Dsnp	PHR	A	G	7	12,868,306	+	GTACCAGGATCAATGATGCTAAGGCACGACACTCG[A/G]AAATACTTGCCACATGCAGTACCCAGGTCAACATT
3,804	7	7001	0.00	89810831	F1Dsnp	PHR	A	G	7	12,976,014	+	GAGAGCAGTAGTTTATTTATAATAAACACAGTGGA[A/G]CCCATTTTACAAGTATACACGGTATGGTAATACGT
3,805	7	7001	0.00	89810834	F1Dsnp	PHR	T	G	7	13,141,093	+	CTCTCTTTCTCTTCTGACCTGAACCTGCTACATCT[G/T]GAACACTTGCTTTAGCTTCACATTGGCTTCTCCCC
3,806	7	7001	0.00	89866793	F1Dsnp	PHR	A	G	7	13,155,089	+	GATAGAAATTTTGTGCCCAAACCACGAACAGTGGT[A/G]ATGTTAATTAAATTTTTCTGTGAAAATCATCATCT
3,807	7	7001	0.00	89866794	F1Dsnp	PHR	T	G	7	13,159,267	+	GCATTGATTGATGGGTATTGCAAGGAGGGAAAGGT[G/T]GAGGCTGCAATGGATATTAAGGCTTTGATGGAATC
3,808	7	7001	0.00	89866795	F1Dsnp	PHR	T	G	7	13,160,302	+	TGGAAGACAATGGATTATCAAATTGCTTTAGAGCT[G/T]TTTGAGAAGATGGTTGTACATGGATGTGCACCCAA
3,809	7	7001	0.00	TP2763	GBS				NGH			TGCAGCAAATTAGCCAAGATTCTGGACTGTTGTCTGTGTGGTTGCGGTTCCTACATACACAGCG
3,810	7	7018	2.44	89866986	F1Dsnp	PHR	T	G	7	920,186	+	CAACTCCAGTCATGGGCACAGGACAGCTAAAGCTA[G/T]TTTGAAGAGGAGCGCACAAGGGAAGCATTCCATGG
3,811	7	7018	2.44	89800217	snp	PHR	A	G	7	1,046,472	+	TCGATGAACATTGGAGCTCATTTAACATTAACATT[A/G]ACATTAACATTAACATGCATAACAATGCTTTACAG
3,812	7	7018	2.44	89810809	F1Dsnp	PHR	T	C	7	1,072,804	+	TTGATGTCCGTAATCATCATCATGACCTGGTTTAG[C/T]GTTGGGGTTTGGGCTTTGATGCCCCAGATGGAACT
3,813	7	7018	2.44	89810830	F1Dsnp	PHR	T	C	7	1,296,816	+	CTAATTGAGTTGTGTATCGTTGCTACCGACTTGCC[C/T]TACTGAAGCTGTTACCTCAGAGAATGTCTTCAGAG
3,814	7	7018	2.44	89800607	snp	PHR	T	G	7	1,350,939	+	GATATCTTTGTTTGATTGGTACCTTCACTTTCATA[G/T]TTAGGAACTAGCTTGCTCTGTTTTTGTTGTTTTAC
3,815	7	7018	2.44	89866805	F1Dsnp	PHR	A	G	7	1,402,823	+	TGATGGGTCGACGTCGTCGGATTTCGAGTGTGATC[A/G]GTCTCGGATAATACCTAATGTTGCAGCCGGTGGGG
3,816	7	7018	2.44	TP4152	GBS				7	13,479,470	13,479,451	TGCAGCCGCGAGCCTTGGGATTTGCCCGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACC
3,817	7	7018	2.44	89866799	F1Dsnp	PHR	T	G	7	13,482,774	+	CCACAGAGTATGATGGGCATATGGTTTAGCTTGTT[G/T]TCATTTTGATAAGCCTCCACAAATTGCAAAATTTT
3,818	7	7018	2.44	89866800	F1Dsnp	PHR	T	C	7	13,490,033	+	ATCAAGTATGTGTTCTTCGAGGCATCAACCATCTC[C/T]GGAATTTTACATGCAAGCATGTACCTGGATGCTGT
3,819	7	7018	2.44	89866801	F1Dsnp	PHR	T	C	7	13,702,780	+	ATCGCTCTACAACCCTCCCCAAAGTCCTTACTGAT[C/T]TCCCCTCTCACAACATGGCAAACCATTCTTTGCTC
3,820	7	7018	2.44	330_76442	GBS				7	13,856,853		TGTTTCCTACACCCAAAACTTTCAGTACAGARAAGATTCATCAAAAAAAATAAAAAAAATTAAC
3,821	7	7002	4.88	89866802	F1Dsnp	PHR	A	G	7	13,901,015	+	CAAGGAGTTGAACTGCGGCATCTTTCGGCTGAGGC[A/G]ATTCAAACTGACTGTTCCAAAGTGGTTTACCTTGT
3,822	7	7002	4.88	89810838	F1Dsnp	PHR	A	G	7	13,972,373	+	GTTCCAGCTGGTGGAGTTATTGCGTCGATTATGGT[A/G]GTTCTTTGCTTGTTTTGGGTTGGTCTTGTAGATGG
3,823	7	7002	4.88	89866803	F1Dsnp	PHR	A	C	7	13,977,180	+	ACACTGGATTGCTTCTGCGTTACTGCTTGGATAGT[A/C]AACCTGAGCTTGAGACTTACCCGGATATTGGCCAG
3,824	7	7002	4.88	89866804	F1Dsnp	PHR	T	C	7	14,011,151	+	AATGTCGTGGAGAAATGCTTGATTTTTGGGAGTCC[C/T]GAGGAGCGCCAGTTCTTGGTAAAAGAGATGCTTGG
3,825	7	7002	4.88	89866806	F1Dsnp	PHR	A	G	7	14,158,920	+	GCTGGCAACCCCAACATAGTTCTGGTGGTTAAGTT[A/G]TTGTCTCTAAGAGTTAAAATTCAGGTGAGAAAATA
3,826	7	7002	4.88	TP941	GBS				7	14,168,884	14,168,821	TGCAGAATTTTTATTGGAAGAGCTTCTCTCAGCAGCCACAGATTGGTGATCCAAGGGTTCATCA
3,827	7	7002	4.88	89810839	F1Dsnp	PHR	T	C	7	14,203,920	+	AGACTTCCTCAAACCACCAATCTTCATTAACTGCA[C/T]GTGGTTTGGCTGTTGTGCTTATTCCATTCCAGAAC
3,828	7	7002	4.88	89866812	F1Dsnp	PHR	T	C	7	14,759,436	+	TCCTGCGACTCCAGAAAGACCTCAGCCGAATTTTC[C/T]GATTTCTGGTCAACCCGCACTTTTCTCTACATAAC
3,829	7	7002	4.88	89810842	F1Dsnp	PHR	A	G	7	14,883,529	+	CAATCCGCTTAATGTGGCTGACTGCATTGTGAAGC[A/G]TCTCAAGAGAGTTAAGTACTGCCTAATTTAATTGA
3,830	7	7002	4.88	89810843	F1Dsnp	PHR	A	G	7	14,902,774	+	ATAAACAAGGCATGTCAGCTAGTTCTCTCACCGTC[A/G]TCACGCTTATCACTATAAATGTCAATCTTTTCACC
3,831	7	7002	4.88	89901098	snp	PHR	A	G	7	14,902,831	+	TCAATCTTTTCACCCTTCCTCTGGACATTCAAATC[A/G]TGAGAAAACTTGCACTTGAACCCCTTAGTACATTG
3,832	7	7002	4.88	TP2480	GBS				7	14,917,570	14,917,507	TGCAGATTCAACCAAACATATGAATCAAATTCTATACACTTTCTCAGAATCCAAGCACAACAAT
3,833	7	7002	4.88	89866814	F1Dsnp	PHR	A	G	7	14,932,235	+	TCGCATTCAGATCGAAGAGGTGGATCCTCCATGTC[A/G]AGCCACAGGAAAGATGAGTACAATTGGAGATATGA
3,834	7	7002	4.88	89810845	F1Dsnp	PHR	T	C	7	14,942,316	+	TCTGGAACTCCTTTTCAGAATAGTTTTGAGGAGCT[C/T]CACAATACAGTCCGTTTGGTGAGGCCTGAGTGGAC
3,835	7	7002	4.88	89805980	del	PHR	-	TAAT	7	15,032,396	+	CAACAGAAATAAAATATAAAAGAAGATACATCTGC[-/TAAT]TAATGGGAGTAAGAGCCTTAATTAGCTACATTTGA
3,836	7	7002	4.88	89866815	F1Dsnp	PHR	T	C	7	15,034,417	+	TACTTTTAGCTGTCAAGATCATCCTACCACTAATA[C/T]GATCAAATTGCTAAATGATTCATGTCCCATAAGTC
3,837	7	7002	4.88	89810847	F1Dsnp	PHR	A	G	7	15,034,461	+	TGCTAAATGATTCATGTCCCATAAGTCCATCAAAT[A/G]CAACGATTTTTGACTTTGGTATATTTCTCAATGCT
3,838	7	7002	4.88	89866816	F1Dsnp	PHR	T	C	7	15,035,184	+	TTGAACGGAGCAAGGGTCCGGAGGTAGAACAATGG[C/T]TAACCAAAAATGGTCTTCCTATGCGCTTTATGCCC
3,839	7	7002	4.88	89866817	F1Dsnp	PHR	T	G	7	15,035,213	+	CAATGGTTAACCAAAAATGGTCTTCCTATGCGCTT[G/T]ATGCCCGAGATCATGGAAAAGGTGGTGCAAGTGGA
3,840	7	7002	4.88	89866818	F1Dsnp	PHR	T	G	7	15,035,279	+	GTGGATTTAGAACAAAACAGGGATGTTAATGTGGA[G/T]AATATCCTCTCGATTCTTCCCTTGCAACTTCAAAG
3,841	7	7002	4.88	89810850	F1Dsnp	PHR	A	G	7	15,035,691	+	CGGCGGAGAATATTATCCTCCCTGCTAGTCTTCCC[A/G]TGCCACTTGAGGAGCGTGTCAGAGAGTATAAGTGG
3,842	7	7002	4.88	89810851	F1Dsnp	PHR	T	C	7	15,036,856	+	CACGACCATGACAATGCAGCTGTTGAGCTGTCTAT[C/T]ACTGCGGAGGAATTGAAGAGTGTAGGTTCTAAATT
3,843	7	7002	4.88	89810852	F1Dsnp	PHR	A	G	7	15,051,125	+	GGAAAAGGTAGTAGAAGTGGATTTAGAACAAAACA[A/G]GGATGTTGATGTGGAAAAAATCCAATCGATTCTTC
3,844	7	7002	4.88	89866819	F1Dsnp	PHR	A	G	7	15,075,851	+	GTTGTAAAGATGATAATCAGATGGCTGCCTGTCAG[A/G]TTGTCATGAAGGAGGTAAGCTCAGGGATAATATAT
3,845	7	7002	4.88	89866822	F1Dsnp	PHR	A	G	7	15,100,741	+	GCAACTTTGACCATCAAATTCTCATCTAGCAGTAT[A/G]TTCGCAGACTTAACATCACGGTGAATGATCGTCTT
3,846	7	7002	4.88	89810854	F1Dsnp	PHR	A	G	7	15,122,707	+	CTCCGCAATACCAGGGAAGAGAGGGACCAATTTGA[A/G]GAAGCTAATACCAAGATTGTTGCCCACTTGGAAAC
3,847	7	7002	4.88	89800872	snp	PHR	T	C	7	15,180,533	+	AGAAGGAGAGTTGAAGATGGAGAATGACAAAGAAG[C/T]TTATAGTAGATAAAAACAGAGCAAGTAACTTGCAG
3,848	7	7002	4.88	89866823	F1Dsnp	PHR	A	C	7	15,183,565	+	CCTATCAAAGACACGGCAAGTGTAGCGGTGGTATC[A/C]AGAAATCCACTGTCAATAACTTCTTCGACTGTCTC
3,849	7	7002	4.88	89810856	F1Dsnp	PHR	A	G	7	15,187,493	+	AGTCCTGAGCTGCCATTTTCGAAACCACTAGGAGT[A/G]TTTCCTCCAAATGGAGGAGTCCCCATCTCAGAAAT
3,850	7	7002	4.88	89866824	F1Dsnp	PHR	A	G	7	15,194,794	+	AATCAAAATTTCTAGGCCCTATTTCCTGGACAGGC[A/G]TGGAAAGCAAATCCCCAATGGTAATGCCACGGTTA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,851	7	7002	4.88	89866826	F1Dsnp	PHR	A	G	7	15,225,928	+	TCAGTAATCAAAGTGTGGGAGACTCGGTAACTGAG[A/G]AGATACCTTATTCATGTAATAGCAGCAAGTGGATT
3,852	7	7002	4.88	89810879	F1Dsnp	PHR	T	C	7	15,962,153	+	TCTTACAACTTCATATGGAATTCAGCTGTGATGGA[C/T]GACTCAACTGCATTAGTAATTGATGACTCCAAGAT
3,853	7	7002	4.88	89866847	F1Dsnp	PHR	A	G	7	15,964,437	+	CTGAGGTGAAGAATGCAGCCTTGGAATGTGCGGTC[A/G]TGCTTATTGGTGAATACGAGGAAGGTTTGGAGAAA
3,854	7	7002	4.88	89810880	F1Dsnp	PHR	T	C	7	15,967,905	+	TTCGCATTTGAATGCATCCTGCATGCACCTAATAA[C/T]GCTCCCCAGACTCCAGCATCAGGCTCCATTGGCAT
3,855	7	7002	4.88	89810881	F1Dsnp	PHR	T	G	7	15,969,922	+	CACCCGCTTCAAAATCCAATGCAGCAGTGCAAGCT[G/T]TCAGGGCAAAGTTGAAGGTGTACTTGTCTGGCTCT
3,856	7	7002	4.88	89866848	F1Dsnp	PHR	T	G	7	16,004,942	+	GAGATGATAATTTGATCTCAGCGGCTCCGACCTAT[G/T]ATAAGCATGCTGATAACACTATATCAATGGGTCTG
3,857	7	7002	4.88	TP7709	GBS				7	16,120,032	16,120,091	TGCAGTAAAGGCCATGTACCGAAGCGCCAGAGTGAGATTAGGTCAATACGATTATTTTGTTATC
3,858	7	7002	4.88	89801028	snp	PHR	T	C	7	16,279,176	+	TGAGGAAGAAGAGGTTGAGGAAGATGAAGAGTGTG[C/T]GGCTGAAGGTGATATAGAACTTTTAGCAGACTGAA
3,859	7	7003	7.32	89872924	snp	PHR	T	C	1	10,007,279	+	TGCTGTTATCACTGTCCCTGCTTACTTTAATAACT[C/T]GCAGTGTGAGGCTACAAAGAAAGCTGGTTTTGTTG
3,860	7	7003	7.32	89810861	F1Dsnp	PHR	A	G	7	15,299,582	+	ACAATCATGCTTGAGATGGACCGTATGCTAAGACC[A/G]GGTGGACGAGTTTACATCCGTGATACTCTTGCAGT
3,861	7	7003	7.32	89866828	F1Dsnp	PHR	T	G	7	15,319,939	+	AATATGTTGAGCCTTCCAGCGAAAGAAACACCCAC[G/T]TGCTCCATTAGCTTCTCTCTCTCGGATTTAACCGA
3,862	7	7003	7.32	89866829	F1Dsnp	PHR	A	G	7	15,334,541	+	ACCCGACCCGTGAGTTCGAACCCGTGTGAGAAGCC[A/G]ATCACTTATTTCTTGGAGCATGTTAAGGACGGCAA
3,863	7	7003	7.32	89866830	F1Dsnp	PHR	A	G	7	15,356,694	+	CTTAAGATTACACAAGCTTGGTCTTCTTCCTGCTC[A/G]TGTGGTTCAAGATGCAGCTGATGAGTCGGAGTTTC
3,864	7	7003	7.32	89866831	F1Dsnp	PHR	A	G	7	15,396,671	+	TTTGAGGATTATGTGCATTCCTATTCGTATCCTCC[A/G]TCATCATATTTTGATAAGACAAGCACTTGGTCATG
3,865	7	7003	7.32	89810862	F1Dsnp	PHR	A	G	7	15,400,425	+	GCAAATCATAAAGAGCATCTGAGGAATTTATAATC[A/G]CTGATGCGTCCACTGATTCCAAAAACACAGTTCCT
3,866	7	7003	7.32	89810863	F1Dsnp	PHR	T	C	7	15,408,660	+	CCCAGTGAGCTGATCAGCGAGTTCTCTAATTTGTG[C/T]TGCAGAACCATGCTCGAAAAACTGAACACAAAATG
3,867	7	7003	7.32	89850543	SnpSnp	PHR	A	G	7	15,408,851	+	ATCACCTTCTGAATCACATAATTACCGAACACGTC[A/G]GTCATCAAAGAGAGGGCTTGGGGCATAATTTCATC
3,868	7	7003	7.32	TP5364	GBS				7	15,409,599	15,409,550	TGCAGCTGCTGAGTTGCAGAGTATGGGCAGGGGTGGAAATCACACTGCCGAGATCGGAAGAGCG
3,869	7	7003	7.32	89866832	F1Dsnp	PHR	T	C	7	15,467,307	+	GACTTGTGGCAATTAGATGAAGCAGAGCGGCTTGA[C/T]CTTGAAGAAGACAAGGACAGAGACGACCCTTCTTT
3,870	7	7003	7.32	89866833	F1Dsnp	PHR	T	G	7	15,516,100	+	TATTTCAGCAAGACTGCCTGAATTGGTCAGAGGAG[G/T]GGGATCAGATATTGCATCAGGAATCCCTGGATCCA
3,871	7	7003	7.32	89810864	F1Dsnp	PHR	T	G	7	15,545,604	+	TACAACATCAGTTTCAGCTCTTCCATTTTTCTTTC[G/T]AGCCCACTGATCTCATCTTCTACCATTTCCAGCTC
3,872	7	7003	7.32	89810865	F1Dsnp	PHR	A	G	7	15,570,947	+	GGTTTGGAGACTTAACTTCAAATGTCATGTTTAGG[A/G]TGGTTGTTGGAAAGAGATTTTTTGTGGCAAACTCG
3,873	7	7003	7.32	139_183098	GBS				7	15,573,344		TACACCGGTTTATTATAAATTTAAAGTACTTTAAGTCATGGCCAAGAGAAGGCCTTATACAGCA
3,874	7	7003	7.32	89810866	F1Dsnp	PHR	T	C	7	15,575,421	+	GGTGATAACTCAGCAGATCTGGACCTAGAACCAGA[C/T]GGTGATCTTGATGCTTTATCGGGAGACCTCCAATT
3,875	7	7003	7.32	TP4833	GBS				7	15,586,632	15,586,695	TGCAGCTACAGAGTACTGGCCGTCAATACTCGCATCAAAAATGTGGAGAACTCTGCGTTTTCTG
3,876	7	7003	7.32	139_122148	GBS				7	15,659,658		GTCCGTACAATTTTACAAATAATTATGCCTATTGTATTCCGATCAGCACCCGGTTCTGGGTTTT
3,877	7	7003	7.32	89810867	F1Dsnp	PHR	T	C	7	15,675,502	+	GTGATCGATGTACACACCATGTAGATCCTTCCATG[C/T]TCCATCTTTCTCCTTTCGGCTAGCCAGCCTCTTCG
3,878	7	7003	7.32	89866834	F1Dsnp	PHR	A	G	7	15,710,613	+	GGCATTTGTTGGTGAAGAAACAACTGCAAATTGGT[A/G]ATCAAGACATCATCTCATTGAAACCTGAAATGAAT
3,879	7	7003	7.32	89866835	F1Dsnp	PHR	A	G	7	15,734,347	+	TCCTCAATTCCATCAAAAGATCTCCTGTCACTGTT[A/G]ATTGTAATCCCTCTCTTCCTACCAGTGGACTTGTC
3,880	7	7003	7.32	89866836	F1Dsnp	PHR	A	G	7	15,734,548	+	GAATTCTCACCCTCATAAATGGCTACCCTGCCACT[A/G]CATTGTCCATTGGAAGTAGTAGTTGAAGTTCGCTT
3,881	7	7003	7.32	89810869	F1Dsnp	PHR	A	G	7	15,735,631	+	GGCCAGAGTTTCAAATCTTCTTGAACAGAAGTATC[A/G]TTGAACCTTCTACCAATTAGCCTCTTTGCATCTGC
3,882	7	7003	7.32	89866837	F1Dsnp	PHR	A	G	7	15,742,976	+	TGTTGAATTTGATCCCTTTGTTTTGTCCAGTGGAT[A/G]GGTCCACGGTAGAGACACTCAAAATACCATTTGCA
3,883	7	7003	7.32	89866839	F1Dsnp	PHR	T	C	7	15,755,491	+	TTGGAATGACAATACTCATTGTATCATCAACTGAA[C/T]CAATTCGGGCCTTAACACCGAGTGACAGAGGGGTC
3,884	7	7003	7.32	89810870	F1Dsnp	PHR	T	C	7	15,756,325	+	CAGTTATAACAGCATTCTTCACAGTTGAGCCCAGG[C/T]AGGCCTCAGCAACTTCTCGCATCTTTCCGAGAATA
3,885	7	7003	7.32	89866840	F1Dsnp	PHR	T	G	7	15,769,463	+	TCTCAAATACAGCCAAAAGGTTATTCTCTGAGGTT[G/T]TTTTGCTCTCACCCTCAAATATGGCGAACTCAATA
3,886	7	7003	7.32	89810871	F1Dsnp	PHR	T	C	7	15,769,656	+	GACATCCAAAAGAGTAAAGCCTTGAAGCTTCTCAT[C/T]CCTACTTCCATTCAAGAGGGCAGCTAGAACAGCAG
3,887	7	7003	7.32	89810872	F1Dsnp	PHR	T	C	7	15,769,741	+	GACTCATCAGGATTTATACCTTTACAGAGCTCCTT[C/T]CCCTTAAAAGTATCTTGTAATAGCTGTTGCACTTT
3,888	7	7003	7.32	89866841	F1Dsnp	PHR	T	C	7	15,770,360	+	CAGCAGCAGTTTTTGTAGCTTGTCTCTGTGAGTCA[C/T]TGAAGAAAGCAGGGACAGTTATTACTGCATTCTTC
3,889	7	7003	7.32	89810874	F1Dsnp	PHR	A	G	7	15,770,389	+	GAGTCACTGAAGAAAGCAGGGACAGTTATTACTGC[A/G]TTCTTCACAGTTGTGCCGATATATGCTTCAGCGGT
3,890	7	7003	7.32	89866842	F1Dsnp	Other	T	C	7	15,770,452	+	TCAGCGGTACCACGCATCTTTGTGAGAACCATGGA[C/T]GAGATATCTTCAGCAGAAAACTGTTTCTCCTTATC
3,891	7	7003	7.32	89810875	F1Dsnp	PHR	T	G	7	15,770,489	+	AGATATCTTCAGCAGAAAACTGTTTCTCCTTATCC[G/T]CCTGGGTAACCACAATCATGGGCTCGTCATCAGGA
3,892	7	7003	7.32	89866843	F1Dsnp	PHR	T	C	7	15,771,464	+	ATTTCGACATGATCATTTTCCCATACTGCGACACA[C/T]GAATTTGTAGTTCCCAAATCAATCCCAATAGCATG
3,893	7	7003	7.32	89810876	F1Dsnp	PHR	A	G	7	15,777,059	+	GGATCAAATATGACAATCTCATCAAGCCGATTTAG[A/G]AACTCAGGACTAAAGTGACTTCTCACCTATCCAAT
3,894	7	7003	7.32	89844061	snp	PHR	T	C	7	15,777,234	+	GCAACTTGCATTGAACACTCTCCCACTAAACCAGA[C/T]AGGAGATGTTTTGCTCCAAGGTTAGAGGTCATGAT
3,895	7	7003	7.32	89810877	F1Dsnp	PHR	A	G	7	15,777,399	+	TGTGCCTTTTCCACTTCATCAAATAATACAACACT[A/G]TAGGGTCTCCGTCTCACGGCCTCTGTCAGTTGGCC
3,896	7	7003	7.32	89866844	F1Dsnp	PHR	T	C	7	15,782,589	+	AATTTAAACAAACTGAATGCATATATGTCTGTGTC[C/T]CTGTGATGTGGGAAGAAAATCTTACCAAAGATTGA
3,897	7	7003	7.32	89866845	F1Dsnp	PHR	A	G	7	15,785,993	+	AAATTAATGATCCTACCAAAGATTGAGTTGGTAGG[A/G]TTTCTCAGAATTTGGTTAAATGCTGCATCGCCTAC
3,898	7	7004	9.76	89810859	F1Dsnp	PHR	A	G	7	15,265,985	+	TTTGCATTCACATTTTCCAGAACAGGAGCATCCAA[A/G]AGCCTCGGAATAGTCTGGATTACAATTCAAGAAAA
3,899	7	7004	9.76	TP7438	GBS				7	16,767,287	16,767,337	TGCAGGTGCCATAACATGAAGTCTCTAACAATTGATTTTGAAAGTCTTTTTATGCCGAGATCGG
3,900	7	7004	9.76	89850590	SnpSnp	PHR	A	G	7	16,789,600	+	GATGAAACTTGTTTCGCATCTTGAAGGTACTAGGA[A/G]CCACATGGATGGTCCAATTTGGCTTGAGATTCAGA

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,901	7	7004	9.76	89810886	F1Dsnp	PHR	T	G	7	16,811,994	+	AATACCTCCATATCATCCTTGAAGTTAAAAGTAGA[G/T]AGAGGAGGATGCAATCTTGGCAATGTTCCACCCGG
3,902	7	7004	9.76	89810887	F1Dsnp	PHR	A	G	7	16,812,085	+	GTGTATCCTCTGCACTAGATACATTGAGTGTGGTT[A/G]ACCCTAATCCACTGCCAGTTCCTGTAACTGAAAAT
3,903	7	7004	9.76	89866852	F1Dsnp	PHR	A	C	7	16,812,793	+	ATGCAAGATGAATGTCTTCTAGACCCAGAGTCATA[A/C]GTATACAACTTTTTATCAAGCCCGACACTAGCAAA
3,904	7	7004	9.76	TP7414	GBS				7	16,813,502	16,813,462	TGCAGGTGATGACGGTTCTGTGCATCTGTGGGACACAACCGAGATCGGAAGAGCGGTTCAGCAG
3,905	7	7004	9.76	89866853	F1Dsnp	PHR	A	G	7	16,824,102	+	ACGAGGCAAATTCCTGATCTGATCCAAATTTGTCA[A/G]ATCAGGGGAAAGACCACCATGCATACATAATATTT
3,906	7	7004	9.76	89866854	F1Dsnp	PHR	A	G	7	16,841,150	+	ATCTTAATCCTGAAGTAGAGGAAGGTATCTGTCAA[A/G]TGCTTTCATACATGTGGCTTGAAACAGAAGTAATG
3,907	7	7004	9.76	89866855	F1Dsnp	PHR	T	C	7	16,850,209	+	CATGTACGGTGCTGCATTTCCAATCCCATCAATAG[C/T]TTCAAACGATGCAACAACTGACTCCATCTGCTGGC
3,908	7	7004	9.76	89866856	F1Dsnp	PHR	A	C	7	16,860,357	+	CAACAACCACGAACCTTGACCATCTCTTTGGTCCT[A/C]GGGACTCGTCGACGTCTTCAGCTTCTTCATCTCTG
3,909	7	7004	9.76	89866857	F1Dsnp	PHR	T	C	7	16,891,942	+	TTAAGGCAAGACGGGCCATTAAACTATGAAGTGCG[C/T]TTGCCTCAGGAATGGACCTACTGATCCCAACTGAT
3,910	7	7004	9.76	89810889	F1Dsnp	PHR	A	C	7	16,919,055	+	AGTAATTTTCAATACTTCTGAAGATCTTGAAGAAC[A/C]AGCACTGCTTACAATCCGACCAGACTTTCCCATCC
3,911	7	7004	9.76	89866858	F1Dsnp	PHR	A	G	7	16,938,862	+	TACTGCTCTCTGAATCATCATCATAAACATCAATG[A/G]CGGCTATTTTGGAAGCTCGCACTTTTGAAGATGAT
3,912	7	7004	9.76	89866859	F1Dsnp	PHR	A	G	7	16,981,919	+	GAGCTTGCAGACGTGAAGCCTCTCCTCAGGGCTCC[A/G]GTTTCCTGGTCCAAGGTATGGTCAGAATTGTTTAC
3,913	7	602	12.20	89810892	F1Dsnp	PHR	T	C	7	17,051,744	+	TCCATGTCCATTGGCGTCTCTTGGAGACTCAAATT[C/T]GTCTGTCAAGTCTTCTGAGTTGGAGGATCCAGAAG
3,914	7	7005	14.66	89810893	F1Dsnp	PHR	T	C	7	17,091,986	+	AGCCTCAGATTGCTCATCCTCACGTCTTCCACATA[C/T]CCACGGCTCGTCACGATCTGATTCGAATTGCGGAG
3,915	7	7005	14.66	89866862	F1Dsnp	PHR	T	C	7	17,096,884	+	GTTCCGAGCTTCCTCCTCGCCTTCTTCAGATCACG[C/T]TCCGTTTGCTGACGAGTGTTCACCTACAAGATCAC
3,916	7	7005	14.66	89810894	F1Dsnp	PHR	T	C	7	17,098,750	+	AGGGGTTTATAGTTTTGGCAATGTGTCTGGAAGGG[C/T]TTACCTATTATTAAGCGATTATATATATATTTTTT
3,917	7	7005	14.66	89810895	F1Dsnp	PHR	T	C	7	17,099,826	+	AGATACAATACAAGGGAGGTATGAACTTGTGAAGC[C/T]TGATGGAGCCGGGAACATGAGGATCGCTGGTGATA
3,918	7	7005	14.66	89810896	F1Dsnp	PHR	A	G	7	17,118,621	+	CCACTCATCATTCCAACAATCATAACAAGTTACTC[A/G]TCGGAAAGTTTGGGGAGATGATGATGGAAATGTTG
3,919	7	7005	14.66	36_379716	GBS				7	17,119,289		ACCATCAGGCAAGTTCTATATGCATTCCTCCRTTTCAAACTTGAAATACGTCGATTGATGGAAT
3,920	7	7005	14.66	89810897	F1Dsnp	PHR	T	C	7	17,222,292	+	TTGTATGGCGGTCTTAACAAAAGTATGGATATTGT[C/T]ACCGTCTACAAATATTTGATCAGTGGGTCTTCTTC
3,921	7	7005	14.66	TP5198	GBS				7	17,264,465	17,264,522	TGCAGCTCTTCAGGCTGCTCGGCCGACTTGAACCGCGCGTGTCCCAATGAGCTGAGGGTGGCGC
3,922	7	7005	14.66	89866863	F1Dsnp	PHR	A	G	7	17,346,421	+	ATCAAGTACCAGCTAGTTTTGACAGTTGTGATGAA[A/G]AACTGTGATCCATTGGTGTCTTGGCCAGAATTTGC
3,923	7	7006	17.10	89810898	F1Dsnp	PHR	A	G	7	17,451,964	+	TCTACTAAGTTGTAGTGTGGGATTTGAGGGAATAG[A/G]TGATGTATGACATGGGTACCAATATCATGATGAAT
3,924	7	7006	17.10	89810899	F1Dsnp	PHR	A	G	7	17,459,565	+	GAGGTGAAGAGTATTTCCCATCTCTATCGACCAAA[A/G]CAAGCTTTGCCACTGTCATACAAGGTTCGGTAGTA
3,925	7	7006	17.10	TP996	GBS				7	17,467,556	17,467,618	TGCAGACACCCTCTCGAGGATGCTCCACCGTCTTCCACCCACTCTCTCCCTTCCCACGCGCCGT
3,926	7	7006	17.10	89810900	F1Dsnp	PHR	A	G	7	17,473,065	+	TTTCAACACATACATTTGGTGGATGAACACGTTCA[A/G]CATGAAAATTCTGTAAGTAGCTACCTAAATTGTCT
3,927	7	7006	17.10	89810901	F1Dsnp	PHR	T	C	7	17,475,060	+	AGTGGATGAAAAGAGCTTATCTATCTCAGTAATAG[C/T]ATTGACATGAGCTTTTGGAAATAATAACCGCAGAA
3,928	7	7006	17.10	89810902	F1Dsnp	PHR	A	G	7	17,529,985	+	TCCAAACTAGTGCCATTGATGAGCCTAGTTCTCAA[A/G]CCTCTGAGGCTTCCAATGGATCATCAGTTATTTCA
3,929	7	7006	17.10	89866866	F1Dsnp	PHR	T	G	7	17,644,245	+	AACTGTTGTTTCTCGACGGAGCAGACATTAGATAC[G/T]GTGATCAATATGGATTGACAGCTCTTCATGCGGCG
3,930	7	7006	17.10	89810903	F1Dsnp	PHR	A	G	7	17,713,393	+	CCCAATCCATGGCTAAAGTCTTTTCTGTCACTTAA[A/G]CAATGCCTGGATTCCCAAAATCCCATTCTGTAGAA
3,931	7	7006	17.10	89844408	snp	PHR	A	C	7	17,737,454	+	ATCAGAAGTTCTAGTTCCAAGGGATACCCTTTGTA[A/C]GTGGCCATTATTTGTTGCAGTCTATCCAAAATCAC
3,932	7	7006	17.10	89810904	F1Dsnp	PHR	T	C	7	17,738,114	+	CAATCGAGAACATGCATCACATCATCAGTTGGCTT[C/T]GGGCCTCTTGTATAGCTTGCTGAGTTATTCCTGAA
3,933	7	7006	17.10	89866868	F1Dsnp	PHR	A	C	7	17,827,062	+	CTGCATTGTGCTGCAAAATTAGTTTGAGAAATAGT[A/C]TCTTGCTCGGTGTGATGATGAATATCAGGGGTATT
3,934	7	7006	17.10	89810906	F1Dsnp	PHR	T	C	7	17,827,329	+	TTGTTACATTTCACGTACAGGGCTCATCTTAGACT[C/T]GGGCCATCACTCAAAGGTCCTCGCATTAAAAACAT
3,935	7	7006	17.10	279_98905	GBS				7	17,857,555		TTTAGATGTAGCAATGAGACTATGGATTCCATAATGCAAGCCGGCAACTCGGTAATCCCACATC
3,936	7	7006	17.10	TP5294	GBS				7	17,857,711	17,857,648	TGCAGCTGCACCCAATCGTCCAGCGGACCTTTTTCCCTTGGTTTGCTCCCGAAGACGTTGAAAT
3,937	7	7006	17.10	89810907	F1Dsnp	PHR	T	C	7	17,861,778	+	CAATTCTCTCTGAATTACCACCAGCTTGAGGGTGT[C/T]CTTCAGTTCAATTACAAAGTCATAGTGAAAGAGAG
3,938	7	7006	17.10	89810908	F1Dsnp	PHR	T	G	7	17,902,040	+	TTGGCAGAAGTTGTTACTTCTTCGTTTTGGAAAAA[G/T]TCAGCTGCTTTTTCATAGAAGTCAATAGCCTTCTC
3,939	7	7007	19.54	89810909	F1Dsnp	PHR	A	C	7	17,909,917	+	TGATGTTGGTGTTTCCACTCTTGAACTTCTCTTTA[A/C]GAGCAAACTTGGATGAGTTTCTTTTCCCTAAGAGA
3,940	7	7007	19.54	TP2970	GBS				7	17,964,836	17,964,899	TGCAGCAATGGCATTTGCAACAAGGCCTCTACCTCACAAATCGCTTTCTTCTACCTCTCTCTAT
3,941	7	7007	19.54	89810910	F1Dsnp	PHR	A	G	7	18,042,407	+	ACATAAGAAAGCTCTTGTTTGGAATCCTCAACACA[A/G]ATCCGAATGAAAGGTTTCTTGCTTCAGACATAATG
3,942	7	7007	19.54	89866869	F1Dsnp	PHR	A	C	7	18,044,776	+	AAATATGATAATCATGTTTAGAAAAATATGCGCAG[A/C]AGATTATAGATGTCCGAGGTGGTTTTCAGATGAAG
3,943	7	7007	19.54	89866870	F1Dsnp	PHR	T	C	7	18,060,605	+	TAGCTAACCTGATGGGTGTTAGTTCCTCATGGAGA[C/T]GAGGTACATCATGTGTTATCCCTTTTGATGACTGT
3,944	7	7007	19.54	89810911	F1Dsnp	PHR	A	G	7	18,149,709	+	ATAATAATTTTTCTTCCCTTTACAGAAAGAGGATG[A/G]CCATCCTTCCCAGTCTCAAGAGTTAAACATCGAGG
3,945	7	7007	19.54	89901767	snp	PHR	A	C	7	18,173,965	+	TTTACTATTGCCATCAAAGGCCTGTGGGCAATTCC[A/C]TTAAACCTTCCAGGCACTCAATTCTACAAAGCAGT
3,946	7	7007	19.54	89810912	F1Dsnp	PHR	A	G	7	18,174,832	+	ATTGAAGCGCTGCTAACGATTCATCATTTGATAAC[A/G]AAGTATTCATGGACGAAGATGATCAAGGATGAGCC
3,947	7	7007	19.54	TP5300	GBS				7	18,240,956	18,241,019	TGCAGCTGCATCTGTAGTAGTAAGTAAGTTGAAAATGAGGGGATCGTCAAGTTTATTCAACAAG
3,948	7	7007	19.54	89866871	F1Dsnp	PHR	A	G	7	18,247,101	+	TCTGATGATCAAATTAAGCAAGAGACTATGACCCA[A/G]ACTCATGCAGCAACCACTACTCAACCCTTAGGAAC
3,949	7	7007	19.54	89866872	F1Dsnp	PHR	T	C	7	18,253,010	+	ACCCGGTTCCCATTTCGAACTTACCCGAATCCGAT[C/T]CCGATTCGAATGTTCTGGTGGTGGTCTCCTTCTAC
3,950	7	7007	19.54	89866873	F1Dsnp	PHR	T	C	7	18,267,975	+	AGGAAAGCTGGTCAATGAGCGGTATTACACTGAGG[C/T]CACATTTGAGATTGTTGTAGAAAATAGACATGTAT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
3,951	7	7007	19.54	89866874	F1Dsnp	PHR	A	G	7	18,338,628	+	TGAAGACTCAACTCTACGAGCCTTGTCAGGTTACT[A/G]ATGATGGTTGGAATGATCCCAGATAAAGAGTTGAA
3,952	7	7008	21.98	89866875	F1Dsnp	PHR	A	G	7	18,372,736	+	CTGACTGCTGGAGTCCACCACATGATCAACCCCCA[A/G]CGACTTCAAATACTCCACCTTCTCAGCTCCCCTGC
3,953	7	7008	21.98	89866876	F1Dsnp	PHR	A	G	7	18,381,472	+	GCTTTCGACCTGCGCGCTTAACCATCTGTCCTTCG[A/G]GATTAGTTGAACCACTAGCAGTTCTTGTATACATC
3,954	7	7008	21.98	89866877	F1Dsnp	PHR	A	G	7	18,382,117	+	TGAACAAGTTTCATGTATACCATAACATCGTAGAT[A/G]GAGGCTGTCAATCCTTGATCAGAAACAGCTCGGCC
3,955	7	7008	21.98	89810914	F1Dsnp	PHR	A	G	7	18,456,915	+	AGAACCCCAAGTTGCCATCACAAAGAAAGCATAAG[A/G]AGTGCATGGCCTTATGGGAGACCTATGCCTTCTCA
3,956	7	7008	21.98	89810915	F1Dsnp	PHR	T	G	7	18,459,260	+	TCCGGGGAACTTCTAGAACTAATTAATAGAGATTT[G/T]GGTTCTTTTGAGAAATTCATTGATGATATAAGGCT
3,957	7	7008	21.98	89810916	F1Dsnp	PHR	T	C	7	18,460,024	+	AACAACCTTTTTGGAGAAACTTGTTTCATGGGAAG[C/T]AGTCAGTTATAGACTTGAAAGTGCAAAGGCTCGAG
3,958	7	7008	21.98	89866879	F1Dsnp	PHR	A	G	7	18,482,209	+	CCAATGAACTGCTTATACAGGAATGTGATGTTCTC[A/G]TCCCTTCTGCTTTGGGTGGAGTTCTCAACAGGTCT
3,959	7	7008	21.98	89810918	F1Dsnp	PHR	A	G	7	18,483,480	+	GCTTCCATTGCCATTTCTGCTTCTTTGCAAATAGT[A/G]TGTGGCTCTGGTTCACAACATGTAACTAAGAAACA
3,960	7	7008	21.98	89866880	F1Dsnp	PHR	T	C	7	18,544,560	+	TATGCCGGCTTAAGGGAAGAGATCAATGGACTCCT[C/T]TTCATCATGCTGCAAGGAGAGGTAGGGAAGATATT
3,961	7	7008	21.98	89866881	F1Dsnp	PHR	T	G	7	18,563,574	+	TCGTCACCTTGACTTCGACGATAGTGTCGACCGGC[G/T]GTGGAGACTGCAAATTCAAAATGAAATTCAGAATC
3,962	7	7008	21.98	89810920	F1Dsnp	PHR	A	G	7	18,581,122	+	GAGAGCACGAGACATAGTCCACACTAATCACAACC[A/G]TACCGTATTAAGTATCCCTGACGAGAGCCAGCATA
3,963	7	7008	21.98	18_1175784	GBS				7	18,591,398		TCTGCYTCAGCATTGCCACCAATGAGTCAATTTGATGCACCCGAATCGGCACAGTCCTCCCCAA
3,964	7	7008	21.98	18_1175758	GBS				7	18,591,424		ATCATACCGCCTCTGAGTCTGCAGCTTCTGCYTCAGCATTGCCACCAATGAGTCAATTTGATGC
3,965	7	7008	21.98	89810921	F1Dsnp	PHR	T	C	7	18,621,391	+	GCCAGATTCAACCACACTTGTGGCAATTGGATTCC[C/T]GTTCTTCGTCATATAATCAATACCACATTGAAAGT
3,966	7	7008	21.98	89844620	snp	PHR	A	G	7	18,621,392	+	CCAGATTCAACCACACTTGTGGCAATTGGATTCCC[A/G]TTCTTCGTCATATAATCAATACCACATTGAAAGTG
3,967	7	7008	21.98	89866883	F1Dsnp	PHR	A	G	7	18,621,998	+	TCAACTCTAAGCCTCTTAAGATTGGGACGAAACCC[A/G]TTCTCTTTTCCAGGTGTTTTCAGTGAAACCATAAC
3,968	7	7008	21.98	89844628	snp	PHR	T	C	7	18,658,653	+	TCGAGGAAATATGTGAATGAATGAAAGTGAAGGTG[C/T]TAGGGTTTTGGAAGTGAGGGAGAAGTGGAGGTGGG
3,969	7	7008	21.98	89810922	F1Dsnp	PHR	A	G	7	18,717,883	+	TGATGTATCTGCATTGCAGGATTCATGTGTACAAC[A/G]TTGAGGAATTGGTTTTGTGTGCCCTGCCGTACCAT
3,970	7	7008	21.98	89866885	F1Dsnp	PHR	A	G	7	18,718,278	+	GCATCCCCGTCAAAGAAGTATCGGCCTTCAAAGCC[A/G]GTGATCAGATTTTGCACGGCAGTTGTCATTGAGGT
3,971	7	7008	21.98	89866886	F1Dsnp	PHR	T	C	7	18,718,869	+	ATGCGAAAGAGTCGGCTGATCTTCAGCTTTTTCGC[C/T]TATCACTTATGACTTTGATCAACCTTGTTCAGGTA
3,972	7	7008	21.98	18_1031965	GBS				7	18,722,040		TCCCAATTCAGCATCTCGGTTTTGAACTACAMAAGACAACAGAGAACCGGATCAACAATGTCAT
3,973	7	7008	21.98	89866887	F1Dsnp	PHR	T	C	7	18,722,145	+	CTTTTGGAGGTTGATGGAGGCATTTCTATCTGCGA[C/T]GCCTGCAGATGTCCCATTGGTTAGTAATTCCTTCT
3,974	7	7008	21.98	TP6458	GBS				7	18,722,152	18,722,091	TGCAGGCATCGCAGATAGAAATGCCTCCATCAACCTCCAAAAGATGCAAATTAGAATATTTGCA
3,975	7	7008	21.98	89810924	F1Dsnp	PHR	A	C	7	18,724,499	+	GGCATGTATTTGAGGACCAATTATTGGAGGCTTTG[A/C]AAGTAAGAAGCTATCTTGAATTTGTAATTTCAGTC
3,976	7	7008	21.98	89810925	F1Dsnp	PHR	A	C	7	18,763,796	+	TTCTTTCCATTTAGTCCACTTCTCCATAGACTCTG[A/C]TGAACTGAGGTTTGTTGGTCCTGAAAGACCCATTG
3,977	7	7008	21.98	89866889	F1Dsnp	PHR	A	G	7	18,772,348	+	GCAGAGTAAACCTAAGGTGCAGCACCTGATAATAC[A/G]AGATAATCTGCACATTTCACCAAAATATGAGGAAT
3,978	7	7008	21.98	TP9343	GBS				7	18,778,678	18,778,633	TGCAGTTCCTGCCTCAATCTTAACACTCGGCGCATTTTTCCTTCCGAGATCGGAAGAGCGGTTC
3,979	7	7008	21.98	89866890	F1Dsnp	CRBT	T	C	7	18,793,117	+	AAGCGTACTGACATTTGCTCATGATCAATTGCATG[C/T]AGGAGGGTCTTGTGGGTATGGAGATTTAGTTTCAA
3,980	7	7008	21.98	89866891	F1Dsnp	PHR	A	G	7	18,877,832	+	GTAGAGTTGACATTGCTATCAAACCTCACCTACTT[A/G]GACATCTCCAATAACTTGCTCTCCGGGTCACTCCC
3,981	7	7009	24.45	89809208	F1Dsnp	PHR	T	C	1	7,148,694	+	CTATGCTGTAGCAGTGACTTATAGAGTTGTTGCTG[C/T]CTTAGAGGCTGAGGTCGATTCCTGATTGAAGCAAG
3,982	7	7009	24.45	89810927	F1Dsnp	PHR	T	C	7	18,896,655	+	CAGCGGTGCAGGAGGAGAAAAAGGGATGAAGAAGA[C/T]AAACTTCGGGATCTTAACGAGGAACTCCAGAGTGT
3,983	7	7009	24.45	89844680	snp	PHR	A	G	7	18,904,972	+	TTCCTATCTCTAGAGGGATGCTCACTTCTAACAAC[A/G]GAAGGTCTGGAGTCTGTGATTCTCTCCTGGAAGGA
3,984	7	7009	24.45	89866892	F1Dsnp	PHR	T	C	7	18,907,057	+	TGGGCACGAAACTTCAGCTCTTCGGAAGAGTTGAT[C/T]ACTGAATTTTGTAGAGAATGCCGGGTTGTTCGAAA
3,985	7	7009	24.45	89810930	F1Dsnp	PHR	A	G	7	18,983,934	+	ACCGTTTCACTAAGTTCAATTCCCTGAGCTCCCAC[A/G]CCACGAGTGACAGCTCCTCTTAGATCCACCCCAGC
3,986	7	7009	24.45	89866893	F1Dsnp	PHR	T	C	7	18,985,673	+	GTAAGACGCGGTTGCACCATCGAATCAAGCCTGTC[C/T]TCTAAGACCTCAAGTTGCTTCCTCACATTAGCAAA
3,987	7	7009	24.45	89866894	F1Dsnp	PHR	T	C	7	19,003,961	+	TGGAGAAGAAGACCCTTTTCTTGGATTCTTGGGGA[C/T]GGATGGGCACCATTTGATGGATCAGATGGAACAGT
3,988	7	7009	24.45	89810931	F1Dsnp	PHR	A	G	7	19,005,087	+	GGAACTCATAGCTCATTGCGTGGAAACTCAAGGGC[A/G]TTGGCAACTGTAACTGCTATTATTGATGGAACAGG
3,989	7	7009	24.45	TP8099	GBS				7	19,035,887	19,035,824	TGCAGTATCATGCGCAACCCTGGTTTTGATCAAATTCCCTTGTATCCCTTGGCAACTTTACTCC
3,990	7	7009	24.45	89866895	F1Dsnp	PHR	A	G	7	19,236,443	+	TGGCAGAAGCTGTGTCAGGAAGACCCACTCTCGTT[A/G]ACGACAGGAACTGCTTTAAGAACCAGATTCTTACA
3,991	7	7009	24.45	TP5214	GBS				7	21,616,751	21,616,718	TGCAGCTGAACTTAGGTTTTTGGGATTAGGGTTCAGCTAATTCCTTCAAAAATCTCCTTCTATA
3,992	7	7009	24.45	89866939	F1Dsnp	PHR	T	C	7	21,624,395	+	TAGGCATCTGTTATCAGAACAGCAGGCCGCACAAA[C/T]GACGACTGATTAATTCCATTCAAATGCCTGACAAA
3,993	7	7009	24.45	89810979	F1Dsnp	PHR	T	C	7	21,731,110	+	TACCTGGATTGGCATCTTCTTGAGAAAGATAGCAC[C/T]AGCCAGATTGATTTCTGTCAGAAAAAGATGTTGGA
3,994	7	7009	24.45	89810980	F1Dsnp	PHR	T	C	7	21,760,450	+	ACTACAATCACAAAAAAGTCTAAGAACAAAATCTT[C/T]TATATATCATTTGATTCTCTCCAATACTTGTTTAT
3,995	7	7009	24.45	89810981	F1Dsnp	PHR	A	G	7	21,817,922	+	CAGCTACTTGATAGTGAAAGTAATGGAGCAAGTGC[A/G]TCCCTTACTGAACATGCTCCGGAATCAAGCAGCTT
3,996	7	7009	24.45	89866940	F1Dsnp	PHR	A	G	7	21,818,673	+	ACCCACATATCGAGGAATTCTTCCAGAAGCAACTT[A/G]GTTCATCACAACAACACAAGGACAACCTCTTGCAG
3,997	7	7009	24.45	89810982	F1Dsnp	PHR	T	C	7	21,820,198	+	ATTGCTTCTTGGTTTGCTAACTGATGGCAGCACAA[C/T]ACTCTGCACATTGCTGTAGACTCTTCGTTCCGAAA
3,998	7	7009	24.45	89810983	F1Dsnp	PHR	A	G	7	21,825,667	+	TTTTAGAACTTTTTTCTGAATCAGTAACCGAGGAA[A/G]AGTTAGATGGGATGAGGCTAATCTGGGAGAAATTG
3,999	7	7009	24.45	89866941	F1Dsnp	PHR	T	C	7	21,826,078	+	ATACGGGGGAGTCGGTTTGATGAATGTGTCGGTGA[C/T]GCAATGCATGCAGAAGCGATAAGAACTGCTTTGAC
4,000	7	7009	24.45	89810984	F1Dsnp	PHR	T	G	7	21,848,089	+	ATTTCTGGGTTTTCGAGGCTGGATTTGAAGGAGAG[G/T]AGGGCATTGGCTTCTGGGTTTTGGTCATCAATGGC

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
4,001	7	7009	24.45	TP3880	GBS				7	21,861,248	21,861,311	TGCAGCCAGAAGAAGATGATGAGTAATTGACTAGCTCAGACCACATCAATAAGGGAAAACGTAC
4,002	7	7009	24.45	287_224414	GBS				7	21,886,710		GCTAGGGTAACCAGCATAGCTGCTAAAGAAACCCCACGAGTGCTCGCTCCTTGTTGGCGAGAAG
4,003	7	7009	24.45	89810985	F1Dsnp	PHR	T	C	7	21,913,079	+	CAATTTTTCGTTCATGGGGGCTGGTTACTCTATGT[C/T]TTCAATCAGTGCCAGCAGATCAGGTTCGCCGGATC
4,004	7	7009	24.45	18_47391	GBS				7	21,970,638		TATGCACGAAACCAGGAATCTTACTATTCCTRCTACTGCAGATCGAGAAATGAGATAGCCAAAA
4,005	7	7009	24.45	89810986	F1Dsnp	PHR	T	C	7	21,985,364	+	TAATTATAGTTCGAGTCCTTGACTTGCCTGAGAAG[C/T]GAACTGTTGATCAAGTAGACTAGAATAGTCATCCG
4,006	7	7009	24.45	89866943	F1Dsnp	PHR	A	G	7	22,043,701	+	CCATCCCAGGGATCAGATGGGAACCTCAGATCAGC[A/G]GTCCTAACGGCATCAAATATGCTTGACTTTGTCTT
4,007	7	7009	24.45	89810988	F1Dsnp	PHR	T	C	7	22,142,930	+	TTTCTGCGTAGTGCTTCTAATTGATCTAACATCAT[C/T]TGCATCTGCATATATAAACCAGAAAAGGACCGCTG
4,008	7	7009	24.45	89810989	F1Dsnp	PHR	T	C	7	22,176,494	+	CTCGGCGTGGGCAGAACACATTTCAAAGAGTTTTT[C/T]GGAGACAATGATTCGATAATGAGGTTGAATTACTA
4,009	7	7009	24.45	89810990	F1Dsnp	PHR	A	G	7	22,184,839	+	TGATTGGTTGATGGGGATGTCTTTGGATAGAACCG[A/G]AGTGGGAAGCTTAGGATCAGATGAGGGCGGCGCGT
4,010	7	7009	24.45	89810992	F1Dsnp	PHR	T	G	7	22,236,498	+	AATACAAATCCAAGTAATTCCAAACAAAATCTGCA[G/T]ACTTGGGAAGAAGCTTCCTATCCCATTACCAATAT
4,011	7	7009	24.45	89866945	F1Dsnp	PHR	T	C	7	22,236,514	+	ATTCCAAACAAAATCTGCAGACTTGGGAAGAAGCT[C/T]CCTATCCCATTACCAATATGACAGGACCTAATATG
4,012	7	7009	24.45	89810993	F1Dsnp	PHR	A	C	7	22,264,464	+	GTCCATTTGGATGATGTAAGTTTGGGTTTTTGCAG[A/C]GAGGGCATTGGTGAAGAAGAAGACAGAGCTTGCTA
4,013	7	7009	24.45	TP141	GBS				7	22,346,790	22,346,853	TGCAGAAACCATTATACCGATGGCAAGTGCAAGTCTACAAGAGAAGCGACACAAGAAGCCCAAC
4,014	7	7009	24.45	TP9300	GBS				7	22,372,758	22,372,695	TGCAGTTCCAATGGTAATCTAACAAATCAGATAAATGTCACACCTCGAATGTTAAGAATTTTCG
4,015	7	7009	24.45	89866946	F1Dsnp	PHR	T	C	7	22,398,641	+	CTTCTTTTTGCTCTAGGGTTGGAGTTTTCTTTGGC[C/T]AAGGTATGTTGGGTTTTGGAACTTCATATAGTTTT
4,016	7	7009	24.45	89866947	F1Dsnp	PHR	T	C	7	22,398,999	+	GGAGCTGGGTTGTCTGAGGGAATTTTTGTTGGCTC[C/T]TTCCTATCAATGTCATCAACAGCAGTAGTACGTTT
4,017	7	7009	24.45	89866948	F1Dsnp	PHR	A	G	7	22,461,683	+	ATTTTGCAGGTTGAGGCAGAAGTGTCACGGTTGGA[A/G]GAGCTGAAATCAAGTAAAATGAAAGAGCTTGTTCT
4,018	7	7009	24.45	89810995	F1Dsnp	PHR	T	C	7	22,477,242	+	ATAACAACATACCCCATTGATGGTGGAACAGTAAG[C/T]CTTCTTTTATCCCCAACACGCATGCCTAAAGGTGG
4,019	7	7009	24.45	89866949	F1Dsnp	PHR	A	C	7	22,477,812	+	TTGCTTTTTCCCACGTCAGCAGCAGTTTGATCGGC[A/C]TTAGTTTTTTCTTCAGTCTCCTGGGATTTCTTCTT
4,020	7	7017	26.88	TP2722	GBS				7	21,393,447	21,393,510	TGCAGCAAAGCGAGAGCATGTGTAAGAATTGGATCTCTAAATTAAAGCAATGCATGAAATTAAC
4,021	7	7017	26.88	TP9822	GBS				7	21,395,165	21,395,228	TGCAGTTTTCCTATGGAACAAGAAACAAAATTCAAAGGAGACGGGACAGATTCAAGGCATAGAC
4,022	7	7017	26.88	17_246286	GBS				7	21,395,452		ATCTCTGCAAAGAATGATAACACCCAGGTTTTAGAAATCATTTCTTTCTAGATGAAAGCATACA
4,023	7	7017	26.88	89866938	F1Dsnp	PHR	T	G	7	21,396,737	+	CGTTTTGGCGGGGAAAAGAACCCTGCTTCATACTT[G/T]GGTCCGAAACTGTTCTTCTGAAAGGGCACTCTCCC
4,024	7	7017	26.88	TP8559	GBS				7	21,449,169	21,449,106	TGCAGTCTGTTCAAGATACATAAGCTAAAGAGTAAGTATATAGTAATGAAATGGATTATGAAGG
4,025	7	7017	26.88	89810978	F1Dsnp	PHR	T	C	7	21,523,028	+	AGTGAGATCCATATTCCAAGGAACATATCATGCCC[C/T]GTGTCACCCATTGGAAGCCCTCTATTGTACTCCAG
4,026	7	262	29.32	89810976	F1Dsnp	PHR	A	G	7	21,331,516	+	CATCAAGCAGCTATGCCTGCGGCAGACATTCTTTC[A/G]TTGAAGCCATGTGTTTGCTATTGAGTGAAGTACTG
4,027	7	262	29.32	89810977	F1Dsnp	PHR	A	G	7	21,338,154	+	CTGGATTTTTTCTATGTTTTTTAGGTGGGGATGGA[A/G]TTTTGGGCAAGATGGGCGCACAAAGCTCTATGGCA
4,028	7	262	29.32	89866937	F1Dsnp	PHR	A	G	7	21,359,644	+	CTGCCAAACACAGAACAAGAAAGCCTCCTCCAACA[A/G]CTGGAGCCACCCAAATCCATATGTTTTTCTTCTTA
4,029	7	7016	31.76	89810972	F1Dsnp	PHR	T	C	7	21,182,974	+	GGGATTCGAGTTGTTTGTAAGCATCTTGGGAAGAG[C/T]AAGTCGGCCACGGCGGCGGTGGCTGTGGCGTCTCC
4,030	7	7016	31.76	89810973	F1Dsnp	PHR	T	G	7	21,189,554	+	TTTCGGGCGGTACAAGTATGATCAGACCTCCATTA[G/T]CTTCATTTACGAGGGCACTCAAGTTGGGGACGCTG
4,031	7	7016	31.76	TP2107	GBS				7	21,255,078	21,255,141	TGCAGATATTTTAGACCCATGCTTATGCTTTTGAACAGTAATGTCCTGAAGTATCAAGTAAAGG
4,032	7	7016	31.76	89866934	F1Dsnp	PHR	A	G	7	21,255,521	+	TTTTTGCAGCTGCCACATTTTAGTGAGGCTGTTGT[A/G]AAAAAGATAGCCCGCAAGGTAAGTCTATTTTGGAG
4,033	7	7015	34.20	89866924	F1Dsnp	PHR	T	G	7	20,859,284	+	TTTGTTTGTCATTCCGCAGAGACGATCGCTTTTCA[G/T]CTGGATTCTGTGGATCCTGTGAAAGCCCTCAGAAT
4,034	7	7015	34.20	89866925	F1Dsnp	PHR	T	C	7	20,897,506	+	GTACACTCCCACGGCAAGTTCCTCAAATGGAGTAC[C/T]TTGGATGGTGGCTGAGTGTATCGGAACTGTGGCTG
4,035	7	7015	34.20	89866926	F1Dsnp	PHR	A	G	7	20,898,008	+	CAGCCAATATCACGGCGGTAAAACCCTCCTGGCCA[A/G]TTAATTTGTTCAACACCTTGATAAGCCCTTTCATG
4,036	7	7015	34.20	89866927	F1Dsnp	PHR	T	C	7	20,917,699	+	TGTGGTGCTGCAATATGGATACTTGGTTCCTGTTG[C/T]TGCTGGGATAGTTGTCTTTTTCTCCTCCTTTGATC
4,037	7	7015	34.20	89810966	F1Dsnp	PHR	T	C	7	20,921,638	+	TAAAGGAGACAGTTGAGCAGTGCAGTGATGTAAGG[C/T]ACGCATGAAAACTCTTCTGTACTTTTCTTCCTTAT
4,038	7	7015	34.20	89866928	F1Dsnp	PHR	A	G	7	20,943,816	+	GGTTCGAGTGATGAGCTAGCCGCAGTTATGGTCGG[A/G]CTAGAGAGGTAAGTCGGTTGTTGCAACTGTTGTAA
4,039	7	7015	34.20	89810967	F1Dsnp	PHR	A	G	7	21,016,758	+	CCACCTGTTGTATGTATTGGGCTTTTTCCAGTGAG[A/G]AGCTCGAGCAACAGCACCCCGAAACTATAAACATC
4,040	7	7015	34.20	89866930	F1Dsnp	PHR	T	G	7	21,063,382	+	AGAAATGCAGTGCATGCTCTCTACCATTTCCTACA[G/T]ATACATAGTTATGCTCTCCTTCCCAATGCACCCAT
4,041	7	7015	34.20	17_511757	GBS				7	21,089,993		TGTGGTGTGGTTTTCGAGAGAGGGATCTGCTGCTGCTGCAGTAGCTAAAGCATTTTACATTTTC
4,042	7	7015	34.20	89810969	F1Dsnp	PHR	T	C	7	21,123,690	+	TGAAGATCTCACTAAAAAAATTCCTCACAGATAAC[C/T]GCAGGGCCTCATACCATTCCTTTGAGAAATATATA
4,043	7	7015	34.20	89866931	F1Dsnp	PHR	A	G	7	21,131,089	+	CCATCTGAAAGGCTTCCCTTGTACACGCTCCCAAA[A/G]CCACCTGAAAAAGTAGCACATATACTACTTACTAT
4,044	7	7015	34.20	89866932	F1Dsnp	PHR	A	G	7	21,143,556	+	AGAAGGTAGATGCAAGTCACACCAACTAATGTAGC[A/G]ACAGCAATGCACCACAGAACCAAATTTATTGTTAG
4,045	7	7015	34.20	TP7160	GBS				7	21,143,892	21,143,955	TGCAGGTAAAGGGTCAACCTGATCTGTACTTGGAGCAAAAGCATTCTCCGTTTGATCACCTTTT
4,046	7	7015	34.20	17_465991	GBS				7	21,144,000		GAAACTTGAAAGGCAGTTAACACTACTGMGGRGAAAGACACCGCGAAAAGGTGATCAAACGGAG
4,047	7	7015	34.20	89810970	F1Dsnp	PHR	A	G	7	21,160,966	+	CCCGAGTATCGTAATGGAAAGCTTGTTATATCATC[A/G]ATGAGGTACATACCAACCTTCTGTGTGCATGATTT
4,048	7	7015	34.20	89810971	F1Dsnp	PHR	T	C	7	21,175,202	+	GCATGGTGTGTCTAATCCCTCTTCTTCTCTTTCAC[C/T]GGACCTTTGGGTATCTTACTCAAAACCTTTTCATT
4,049	7	267	36.67	89810958	F1Dsnp	PHR	T	C	7	20,394,660	+	TATTTTGATCCAATTTTATGTTTGTTTGTTTTCAG[C/T]CACAACAATGATTATGCTGCAACCAACCAAGATGA
4,050	7	267	36.67	89810960	F1Dsnp	PHR	T	C	7	20,463,328	+	TTGGAATGTGGTACAAGATATTCGTGATTTCATGT[C/T]TGATTTCAGTAACCACAGACCCTTTGTTCTTCTAT

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
4,051	7	267	36.67	89866912	F1Dsnp	PHR	T	C	7	20,541,020	+	CTTACCGAATGATTGATCAGCCGTGCTATATTTCC[C/T]TTATCGGTGGCATCTACTACCACTTCTTCGCTAAT
4,052	7	267	36.67	89866913	F1Dsnp	PHR	A	G	7	20,542,736	+	AATAAGAATCTAACCTCCATGCGGTACCCTGCTCT[A/G]GATGCACACATGGCATGGTAATAAGTGGAGCACCT
4,053	7	267	36.67	89810961	F1Dsnp	PHR	T	C	7	20,544,833	+	ACCTTAAAATAATTGGTGTTAATTCTATCACATTC[C/T]GCATGCACCCATACTCGGCAACCATCACACCGGAC
4,054	7	267	36.67	89866914	F1Dsnp	PHR	A	G	7	20,562,463	+	AACAATATCCCTTGATTTAGTTCCAGCAGGCACTG[A/G]GATGATTATATTAACCTCCTGCAGACTCTGGGTCC
4,055	7	267	36.67	89866915	F1Dsnp	PHR	T	C	7	20,610,716	+	AGCCTAAGTACCAAGTGCAACAGGTTCCCATCAGT[C/T]ACCCCATAGTCCCTAACACAAGAATTGTTCCTAGC
4,056	7	267	36.67	89866916	F1Dsnp	PHR	T	C	7	20,636,937	+	GAGACAACCATGAGAAAAAAAGGTGTAATGTTCAA[C/T]GTTTCCTTCAGACCATGAAGGCCAGCATTGTGTGC
4,057	7	267	36.67	89866917	F1Dsnp	PHR	A	G	7	20,641,766	+	GAAAATTCAACCTGTTGAAATTGCACACATACCTC[A/G]CACCAATCAAGGCAATCAATGGCTTTGACCTTCGC
4,058	7	267	36.67	89810962	F1Dsnp	PHR	T	C	7	20,654,501	+	ATTCTATAGCTTTATTGATCATTTTCAACTTTGAC[C/T]TCTTCTCCTCAATCTGCTTCTCAACTTCAACAACA
4,059	7	267	36.67	89810963	F1Dsnp	PHR	T	G	7	20,654,914	+	GCGAAATAGCACCATGTTTAATACAAGCACGAGCA[G/T]CCAACATATCCTCCCTGGTTTTATATACTTGGAGC
4,060	7	267	36.67	89866918	F1Dsnp	PHR	T	C	7	20,657,838	+	ATACCATTTTTCTCATAACCTGCGGTTACTTTCAA[C/T]AGGCCACCAAGGTCAATGCATCCATGATGATCAGC
4,061	7	267	36.67	89866919	F1Dsnp	PHR	A	G	7	20,658,136	+	TGAATAGAAAACCCCTCCACATTCAATTGAACTTC[A/G]GTGCCTTCAATTACATGATTGCCATATTGATCAAA
4,062	7	267	36.67	89866920	F1Dsnp	PHR	T	G	7	20,665,311	+	AGGATTACCCCCTATTGCCTGTTCCTTATAAGACC[G/T]GTGAAGTGAAGCACCCATCTTTCCCCTGAAAAGAA
4,063	7	267	36.67	89866923	F1Dsnp	PHR	A	G	7	20,760,018	+	AAAGTGAACAAAATGCAAAACAAGGTTTCAAGTGT[A/G]GCGGCAATGCATTGTAGCTCAATTTTAGTGCAGCC
4,064	7	7013	39.11	TP524	GBS				7	19,799,044	19,798,984	TGCAGAAGAATGAAAGAATTTCAGCACAACCCATTGAACCGTCTTCCTTTGTGCTGGTTTAAGC
4,065	7	7013	39.11	89866904	F1Dsnp	PHR	A	G	7	19,989,184	+	CTCGGAATATCGAAACTCTGCACTTACGTTCCTCT[A/G]TCACCTCCAGCACACATATGTCACCTTCTTCCAGA
4,066	7	7013	39.11	TP2685	GBS				7	20,059,218	20,059,280	TGCAGCAAAAGCGCCGCCGTCTCGGTGGCCAACAACAACCACGACTCCTCCACCGCCACCGCCA
4,067	7	7013	39.11	89810949	F1Dsnp	PHR	A	C	7	20,068,708	+	AACAAGAACCACATGAAATACGTAACCGCAAAGAC[A/C]CCAAATATCACGGTGCTCAACAAAGGGTACTTGCA
4,068	7	7013	39.11	89866905	F1Dsnp	PHR	T	C	7	20,091,778	+	GGTTACTGCCAGGGTATGAGTGATCTACTTTCTCC[C/T]ATAGCTGCTGTAATGACAGAGGATCACGAGGCTTT
4,069	7	7013	39.11	23_313091	GBS				7	20,108,735		TCACCGTGTGAACACTCTCCCTACAAAACACTGTACTCCCTCCCTCACCCTCCTCCGACCGACC
4,070	7	7013	39.11	89866906	F1Dsnp	PHR	T	C	7	20,180,449	+	TGTAGTGGTTTAAAAGGCAGTAATAGCACCAACTT[C/T]AAAGCCATGAAGCAATCTATTTCAAGAAAGATCTG
4,071	7	7013	39.11	89810950	F1Dsnp	PHR	T	C	7	20,234,340	+	AACACATCATCTGGTATTTCGTCTTTTAGGGATTC[C/T]GGTAAGTATTTTAATAATTCTGGCATCTCTTCGAA
4,072	7	7013	39.11	89810951	F1Dsnp	PHR	A	C	7	20,266,871	+	GAAGGCCTAGTTAATGCTTTGGAGATTGTCAATCG[A/C]GAGGTGGAAGTTGCCAAGCATCTAGCTCTTGATTG
4,073	7	7013	39.11	89810952	F1Dsnp	PHR	A	G	7	20,270,744	+	ACAGCGAGAATCCATTTTTGTTTGGGGAAAGCCCT[A/G]TGCGCAAGCCAAACAAGAACTGGAGCAACGGCGCC
4,074	7	7013	39.11	89810953	F1Dsnp	PHR	A	G	7	20,270,879	+	ACGAGACCCCAGATAACAGATGCATCAAAGAACAC[A/G]CGGTCCATTGGACAAGTCCAAGGGCTGCCTGGTGG
4,075	7	7013	39.11	89866908	F1Dsnp	PHR	T	C	7	20,286,874	+	AGATTATACAGCTGCTGTAATTGTCGAAACCATGT[C/T]TCACTTCATGATGATATTGTTTCTAAAGCCTTTCA
4,076	7	7013	39.11	89810954	F1Dsnp	PHR	A	C	7	20,323,196	+	TTCATCCTTACAACTTTATTACATATATCAAACTT[A/C]TCAAGAAGTACTTGTTTCAACCCAAGGTTCACAAT
4,077	7	7013	39.11	89810955	F1Dsnp	PHR	A	G	7	20,339,114	+	CGTCTTCAGTTGACAAAACTGTTCGTCTATGGCAA[A/G]TGGGATGCACTGATTGCGTCAAGGTCTTTGCCCAT
4,078	7	7013	39.11	89810956	F1Dsnp	PHR	A	G	7	20,339,329	+	TTTATGTTGTGGACTCTTGCAGTGACCTGTGTTCA[A/G]TTCAATCCTGTGGATGATAATTACTTCATTAGTGG
4,079	7	7013	39.11	89866909	F1Dsnp	PHR	A	G	7	20,364,624	+	GATAGAGCCATTTCTTTCAGGGAGTATCTGCCACA[A/G]TTTTCCATTGAGGATATTGGTACAATACTTGTCTA
4,080	7	7013	39.11	89810957	F1Dsnp	PHR	T	C	7	20,382,201	+	GCGGCGGTGACGACGTCGTATCGGATACTGTGCCA[C/T]GATATGAAGGCGGGAGGGGTGATAGGGAAGTCCGG
4,081	7	7013	39.11	89866910	F1Dsnp	PHR	A	G	7	20,384,098	+	GTCTGTTACTAGGGTCCTGATGATGAGCTGTTTCC[A/G]GCTCAGGAAGCTTTATTGCATATCCAAACTCGTAT
4,082	7	7013	39.11	89810964	F1Dsnp	PHR	A	G	7	20,690,050	+	GATCCTGACAAACCTTTACCAGAGGGATTTGCATG[A/G]GTTTCTCTCTTCCTTGGGGGGACTGGAAAAACTTA
4,083	7	7012	41.55	23_552019	GBS				7	19,843,303		AGGAGCCATGGATCATGTCACTGAAGAACATTACAGGAGGAGAAGGAAGAAAGAGATCTTGCAG
4,084	7	7012	41.55	23_551948	GBS				7	19,843,356		TATAAAGTTCYATCTGCTAGCTGCAGAAGAACACAAGCATAGATATTCTTGTTGAGCATTGTAT
4,085	7	7012	41.55	TP5570	GBS				7	19,895,741	19,895,678	TGCAGCTTCATATTCCAACTGACGATCACTATCCTCCTTATCTTGTTGACCATCTCCGCTATGT
4,086	7	7012	41.55	89810947	F1Dsnp	PHR	T	G	7	19,931,523	+	TATAGGCATTCCTACTGGGCTAGTTTTTGCGTTTG[G/T]CCTCCACATTGGAGGAAAGGTAGCAGCAAGATCTC
4,087	7	7012	41.55	89810948	F1Dsnp	PHR	T	C	7	19,968,760	+	CGCACGAATCTCACCTCCTGATCGGCTTCTTGTGC[C/T]GGGGAGTGTCATAGTGTCTTCAAAAATACGGTCCA
4,088	7	7011	43.99	TP9001	GBS				7	19,688,830	19,688,769	TGCAGTGGTTGTTAGGCAAGCTGAGAGAGAGGCAAATCGTGCTGCTTTGCAAGCAACCTATAAG
4,089	7	7011	43.99	89866901	F1Dsnp	PHR	T	C	7	19,700,849	+	TCAGCATTGAGGTTATCACCAAATGTCGACACAAG[C/T]AGTCCCATGCAAGATATAGCACATTCTTTCACCTC
4,090	7	7011	43.99	89810945	F1Dsnp	PHR	A	G	7	19,708,075	+	AAGAAATTGCCGTGGGATGATCGGCTTTTTCATAA[A/G]AACTGGAAGGTGCGAAATGAAGCCAACATCGACTT
4,091	7	7011	43.99	89866903	F1Dsnp	PHR	T	C	7	19,711,805	+	TGATGGAACCCCAGAAGTGAGAGATGCAGCATTTT[C/T]AGCTTTGACAGCAGTAGCTAAGGTAGCATTTAAAT
4,092	7	7011	43.99	89810946	F1Dsnp	PHR	A	C	7	19,725,726	+	AAAGTGTTCACCTGAACAGATAAGACAAGCCAAAG[A/C]GCCCCACGGCGACCGATATCCTAATGAGCCTCCCA
4,093	7	274	49.02	89810364	F1Dsnp	PHR	A	G	5	7,552,723	+	TGTGGTTGCTTATTGCAGAACCTCATTGTGAAGGA[A/G]CACAGGATATGGTCAAAGATTTTGATGATCTTATT
4,094	7	274	49.02	89850691	SnpSnp	Other	T	G	7	19,612,367	+	AAGTAATGCTTATCTGCCTTCCTTTTTCCTGCTTA[G/T]TAAAGATATTTTTCTTGTTGTATTTCTTTTCAGGG
4,095	7	7010	51.53	89810933	F1Dsnp	PHR	A	G	7	19,328,078	+	TGCATAAAATTTGCAGTCGTACCTCAAGGACATCC[A/G]CAGTAAGATTTTTCCAACTGTTGAGCAGCCGACAA
4,096	7	7010	51.53	89810934	F1Dsnp	PHR	T	C	7	19,340,692	+	TTCCTGCTGCCTTACTACCACTGTTTTCTCATGCT[C/T]CGCAACAATGGTACCCTCTTCTCTCTCTCTGGCCC
4,097	7	7010	51.53	89810935	F1Dsnp	PHR	A	G	7	19,404,074	+	TCAATTTCTTCAATTTTGATGTCATCAGGGACTCC[A/G]ATGACAAGCACAGCTATTATGTTATTGACATCAAC
4,098	7	7010	51.53	89866896	F1Dsnp	PHR	T	C	7	19,405,221	+	ACTGATCATTAGTTGCTTCCTGATGATGATCACCA[C/T]CCATAACTATAAGATCCCGGCCGTCGCAGGCTACT
4,099	7	7010	51.53	89866897	F1Dsnp	PHR	A	G	7	19,434,815	+	AGCTTTTCCAAGGTCCAAACCAAGGAGATAAGATC[A/G]TTGAAGAGGCCACCTCAGAGGCACTTGATGAACCT
4,100	7	7010	51.53	89810936	F1Dsnp	PHR	A	G	7	19,438,672	+	ACCTTTTGCTTAAACCCAGCTGGTGATACTCCATC[A/G]TCCGCTAGATTATTTGATGCCATTGTTAGTGGTTG

Table A: Mapped markers of *F. iinumae* 21F2D map and comparison to *F. vesca* reference physical map

Sort	Fii LG	Bin	cM	Marker ID	Marker		Allele		*F. vesca* reference v1.1			Query Sequence
					Type	Class	0	2	PC	Start	Finish	
4,101	7	7010	51.53	89866898	F1Dsnp	PHR	T	C	7	19,442,148	+	GATGATCTCGATAGCGAAATTGGGAGTGGTGACTT[C/T]ATGAACTACACAGTGCACATACCTCCGACCCCAGA
4,102	7	7010	51.53	89810938	F1Dsnp	PHR	A	G	7	19,458,033	+	GCCAAAGAAATCAGCAACTCCAAGGATGCTAAAAA[A/G]GTGAGACCAATTTCGGGGTTTTTGTCAAGTTGGGT
4,103	7	7010	51.53	89810939	F1Dsnp	PHR	A	G	7	19,458,299	+	AAGCAAGAAGAGACGAGGCAGGTTGAGTTGTCTGC[A/G]AAGGAGGCAGAGTTTAAGGCAATGCAAGCTCAAGC
4,104	7	7010	51.53	89866899	F1Dsnp	PHR	T	C	7	19,458,329	+	TCTGCAAAGGAGGCAGAGTTTAAGGCAATGCAAGC[C/T]CAAGCGGAATCTGTGAGTTTTGTAGTTATTTCTTC
4,105	7	7010	51.53	TP1416	GBS				7	19,462,340	19,462,399	TGCAGAGAATTGAATTCGAAAAGCGATATACAGATCCCTAGTAGCAGATAAACGTAAATCAATA
4,106	7	7010	51.53	TP7705	GBS				7	19,475,403	19,475,362	TGCAGTAAACTTGGAGAGTTAAATAAAGCGTGGAAACAGTAAAAATTGAAGCCGAGTGAGAGTT
4,107	7	7010	51.53	89810940	F1Dsnp	PHR	A	G	7	19,511,346	+	GACTATGCCAGGAATTTGCCTGATGCTAGAGAGTC[A/G]GAAGTTTTATCGCTTTTTGCCACAATTATTAACAA
4,108	7	7010	51.53	89810941	F1Dsnp	PHR	A	G	7	19,512,615	+	ACATTTAAGGATCACATCCGAGACTTTCTAGTGCA[A/G]TCTAAAGAGTTTTCAGCACAGGTATGATGCTACAA
4,109	7	7010	51.53	89810942	F1Dsnp	PHR	A	G	7	19,520,769	+	CAGCCTCAAATGTTTAAGAACATGAGAGCTGATCT[A/G]GCTTCCATGTGGAGCTCTAGCAGCAAAGTAGGAAA
4,110	7	7010	51.53	89810943	F1Dsnp	PHR	A	G	7	19,556,446	+	GCAAACACCTTAAGGTCCTTCACAAGAATTTCAAC[A/G]GCCTTCGCCCTATCCTGCCTGAAAGCAGAAAATTG

APPENDIX B

21F2D MAP POSITIONS AND SEGREGRATION DATA

Table B: *F. iinumae* F1D segregation data for the 21F2D map. The *F. iinumae* map includes Array and GBS markers for the 21 F2Ds. Each bin comprises markers that co-segregate without recombination. The locus column includes the bin name followed by a '–' and the number of markers in the corresponding bin. The map positions are given in centi-Morgans, cM. The parents genotypes 0, 1, 2 are the Affymetrix genotype calls for AA, AB, BB respectively.

The F2Ds genotypic calls are in JoinMap code for an F2 mapping population. The cells are colored as follows: the a's are yellow, the b's are white, the h's are green, and the missing data are white.

Table B: *F. iinumae* F1D segregation data for the 21F2D map.

Sort	LG	Bin	cM	Locus	Parents			F2D Plants																		
					J17	J4	F1D	1	5	9	13	21	25	29	33	37	41	45	49	53	57	61	65	69	73	77	81	17
1	1	1015	0.00	B1015-23	2	1	1	a	b	h	h	a	h	b	b	a	b	b	h	h	h	a	b	h	h	h	h	b
2	1	1017	2.44	B1017-5	2	0	1	a	b	h	h	a	h	b	b	a	b	b	h	a	h	a	b	h	h	h	h	b
3	1	1014	4.88	B1014-16				a	b	h	h	a	b	b	b	a	b	b	h	a	h	a	b	h	h	h	h	b
4	1	1018	7.32	B1018-6	0	2	1	a	b	h	a	a	b	b	b	a	b	b	h	a	h	a	b	h	h	h	h	b
5	1	1013	9.76	B1013-17	0	2	1	a	b	h	a	a	h	b	b	a	b	b	h	a	h	a	b	h	h	h	h	b
6	1	1012	14.76	B1012-24	0	2	1	a	b	b	a	a	h	b	b	a	b	b	h	h	h	a	b	h	h	h	h	b
7	1	1019	17.20	B1019-3	2	1	1	a	b	b	a	a	h	b	b	h	b	b	h	h	h	a	b	h	h	h	h	b
8	1	1020	19.67	B1020-9	2	0	1	a	b	b	a	a	h	b	b	h	b	h	h	h	h	a	b	h	h	h	h	b
9	1	1001	22.16	B1001-10	0	2	1	a	b	b	a	a	h	b	b	h	b	h	h	h	h	a	b	h	h	h	h	h
10	1	1002	24.65	B1002-5	0	2	1	a	b	h	a	a	h	b	b	h	b	h	h	h	h	a	b	h	h	h	h	h
11	1	1003	27.11	B1003-6	2	1	1	a	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	h	h	h	h	h
12	1	1004	29.55	B1004-5	2	0	1	a	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	b	h	h	h	h
13	1	1005	31.99	B1005-44	0	1	1	h	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	b	h	h	h	h
14	1	1006	36.99	B1006-34	0	2	1	b	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	h	h	h	h	h
15	1	1007	39.43	B1007-64	2	0	1	b	b	h	a	a	h	b	b	h	h	h	h	h	h	h	b	h	h	h	h	h
16	1	1008	41.90	B1008-20	0	2	1	b	b	h	a	h	h	b	b	h	h	h	h	h	h	h	b	h	h	h	h	h
17	1	1009	44.36	B1009-16	2	0	1	b	b	h	a	b	h	b	b	h	h	h	h	h	h	h	b	h	h	h	h	h
18	1	1010	46.80	B1010-16	0	1	1	b	b	h	a	b	h	b	h	h	h	h	h	h	h	h	b	h	h	h	h	h
19	1	1011	49.32	B1011-148	2	1	1	h	b	h	a	b	h	b	h	h	h	h	h	h	h	h	b	h	h	h	h	h
20	2	2013	0.00	B2013-3				b	h	b	h	h	b	a	b	h	h	h	a	h	b	h	h	a	h	h	a	b
21	2	2008	2.49	B2008-74	0	2	1	b	h	b	h	h	b	a	b	h	h	h	a	h	b	h	h	a	h	a	a	b
22	2	2001	4.98	B2001-64	2	0	1	b	h	b	h	h	b	a	b	h	h	a	a	h	b	h	h	a	h	a	a	b
23	2	2012	7.42	B2012-104	2	0	1	b	h	b	h	h	b	a	b	h	h	a	a	h	b	h	h	a	h	h	a	b
24	2	2010	9.86	B2010-69	2	1	1	b	h	b	h	h	b	a	b	h	a	a	a	h	b	h	h	a	h	h	a	b
25	2	2014	12.30	B2014-18	2	1	1	b	h	b	h	h	b	a	b	h	a	a	a	h	b	h	h	h	h	h	a	b
26	2	2009	17.30	B2009-29	0	2	1	b	h	b	h	h	b	a	b	h	a	a	a	h	b	b	h	a	h	h	a	b
27	2	2011	19.74	B2011-19	0	1	1	h	h	b	h	h	b	a	b	h	a	a	a	h	b	b	h	a	h	h	a	b
28	2	2004	22.18	B2004-66	0	1	1	h	h	b	h	h	b	a	b	h	a	a	a	h	b	b	h	a	h	h	h	b
29	2	278	24.65	B278-2	2	1	1	a	h	b	h	h	b	a	b	h	a	a	a	h	b	b	h	a	h	h	h	b
30	2	276	27.09	B276-3	2	1	1	a	h	b	h	b	b	a	b	h	a	a	a	h	b	b	h	a	h	h	h	b
31	2	2007	29.52	B2007-19	0	2	1	a	h	b	h	b	b	a	b	h	a	h	a	h	b	b	h	a	h	h	h	b
32	2	2006	31.96	B2006-23	2	0	1	a	h	b	b	b	b	a	b	h	a	h	a	h	b	b	h	a	h	h	h	b
33	2	264	34.40	B264-8	0	2	1	a	h	b	b	b	h	a	b	h	a	h	a	h	b	b	h	a	h	h	h	b
34	2	2005	42.22	B2005-15	2	0	1	a	h	h	b	b	h	a	h	h	a	h	a	b	b	b	h	a	h	h	h	b
35	2	307	44.66	B307-3	0	1	1	a	h	h	b	b	h	a	h	h	a	h	a	b	b	b	h	a	h	h	b	b
36	2	2017	47.13	B2017-10	0	1	1	a	b	h	b	b	h	a	h	h	a	h	a	b	b	b	h	a	h	h	b	b
37	2	2016	49.59	B2016-5	0	1	1	a	b	h	b	b	h	a	h	h	a	h	a	b	h	b	h	a	h	h	b	b
38	2	2002	54.60	B2002-25	2	0	1	a	b	h	b	b	h	a	h	a	a	h	a	b	h	b	h	a	h	h	b	h
39	2	215	57.03	B215-1	2	0	1	a	b	h	b	b	h	a	h	a	a	b	a	b	h	b	h	a	h	h	b	h
40	2	2003	59.50	B2003-30	2	0	1	a	b	h	b	b	h	a	h	a	a	b	a	b	a	b	h	a	h	h	b	h
41	3	3007	0.00	B3007-21	0	2	1	h	b	b	a	h	h	a	a	a	h	b	a	b	h	h	b	h	b	h	h	b
42	3	496	2.47	B496-1	0	2	1	h	b	b	a	h	h	a	a	a	b	b	a	b	h	h	b	h	b	h	h	b
43	3	TP6259	7.47	TP6259				h	b	b	a	h	h	a	a	a	b	b	a	b	b	a	b	h	b	h	h	b
44	3	495	9.91	B495-3	1	1	1	h	b	b	a	h	h	a	a	a	b	b	a	b	b	a	h	h	b	h	h	b
45	3	498	12.35	B498-2	0	1	1	h	b	b	a	h	h	h	a	a	b	b	a	b	b	a	h	h	b	h	h	b
46	3	3014	14.81	B3014-4	1	2	1	h	b	b	a	h	h	h	a	a	b	b	a	b	b	a	h	h	h	h	h	b
47	3	3013	17.25	B3013-6	1	2	1	h	b	b	a	h	h	h	a	h	b	b	a	b	b	a	h	h	h	h	h	b
48	3	3006	19.77	B3006-5	0	1	1	h	b	b	a	h	b	h	a	h	b	b	a	b	b	a	h	h	h	h	h	b
49	3	505	37.74	B505-2	2	1	1	h	b	b	h	h	b	h	a	h	h	b	a	b	b	h	h	h	h	h	a	h
50	3	3008	40.28	B3008-24	2	0	1	h	b	b	h	h	b	h	a	h	h	b	a	b	h	h	h	h	h	h	a	h
51	3	507	42.84	B507-8	2	0	1	h	b	b	h	h	b	h	a	h	h	b	a	b	h	h	h	h	h	h	h	h
52	3	TP3055	45.41	TP3055				h	h	b	h	h	b	h	a	h	h	b	a	b	h	h	h	h	h	h	h	h
53	3	1_1627828	47.97	1_1627828				h	h	b	h	h	b	b	a	h	h	b	a	b	h	h	h	h	h	h	h	h
54	3	3009	53.61	B3009-22	0	2	1	a	h	b	h	h	b	b	a	b	h	b	a	b	h	h	h	h	h	h	h	h
55	3	3010	56.15	B3010-16	0	2	1	a	a	b	h	h	b	b	a	b	h	b	a	b	h	h	h	h	h	h	h	h

Table B: *F. iinumae* F1D segregation data for the 21F2D map.

Sort	LG	Bin	cM	Locus	Parents			F2D Plants																			
					J17	J4	F1D	1	5	9	13	21	25	29	33	37	41	45	49	53	57	61	65	69	73	77	81	17
56	3	3019	58.66	B3019-1				a	a	b	h	h	b	b	a	b	h	h	a	b	h	h	h	h	h	h	h	h
57	3	3001	61.30	B3001-34	2	0	1	a	a	b	h	h	h	b	a	b	h	h	a	b	h	h	h	h	h	h	h	h
58	3	149	63.82	B149-1	2	0	1	a	a	b	h	h	h	b	a	b	h	h	a	b	h	h	h	h	h	a	h	h
59	3	3018	66.46	B3018-8	2	1	1	a	a	b	h	h	h	b	a	b	h	h	a	b	h	h	a	h	h	a	h	h
60	3	3017	68.92	B3017-2	2	0	1	a	a	b	h	h	h	b	a	b	h	h	h	b	h	h	a	h	h	a	h	h
61	3	3015	71.41	B3015-30	2	0	1	a	a	b	h	h	h	b	a	b	h	h	h	h	h	h	a	h	h	a	h	h
62	3	3016	73.90	B3016-5	0	1	1	a	a	b	h	b	h	b	a	b	h	h	h	h	h	h	a	h	h	a	h	h
63	3	3002	76.37	B3002-67	2	0	1	a	a	b	h	b	h	b	a	b	h	h	h	h	h	h	a	h	h	h	h	h
64	3	3003	78.88	B3003-252				a	a	b	h	b	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h
65	3	3004	83.99	B3004-45	0	2	1	a	a	b	h	a	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h
66	3	3005	86.46	B3005-46	2	0	1	a	a	b	h	a	h	b	h	b	h	h	h	h	h	h	a	h	h	h	a	h
67	3	3012	88.94	B3012-17	0	2	1	a	a	h	h	a	h	b	h	b	h	h	h	h	h	h	a	h	h	h	a	h
68	3	3011	91.41	B3011-8	0	1	1	a	a	h	h	a	h	b	h	b	h	h	h	h	b	h	a	h	h	h	a	h
69	3	3020	96.52	B3020-4	0	2	1	a	a	h	h	a	h	b	h	b	h	h	h	a	b	h	h	h	h	h	a	h
70	3	186	98.98	B186-10	2	0	1	a	a	h	h	a	h	b	h	b	a	h	h	a	b	h	h	h	h	h	a	h
71	4	4001	0.00	B4001-133	2	0	1	h	a	h	a	b	b	a	a	h	h	h	a	b	h	h	h	h	b	b	h	a
72	4	4002	2.44	B4002-99	0	2	1	a	a	h	a	b	b	a	a	h	h	h	a	b	h	h	h	h	b	b	h	a
73	4	4004	4.88	B4004-73	0	2	1	a	h	h	a	b	b	a	a	h	h	h	a	b	h	h	h	h	b	b	h	a
74	4	4007	7.32	B4007-78	0	2	1	a	h	h	a	b	b	a	a	h	h	h	a	b	h	b	h	h	b	b	h	a
75	4	4023	15.03	B4023-4				a	b	h	a	b	b	a	a	h	b	h	a	b	h	b	h	h	h	b	h	a
76	4	4012	17.47	B4012-3				a	b	h	a	b	b	a	a	h	b	h	h	b	h	b	h	h	h	b	h	a
77	4	4019	22.50	B4019-3				a	b	h	h	b	b	a	a	h	b	h	h	h	h	b	h	h	h	b	h	a
78	4	4021	27.55	B4021-3	0	1	1	a	b	h	h	b	b	a	a	h	b	b	h	h	h	b	h	h	h	b	h	h
79	4	4011	35.40	B4011-1				a	b	h	h	b	b	h	h	h	b	h	h	h	h	b	h	h	h	b	h	h
80	4	4008	40.48	B4008-18	0	2	1	a	b	h	h	b	b	h	h	h	b	b	b	h	h	b	h	h	h	b	h	h
81	4	225	45.54	B225-4	0	2	1	a	b	h	h	b	b	h	h	h	b	b	b	h	a	b	a	h	h	b	h	h
82	4	4010	47.98	B4010-4	0	2	1	a	b	h	h	b	b	b	h	h	b	b	b	h	a	b	a	h	h	b	h	h
83	4	4018	50.42	B4018-9	2	0	1	a	b	h	h	h	b	b	h	h	b	b	b	h	a	b	a	h	h	b	h	h
84	4	4006	52.88	B4006-10	2	1	1	a	b	h	h	h	b	b	h	h	b	b	b	a	a	b	a	h	h	b	h	h
85	4	4013	53.70	B4013-8	2	1	1	a	h	h	h	h	b	b	h	h	b	b	b	a	a	b	a	h	h	b	b	h
86	4	328	55.40	B328-18	0	2	1	a	h	h	h	h	b	b	h	h	b	b	b	a	a	b	a	h	h	b	h	h
87	4	4003	60.40	B4003-16	2	0	1	a	h	h	h	h	b	b	h	h	b	b	b	a	a	b	a	h	h	b	b	b
88	5	5030	0.00	B5030-6	0	2	1	h	h	h	h	h	h	a	h	h	h	a	h	h	a	h	a	b	h	h	a	b
89	5	5031	2.44	B5031-8	0	1	1	h	h	h	h	h	h	a	h	h	h	a	h	b	a	h	a	b	h	h	a	b
90	5	5032	4.88	B5032-18	0	1	1	h	h	h	h	h	h	a	h	h	h	a	h	b	a	h	h	b	h	h	a	b
91	5	683	15.80	B683-1	0	2	1	h	h	h	h	b	h	a	h	h	h	a	a	b	a	h	h	b	h	h	h	h
92	5	5011	18.24	B5011-9	0	1	1	h	h	b	h	b	h	a	h	h	h	a	a	b	a	h	h	b	h	h	h	h
93	5	5033	20.68	B5033-5	2	0	1	b	h	b	h	b	h	a	h	h	h	a	a	b	a	h	h	b	h	h	h	h
94	5	426	25.73	B426-4	0	2	1	b	h	h	h	b	h	a	h	h	h	a	a	b	a	h	h	h	h	h	h	h
95	5	5001	28.20	B5001-2	0	2	1	b	h	h	h	b	h	a	h	h	h	h	a	b	a	h	h	h	h	h	h	h
96	5	428	30.74	B428-1	0	2	1	b	h	h	h	h	h	a	h	h	h	h	a	b	a	h	h	h	h	h	h	h
97	5	5002	33.18	B5002-18	0	2	1	b	b	h	h	h	h	a	h	h	h	h	a	b	a	h	h	h	h	h	h	h
98	5	5003	35.72	B5003-20	0	2	1	b	b	h	h	h	h	a	h	h	h	h	a	b	a	h	b	h	h	h	h	h
99	5	372	38.21	B372-7	0	2	1	b	b	h	h	h	h	a	h	h	a	h	a	b	a	h	b	h	h	h	h	h
100	5	5004	40.75	B5004-8	2	0	1	b	b	h	h	h	h	a	h	h	a	h	a	b	h	h	b	h	h	h	h	h
101	5	5005	45.94	B5005-42	0	2	1	b	b	h	h	h	h	a	h	h	a	h	a	b	b	b	b	h	h	h	h	h
102	5	5006	48.43	B5006-10	0	2	1	b	b	h	h	h	h	h	h	h	a	h	a	b	b	b	b	h	h	h	h	h
103	5	5007	50.89	B5007-15	2	1	1	b	b	h	h	h	h	h	h	h	h	h	a	b	b	b	b	h	h	h	h	h
104	5	5034	53.35	B5034-46	2	0	1	b	b	h	h	h	h	h	h	h	h	b	a	b	b	b	b	h	h	h	h	h
105	5	388	55.79	B388-3	2	0	1	b	b	h	h	h	h	h	h	h	h	b	a	h	b	b	b	h	h	h	h	h
106	5	5018	58.31	B5018-99	0	2	1	b	b	h	h	h	h	h	h	b	h	b	a	h	b	b	b	h	h	h	h	h
107	5	5014	60.75	B5014-35	0	1	1	b	b	h	h	h	h	h	h	b	h	b	a	h	b	b	b	a	h	h	h	h
108	5	5016	63.29	B5016-22	0	2	1	b	b	h	h	h	h	h	a	b	h	b	a	h	b	b	b	a	h	h	h	h
109	5	5022	65.75	B5022-16	2	0	1	b	b	h	h	h	h	h	a	b	h	b	a	h	b	b	b	a	a	h	h	h
110	5	5029	68.24	B5029-167	1	2	1	b	b	h	b	h	h	h	a	b	h	b	a	h	b	b	b	a	a	h	h	h

Table B: *F. iinumae* F1D segregation data for the 21F2D map.

Sort	LG	Bin	cM	Locus	Parents			F2D Plants																		
					J17	J4	F1D	1	5	9	13	21	25	29	33	37	41	45	49	53	57	61	65	69	73	77	81	17
111	6	346	0.00	B346-12	2	1	1	b	a	h	a	a	a	h	h	a	a	h	h	b	h	b	b	a	a	a	b	b
112	6	6011	2.44	B6011-14	0	1	1	b	a	b	a	a	a	h	h	a	a	h	h	b	h	b	b	a	a	a	b	b
113	6	6002	4.93	B6002-12	0	2	1	b	a	b	a	a	a	a	h	a	a	h	h	b	h	b	b	a	a	a	b	b
114	6	343	7.37	B343-13	0	2	1	b	a	b	a	a	a	a	h	a	a	h	h	b	h	h	b	a	a	a	b	b
115	6	6017	9.83	B6017-7	2	0	1	b	a	b	a	a	a	a	h	a	a	h	h	b	h	h	b	a	a	a	b	h
116	6	6019	24.03	B6019-11	2	1	1	b	h	b	a	a	h	a	h	a	a	b	b	b	h	h	b	h	a	a	b	h
117	6	6004	29.11	B6004-13	2	0	1	b	h	b	h	a	h	a	h	a	a	b	b	b	h	h	b	h	h	a	b	h
118	6	6005	31.58	B6005-39	0	2	1	b	h	b	h	a	h	a	h	a	a	b	b	b	h	h	h	h	h	a	b	h
119	6	6007	34.07	B6007-11	0	2	1	b	h	b	h	a	h	a	h	a	a	b	h	b	h	h	h	h	h	a	b	h
120	6	6006	42.16	B6006-91	0	1	1	h	h	h	h	a	h	a	h	a	a	b	h	h	h	h	h	h	h	a	b	h
121	6	6009	44.70	B6009-386	0	2	1	h	h	h	h	a	h	a	h	a	a	b	h	h	h	h	h	h	h	h	b	h
122	6	6020	47.19	B6020-12	0	2	1	h	h	h	h	a	h	a	h	a	a	b	h	h	b	h	h	h	h	h	b	h
123	6	6014	49.68	B6014-95	2	1	1	h	h	h	h	a	h	a	h	h	a	b	h	h	b	h	h	h	h	h	b	h
124	6	6016	52.17	B6016-2	0	2	1	h	h	h	h	a	h	a	h	b	a	b	h	h	b	h	h	h	h	h	b	h
125	6	6021	54.66	B6021-5				h	h	h	h	a	a	a	h	b	a	b	h	h	b	h	h	h	h	h	b	h
126	6	658	57.20	658-1	1	2	1	h	h	h	h	a	a	h	h	b	a	b	h	h	b	h	h	h	h	h	b	h
127	6	6022	59.67	B6022-9	1	0	1	h	h	h	h	a	a	h	h	b	a	b	h	h	b	a	h	h	h	h	b	h
128	6	6010	62.18	B6010-50	2	0	1	h	h	h	h	a	a	h	h	b	a	b	h	h	b	a	a	h	h	h	b	h
129	6	6018	64.64	B6018-28	2	0	1	h	h	h	h	a	a	h	a	b	a	b	h	h	b	a	a	h	h	h	b	h
130	6	654	67.11	654-1	2	1	1	h	h	h	h	a	a	h	a	b	a	b	h	h	b	a	a	h	a	h	b	h
131	6	6013	69.57	B6013-6	0	2	1	h	h	h	h	a	a	h	a	b	a	b	h	h	b	a	a	h	a	a	b	h
132	6	6012	74.71	B6012-34	2	0	1	h	b	h	h	a	a	h	a	b	a	b	h	a	b	a	a	h	a	a	b	h
133	6	523	79.85	523-2	0	2	1	h	b	h	h	a	a	h	a	b	a	b	h	a	b	a	h	a	a	a	b	h
134	6	524	82.31	524-8	1	0	1	h	b	h	h	a	a	h	a	b	a	b	h	a	b	a	h	a	a	h	b	h
135	6	6008	87.60	6008-15	2	0	1	h	b	h	h	h	a	h	a	b	a	b	h	a	b	a	h	a	h	h	b	h
136	6	527	90.07	527-2	0	2	1	h	b	h	h	h	a	h	a	b	a	b	h	a	b	h	h	a	h	h	b	h
137	6	6015	98.17	B6015-43	0	1	1	h	b	h	h	h	a	h	a	b	a	b	h	a	h	h	h	a	h	h	h	b
138	7	7001	0.00	B7001-133	0	1	1	h	h	h	h	b	b	b	h	h	h	h	a	b	b	b	a	a	h	h	b	b
139	7	7018	2.44	B7018-11	2	0	1	h	h	h	h	b	b	b	b	h	h	h	a	b	b	b	a	a	h	h	b	b
140	7	7002	4.88	B7002-38	0	2	1	h	h	h	h	b	b	b	b	h	h	h	a	b	b	b	a	a	h	h	h	b
141	7	7003	7.32	B7003-39	2	0	1	h	h	h	b	b	b	b	b	h	h	h	a	b	b	b	a	a	h	h	h	b
142	7	7004	9.76	B7004-15	2	0	1	h	h	h	b	b	b	b	b	h	h	h	a	b	b	b	a	a	h	b	h	b
143	7	602	12.20	B602-1	0	2	1	h	h	h	b	b	b	b	b	h	h	h	a	b	b	b	a	a	h	b	b	b
144	7	7005	14.66	B7005-9	0	2	1	h	h	h	b	b	b	b	b	h	h	h	a	b	b	b	a	a	h	h	b	b
145	7	7006	17.10	B7006-16	2	1	1	h	h	h	b	b	b	b	b	h	b	h	a	b	b	b	a	a	h	h	b	b
146	7	7007	19.54	B7007-13	2	0	1	a	h	h	b	b	b	b	b	h	b	h	a	b	b	b	a	a	h	h	b	b
147	7	7008	21.98	B7008-29	2	0	1	a	h	h	b	b	b	b	b	h	b	h	a	b	b	h	a	a	h	h	b	b
148	7	7009	24.45	B7009-39	2	0	1	a	h	h	b	b	b	b	b	h	b	h	a	b	b	a	a	a	h	h	b	b
149	7	7017	26.88	B7017-6	0	2	1	a	h	b	b	b	b	b	b	h	b	h	a	b	b	a	a	a	h	h	b	b
150	7	262	29.32	B262-3	2	1	1	a	h	b	b	b	b	b	b	b	b	h	a	b	b	a	a	a	h	h	b	b
151	7	7016	31.76	B7016-4	2	1	1	a	h	b	b	b	h	b	b	b	b	h	a	b	b	a	a	a	h	h	b	b
152	7	7015	34.20	B7015-16	2	1	1	a	h	b	b	b	h	b	h	b	b	h	a	b	b	a	a	a	h	h	b	b
153	7	267	36.67	B267-15	2	0	1	a	h	b	b	b	h	b	h	b	b	h	a	b	h	a	a	a	h	h	b	b
154	7	7013	39.11	B7013-19	2	0	1	a	h	b	b	b	h	b	h	b	b	h	a	h	h	a	a	a	h	h	b	b
155	7	7012	41.55	B7012-5				a	h	b	b	b	h	b	h	b	b	h	h	h	h	a	a	a	h	h	b	b
156	7	7011	43.99	B7011-5				a	h	b	b	b	h	b	h	b	b	h	h	h	h	a	a	a	b	h	b	b
157	7	274	49.02	B274-2	0	2	1	a	h	b	b	b	h	b	h	b	b	h	h	h	h	a	a	a	b	h	h	h
158	7	7010	51.53	B7010-16	2	0	1	a	h	b	b	b	h	b	h	b	b	h	h	h	a	a	a	a	b	h	h	h

APPENDIX C

F. iinumae 85F2D MAP POSITIONS AND SEGREGRATION DATA

Table C: *F .iinumae* F1D segregation data for the 85F2D map. This *F. iinumae* map includes only GBS markers for the 85 F2Ds. Each bin comprises markers that co-segregate without recombination. The locus column includes the bin name followed by a dash '–' and the number of markers in the corresponding bin. The map positions are given in centi-Morgans, cM. The parents genotypes 0, 1, 2 are the Affymetrix genotype calls for AA, AB, BB respectively.

The F2Ds genotypic calls are in JoinMap code for an F2 mapping population. The cells are colored as follows: the a's are yellow, the b's are white, the h's are green, and the missing data are white.

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	1	5	9	13	21	25	29	33	37	41	45	49	53	57	61	65	69	73	77	81	17	2	3	4	6	7	8	10	11	12	14	15
1	1	B1015-3	0.00	a	b	h	h	a	h	b	b	a	b	h	h	h	h	a	b	h	h	h	h	b	b	h	h	h	b	b	b	h	h	a	h
2	1	B1017-2	2.43	a	b	h	h	a	h	b	b	a	b	b	h	a	h	a	b	h	h	h	h	b	b	h	h	b	b	b	b	h	h	a	h
3	1	B1014-3	5.49	a	b	h	h	a	b	b	b	a	b	b	h	a	h	a	b	h	h	h	h	b	b	h	h	b	b	b	b	h	h	h	h
4	1	B1018-1	9.18	a	b	h	a	a	b	b	b	a	b	b	h	a	h	a	b	h	h	h	h	b	b	a	a	b	b	b	b	a	b	h	h
5	1	B1013b-1	11.61	a	b	h	a	a	h	b	b	a	b	b	h	a	h	a	b	h	h	h	h	b	b	a	a	b	b	b	b	a	b	h	h
6	1	B1013a-2	12.21	a	b	h	a	a	h	b	b	a	b	b	h	a	h	a	b	h	h	h	h	b	b	a	a	b	b	b	b	a	b	h	h
7	1	B1012c-4	19.51	a	b	b	a	a	h	b	b	a	b	b	h	h	h	a	b	h	h	h	h	b	h	a	a	b	b	b	b	a	b	h	h
8	1	B1012b-1	20.11	a	b	b	a	a	h	b	b	a	b	b	h	h	h	a	b	h	h	h	h	b	h	a	a	b	b	b	b	a	b	h	h
9	1	B1012a-1	20.70	a	b	b	a	a	h	b	b	a	b	b	h	h	h	a	b	h	h	h	h	b	h	a	a	b	b	b	b	a	b	h	h
10	1	B1019-1	21.29	a	b	b	a	a	h	b	b	h	b	b	h	h	h	a	b	h	h	h	h	b	h	a	a	b	b	b	b	a	b	h	h
11	1	B1020b-2	21.88	a	b	b	a	a	h	b	b	h	b	h	h	h	h	a	b	h	h	h	h	b	h	a	a	b	b	b	b	a	b	h	h
12	1	B1020a-4	23.98	a	b	b	a	a	h	b	b	h	b	h	h	h	h	a	b	h	h	h	h	h	h	a	a	b	b	b	h	a	b	h	h
13	1	B1001-1	26.09	a	b	b	a	a	h	b	b	h	b	h	h	h	h	a	b	h	h	h	h	h	h	a	a	b	b	b	h	a	b	h	b
14	1	B1002-1	26.68	a	b	h	a	a	h	b	b	h	b	h	h	h	h	a	b	h	h	h	h	h	h	a	a	b	b	b	h	a	b	h	b
15	1	B1003-3	27.87	a	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	h	h	h	h	h	h	a	a	b	b	b	h	a	b	h	b
16	1	B1004-1	28.46	a	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	b	h	h	h	h	h	a	a	b	b	b	h	a	b	h	b
17	1	B1005a-1	29.06	h	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	b	h	h	h	h	h	a	a	b	b	b	h	a	b	h	b
18	1	B1005b-1	29.65	h	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	b	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
19	1	B1005c-2	30.24	h	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	b	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
20	1	B1005d-5	30.83	h	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	b	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
21	1	B1006a-1	32.63	b	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
22	1	B1006b-1	34.43	b	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
23	1	B1006c-2	36.84	b	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
24	1	B1006d-6	38.03	b	b	h	a	a	h	b	b	h	h	h	h	h	h	a	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
25	1	B1007a-4	38.62	b	b	h	a	a	h	b	b	h	h	h	h	h	h	h	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
26	1	B1007b-16	39.21	b	b	h	a	a	h	b	b	h	h	h	h	h	h	h	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
27	1	B1008a-2	41.01	b	b	h	a	h	h	b	b	h	h	h	h	h	h	h	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
28	1	B1008b-4	42.84	b	b	h	a	h	h	b	b	h	h	h	h	h	h	h	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
29	1	B1009-3	43.44	b	b	h	a	b	h	b	b	h	h	h	h	h	h	h	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
30	1	B1010-4	44.63	b	b	h	a	b	h	b	h	h	h	h	h	h	h	h	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
31	1	B1011b-16	45.83	h	b	h	a	b	h	b	h	h	h	h	h	h	h	h	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
32	1	B1011a-15	46.42	h	b	h	a	b	h	b	h	h	h	h	h	h	h	h	b	h	h	h	h	h	h	a	a	h	b	b	h	a	b	h	b
33	2	B2013-3	0.00	b	h	b	h	h	b	a	b	h	h	h	a	h	b	h	h	a	h	h	a	b	h	h	h	h	b	b	b	h	h	h	b
34	2	B2008-22	1.20	b	h	b	h	h	b	a	b	h	h	h	a	h	b	h	h	a	h	a	a	b	h	h	h	h	b	b	b	h	h	h	b
35	2	B2001-11	2.39	b	h	b	h	h	b	a	b	h	h	a	a	h	b	h	h	a	h	a	a	b	h	h	h	h	b	b	b	h	h	h	b
36	2	B2012-27	2.99	b	h	b	h	h	b	a	b	h	h	a	a	h	b	h	h	a	h	h	a	b	h	h	h	h	b	b	b	h	h	h	b
37	2	B2010a-12	3.58	b	h	b	h	h	b	a	b	h	a	a	a	h	b	h	h	a	h	h	a	b	h	h	h	h	b	b	b	h	h	h	b
38	2	B2010b-4	5.40	b	h	b	h	h	b	a	b	h	a	a	a	h	b	h	h	a	h	h	a	b	h	h	h	h	b	b	b	h	h	b	b
39	2	B2014-4	6.01	b	h	b	h	h	b	a	b	h	a	a	a	h	b	h	h	h	h	h	a	b	h	h	h	h	b	b	b	h	h	b	b
40	2	B2009a-7	7.85	b	h	b	h	h	b	a	b	h	a	a	a	h	b	b	h	a	h	h	a	b	h	h	h	h	b	b	b	h	h	b	b
41	2	B2009b-3	9.06	b	h	b	h	h	b	a	b	h	a	a	a	h	b	b	h	a	h	h	a	b	h	h	h	h	b	b	b	h	h	b	b
42	2	B2009c-2	9.65	b	h	b	h	h	b	a	b	h	a	a	a	h	b	b	h	a	h	h	a	b	h	h	h	h	b	b	b	h	h	b	b
43	2	B2011-3	10.25	h	h	b	h	h	b	a	b	h	a	a	a	h	b	b	h	a	h	h	a	b	h	h	h	h	b	b	b	h	h	b	b
44	2	B2004a-4	12.73	h	h	b	h	h	b	a	b	h	a	a	a	h	b	b	h	a	h	h	h	b	h	h	h	h	b	b	b	h	h	b	b
45	2	B2004b-2	13.92	h	h	b	h	h	b	a	b	h	a	a	a	h	b	b	h	a	h	h	h	b	h	h	h	h	b	b	b	h	h	b	b
46	2	B2004c-4	15.11	h	h	b	h	h	b	a	b	h	a	a	a	h	b	b	h	a	h	h	h	b	h	h	h	h	b	b	b	h	h	b	b
47	2	B2007c-1	22.88	a	h	b	h	b	b	a	b	h	a	h	a	h	b	b	h	a	h	h	h	b	h	h	h	h	b	b	b	h	h	b	b
48	2	B2007b-1	23.47	a	h	b	h	b	b	a	b	h	a	h	a	h	b	b	h	a	h	h	h	b	h	h	h	h	b	b	b	h	h	b	b
49	2	B2007a-1	24.06	a	h	b	h	b	b	a	b	h	a	h	a	h	b	b	h	a	h	h	h	b	h	h	h	h	b	b	b	h	h	b	b
50	2	B2006-5	28.36	a	h	b	b	b	b	a	b	h	a	h	a	h	b	b	h	a	h	h	h	b	h	h	h	h	b	b	b	b	h	b	h
51	2	B2005b-3	35.99	a	h	h	b	b	h	a	h	h	a	h	a	b	b	b	h	a	h	h	h	b	h	h	h	h	b	b	b	b	h	b	h
52	2	B2005a-2	36.59	a	h	h	b	b	h	a	h	h	a	h	a	b	b	b	h	a	h	h	h	b	h	b	h	h	b	b	b	b	h	b	h
53	2	B2017b-2	37.78	a	b	h	b	b	h	a	h	h	a	h	a	b	b	b	h	a	h	h	b	b	h	b	h	h	b	b	b	b	h	b	h
54	2	B2017a-2	38.37	a	b	h	b	b	h	a	h	h	a	h	a	b	b	b	h	a	h	h	b	b	h	b	h	h	b	b	b	b	h	b	h
55	2	B2016b-2	39.57	a	b	h	b	b	h	a	h	h	a	h	a	b	h	b	h	a	h	h	b	b	h	b	h	h	b	b	b	b	h	b	h
56	2	B2016a-1	40.16	a	b	h	b	b	h	a	h	h	a	h	a	b	h	b	h	a	h	h	b	b	h	b	h	h	b	b	b	b	h	b	h
57	2	B2002-3	46.58	a	b	h	b	b	h	a	h	a	a	h	a	b	h	b	h	a	h	h	b	h	h	b	h	b	b	b	b	b	h	b	h
58	2	B2003-3	54.54	a	b	h	b	b	h	a	h	a	a	b	a	b	a	b	b	a	h	h	b	h	h	b	h	b	b	h	b	b	h	b	h
59	3	B3007-3	0.00	h	b	b	a	h	h	a	a	a	h	b	a	b	h	h	b	h	b	h	h	b	h	a	a	h	b	a	h	a	h	h	h
60	3	TP6279	1.82	h	b	b	a	h	h	a	a	a	b	b	a	b	b	a	b	h	b	h	h	b	h	a	a	h	b	a	h	a	h	h	h

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	1	5	9	13	21	25	29	33	37	41	45	49	53	57	61	65	69	73	77	81	17	2	3	4	6	7	8	10	11	12	14	15
61	3	B3014b-1	5.54	h	b	b	a	h	h	h	a	a	b	b	a	b	b	a	h	h	h	h	h	b	h	a	a	h	b	a	h	a	h	h	h
62	3	B3014a-1	7.35	h	b	b	a	h	h	h	a	a	b	b	a	b	b	a	h	h	h	h	h	b	h	a	a	h	b	a	h	a	h	h	h
63	3	B3013-1	10.41	h	b	b	a	h	h	h	a	h	b	b	a	b	b	a	h	h	h	h	h	b	h	a	a	h	h	a	h	a	b	h	h
64	3	B3006-2	13.54	h	b	b	a	h	b	h	a	h	b	b	a	b	b	a	h	h	h	h	h	b	h	a	a	h	h	a	h	a	b	b	h
65	3	B3008b-2	21.59	h	b	b	h	h	b	h	a	h	h	b	a	b	h	h	h	h	h	h	a	h	h	h	a	h	h	a	h	h	b	b	h
66	3	B3008a-5	22.79	h	b	b	h	h	b	h	a	h	h	b	a	b	h	h	h	h	h	h	a	h	h	h	a	h	h	a	h	h	b	b	h
67	3	TP3055	27.85	h	h	b	h	h	b	h	a	h	h	b	a	b	h	h	h	h	h	h	h	h	h	h	a	h	h	a	h	h	b	b	h
68	3	1_1627828	28.45	h	h	b	h	h	b	b	a	h	h	b	a	b	h	h	h	h	h	h	h	h	h	h	a	h	h	a	h	h	b	b	h
69	3	B3009b-3	30.26	a	h	b	h	h	b	b	a	b	h	b	a	b	h	h	h	h	h	h	h	h	h	h	a	h	h	a	h	h	b	b	h
70	3	B3009a-1	30.85	a	h	b	h	h	b	b	a	b	h	b	a	b	h	h	h	h	h	h	h	h	h	h	h	h	h	a	h	h	b	b	h
71	3	B3010b-1	36.70	a	a	b	h	h	b	b	a	b	h	b	a	b	h	h	h	h	h	h	h	h	h	h	h	b	h	a	h	h	b	b	h
72	3	B3010a-2	39.15	a	a	b	h	h	b	b	a	b	h	b	a	b	h	h	h	h	h	h	h	h	h	h	h	b	h	a	h	h	b	b	h
73	3	B3019-1	40.35	a	a	b	h	h	b	b	a	b	h	h	a	b	h	h	h	h	h	h	h	h	h	h	h	b	h	a	h	h	b	b	h
74	3	B3001a-3	41.56	a	a	b	h	h	h	b	a	b	h	h	a	b	h	h	h	h	h	h	h	h	h	h	h	b	h	a	h	h	b	b	h
75	3	B3001b-3	43.40	a	a	b	h	h	h	b	a	b	h	h	a	b	h	h	h	h	h	h	h	h	h	h	h	b	h	a	h	h	h	b	h
76	3	B3018-2	45.23	a	a	b	h	h	h	b	a	b	h	h	a	b	h	h	a	h	h	a	h	h	h	h	h	b	h	a	h	h	h	b	h
77	3	B3017-1	46.44	a	a	b	h	h	h	b	a	b	h	h	h	b	h	h	a	h	h	a	h	h	h	h	h	b	h	a	h	h	h	b	h
78	3	B3015d-5	47.05	a	a	b	h	h	h	b	a	b	h	h	h	h	h	h	a	h	h	a	h	h	h	h	h	b	h	a	h	h	h	b	h
79	3	B3015c-1	47.65	a	a	b	h	h	h	b	a	b	h	h	h	h	h	h	a	h	h	a	h	h	h	h	h	b	h	a	h	h	h	b	h
80	3	B3015b-2	48.85	a	a	b	h	h	h	b	a	b	h	h	h	h	h	h	a	h	h	a	h	h	h	h	h	b	h	a	h	h	h	b	h
81	3	B3016-4	50.06	a	a	b	h	b	h	b	a	b	h	h	h	h	h	h	a	h	h	a	h	h	h	h	h	b	h	a	h	h	h	b	b
82	3	B3002a-6	51.26	a	a	b	h	b	h	b	a	b	h	h	h	h	h	h	a	h	h	h	h	h	h	h	h	b	h	a	h	h	h	b	b
83	3	B3002c-1	51.85	a	a	b	h	b	h	b	a	b	h	h	h	h	h	h	a	h	h	h	h	h	h	h	h	b	h	a	h	h	h	b	b
84	3	B3002b-4	53.04	a	a	b	h	b	h	b	a	b	h	h	h	h	h	h	a	h	h	h	h	h	h	b	h	b	h	a	h	h	h	b	b
85	3	B3003d-3	53.63	a	a	b	h	b	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h	h	b	h	b	h	a	h	h	h	b	b
86	3	B3003c-2	54.23	a	a	b	h	b	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h	a	b	h	b	h	a	h	h	h	b	b
87	3	B3003b-6	54.83	a	a	b	h	b	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h	a	b	h	b	h	a	h	h	h	b	b
88	3	B3003f-5	55.43	a	a	b	h	b	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h	a	b	h	b	h	a	h	h	h	b	b
89	3	B3003e-22	56.63	a	a	b	h	b	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h	a	b	h	b	h	a	h	h	h	b	b
90	3	B3003a-23	58.47	a	a	b	h	b	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h	a	b	h	b	h	a	h	h	h	b	b
91	3	B3004b-5	60.93	a	a	b	h	a	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h	a	b	h	b	h	a	h	h	h	b	b
92	3	B3004a-1	61.52	a	a	b	h	a	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h	a	b	h	b	h	a	h	h	h	b	b
93	3	B3004c-1	65.34	a	a	b	h	a	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h	a	b	h	b	h	a	h	h	h	b	b
94	3	B3004d-1	65.94	a	a	b	h	a	h	b	h	b	h	h	h	h	h	h	a	h	h	h	h	h	a	b	h	b	h	a	h	h	h	b	b
95	3	B3005a-7	67.14	a	a	b	h	a	h	b	h	b	h	h	h	h	h	h	a	h	h	h	a	h	a	b	h	b	h	a	h	h	h	b	b
96	3	B3005b-2	67.73	a	a	b	h	a	h	b	h	b	h	h	h	h	h	h	a	h	h	h	a	h	a	b	h	b	h	a	h	h	h	b	b
97	3	B3005c-7	69.53	a	a	b	h	a	h	b	h	b	h	h	h	h	h	h	a	h	h	h	a	h	a	b	h	b	h	a	h	h	h	b	b
98	3	B3012-1	71.98	a	a	h	h	a	h	b	h	b	h	h	h	h	h	h	a	h	h	h	a	h	a	b	h	h	h	a	b	h	h	b	b
99	3	B3011-3	73.78	a	a	h	h	a	h	b	h	b	h	b	h	h	b	h	a	h	h	h	a	h	a	b	h	h	h	a	b	h	h	b	b
100	3	B3020-1	74.97	a	a	h	h	a	h	b	h	b	h	b	h	a	b	h	h	h	h	h	a	h	a	b	h	h	h	a	b	h	h	b	b
101	4	B4001-29	0.00	h	a	h	a	b	b	a	a	h	h	h	a	b	h	h	h	h	b	b	h	a	a	b	b	h	a	h	b	a	b	a	b
102	4	B4002b-21	0.59	a	a	h	a	b	b	a	a	h	h	h	a	b	h	h	h	h	b	b	h	a	a	b	b	h	a	h	b	a	b	a	b
103	4	B4002a-3	1.78	a	a	h	a	b	b	a	a	h	h	h	a	b	h	h	h	h	b	b	h	a	a	b	b	h	a	h	b	a	b	a	b
104	4	B4004b-12	4.81	a	h	h	a	b	b	a	a	h	h	h	a	b	h	h	h	h	b	b	h	a	a	b	b	h	a	a	b	a	b	h	b
105	4	B4004a-10	5.41	a	h	h	a	b	b	a	a	h	h	h	a	b	h	h	h	h	b	b	h	a	a	b	b	h	a	a	b	a	b	a	b
106	4	B4007a-4	6.00	a	h	h	a	b	b	a	a	h	h	h	a	b	h	b	h	h	b	b	h	a	a	b	b	h	a	a	b	a	b	a	b
107	4	B4007b-5	7.19	a	h	h	a	b	b	a	a	h	h	h	a	b	h	b	h	h	b	b	h	a	a	b	b	h	a	a	b	a	b	a	b
108	4	B4007c-1	7.78	a	h	h	a	b	b	a	a	h	h	h	a	b	h	b	h	h	b	b	h	a	a	b	b	h	a	a	b	a	b	a	b
109	4	B4007d-1	8.37	a	h	h	a	b	b	a	a	h	h	h	a	b	h	b	h	h	b	b	h	a	a	b	b	h	h	a	b	a	b	a	b
110	4	B4007e-5	8.96	a	h	h	a	b	b	a	a	h	h	h	a	b	h	b	h	h	b	b	h	a	a	b	b	h	h	a	b	a	b	a	b
111	4	B4023-4	12.62	a	b	h	a	b	b	a	a	h	b	h	a	b	h	b	h	h	h	b	h	a	a	b	b	h	h	a	b	a	b	a	b
112	4	B4012-3	13.81	a	b	h	a	b	b	a	a	h	b	h	h	b	h	b	h	h	h	b	h	a	a	b	b	h	h	a	b	a	b	a	b
113	4	B4019-3	19.50	a	b	h	h	b	b	a	a	h	b	h	h	h	h	b	h	h	h	b	h	a	a	b	b	h	h	a	h	h	b	a	b
114	4	B4021-2	21.30	a	b	h	h	b	b	a	a	h	b	b	h	h	h	b	h	h	h	b	h	h	a	b	b	h	h	a	h	h	b	a	b
115	4	B4011-1	26.29	a	b	h	h	b	b	h	h	h	b	h	h	h	h	b	h	h	h	b	h	h	a	b	b	h	h	a	h	h	b	h	b
116	4	B4008a-5	28.70	a	b	h	h	b	b	h	h	h	b	b	b	h	h	b	h	h	h	b	h	h	a	b	b	h	h	a	h	h	b	h	b
117	4	B4008b-1	30.51	a	b	h	h	b	b	h	h	h	b	b	b	h	h	b	h	h	h	b	h	h	a	b	h	h	h	a	h	h	b	h	b
118	4	B4010-1	35.59	a	b	h	h	b	b	b	h	h	b	b	b	h	a	b	a	h	h	b	h	h	a	b	h	h	h	a	a	h	b	h	b
119	4	B4018-3	39.32	a	b	h	h	h	b	b	h	h	b	b	b	h	a	b	a	h	h	b	h	h	a	b	h	b	h	a	a	h	b	h	b
120	4	B4006b-1	46.11	a	b	h	h	h	b	b	h	h	b	b	b	a	a	b	a	h	h	b	h	h	a	b	h	b	h	a	a	h	b	h	b

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	1	5	9	13	21	25	29	33	37	41	45	49	53	57	61	65	69	73	77	81	17	2	3	4	6	7	8	10	11	12	14	15
121	4	B4006a-2	48.54	a	b	h	h	h	b	b	h	h	b	b	b	a	a	b	a	h	h	b	h	h	h	b	h	b	h	h	a	h	b	h	b
122	4	B4013-1	54.85	a	h	h	h	h	b	b	h	h	b	b	b	a	a	b	a	h	h	b	b	h	h	b	h	b	h	h	a	h	b	b	b
123	4	B4003b-2	57.26	a	h	h	h	h	b	b	h	h	b	b	b	a	a	b	a	h	h	b	b	b	h	b	h	b	h	h	a	h	b	b	b
124	4	B4003a-1	58.46	a	h	h	h	h	b	b	h	h	b	b	b	a	a	b	a	h	h	b	b	b	h	b	h	b	h	h	a	h	b	b	b
125	5	B5030-3	0.00	h	h	h	h	h	h	a	h	h	h	a	h	h	a	h	a	b	h	h	a	b	a	a	h	b	b	h	h	h	h	h	h
126	5	B5031-1	0.59	h	h	h	h	h	h	a	h	h	h	a	h	b	a	h	a	b	h	h	a	b	a	a	h	b	b	h	h	h	h	h	h
127	5	B5032a-1	1.18	h	h	h	h	h	h	a	h	h	h	a	h	b	a	h	h	b	h	h	a	b	a	a	h	b	b	h	h	h	h	h	h
128	5	B5032b-1	3.00	h	h	h	h	h	h	a	h	h	h	a	h	b	a	h	h	b	h	h	a	b	a	a	h	b	b	h	h	h	b	h	h
129	5	B5032c-1	7.37	h	h	h	h	h	h	a	h	h	h	a	h	b	a	h	h	b	h	h	a	b	a	a	h	b	b	h	b	h	b	h	h
130	5	B5011-2	14.53	h	h	b	h	b	h	a	h	h	h	a	a	b	a	h	h	b	h	h	h	h	a	a	h	b	b	h	b	h	b	h	h
131	5	B5033-1	17.25	b	h	b	h	b	h	a	h	h	h	a	a	b	a	h	h	b	h	h	h	h	a	a	a	b	b	h	b	h	b	h	h
132	5	B5001-1	20.01	b	h	h	h	b	h	a	h	h	h	h	a	b	a	h	h	h	h	h	h	h	a	a	a	b	b	h	b	h	b	h	h
133	5	B5002a-2	22.44	b	b	h	h	h	h	a	h	h	h	h	a	b	a	h	h	h	h	h	h	h	a	a	a	b	b	b	b	h	b	h	h
134	5	B5002b-1	29.66	b	b	h	h	h	h	a	h	h	h	h	a	b	a	h	h	h	h	h	h	h	h	a	a	b	b	b	h	h	b	h	b
135	5	B5003a-1	33.40	b	b	h	h	h	h	a	h	h	h	h	a	b	a	h	b	h	h	h	h	h	h	a	a	b	b	b	h	h	b	h	b
136	5	B5003b-3	34.60	b	b	h	h	h	h	a	h	h	h	h	a	b	a	h	b	h	h	h	h	h	h	a	a	b	b	b	h	h	b	h	b
137	5	B5004-5	37.03	b	b	h	h	h	h	a	h	h	a	h	a	b	h	h	b	h	h	h	h	h	h	a	a	b	b	b	h	h	b	h	b
138	5	B5005a-3	38.83	b	b	h	h	h	h	a	h	h	a	h	a	b	b	b	b	h	h	h	h	h	h	a	a	b	b	b	h	h	b	h	b
139	5	B5005b-1	41.28	b	b	h	h	h	h	a	h	h	a	h	a	b	b	b	b	h	h	h	h	h	h	a	a	b	h	b	h	h	b	h	b
140	5	B5005c-5	45.64	b	b	h	h	h	h	a	h	h	a	h	a	b	b	b	b	h	h	h	h	h	h	a	a	b	h	b	h	h	b	h	b
141	5	B5006-3	47.44	b	b	h	h	h	h	h	h	h	a	h	a	b	b	b	b	h	h	h	h	h	h	a	a	h	h	b	h	h	b	h	b
142	5	B5007b-1	48.63	b	b	h	h	h	h	h	h	h	h	h	a	b	b	b	b	h	h	h	h	h	h	a	a	h	h	b	h	h	b	h	b
143	5	B5007a-1	49.22	b	b	h	h	h	h	h	h	h	h	h	a	b	b	b	b	h	h	h	h	h	h	a	a	h	h	b	h	h	b	h	b
144	5	B5034d-4	50.42	b	b	h	h	h	h	h	h	h	h	b	a	b	b	b	b	h	h	h	h	h	h	a	a	h	h	b	h	h	b	h	b
145	5	B5034b-5	52.92	b	b	h	h	h	h	h	h	h	h	b	a	b	b	b	b	h	h	h	h	h	h	a	a	h	h	b	h	h	b	h	b
146	5	B5034a-1	54.11	b	b	h	h	h	h	h	h	h	h	h	a	b	b	b	b	h	h	h	h	h	h	a	a	h	h	b	h	h	b	h	b
147	5	B5018b-11	56.55	b	b	h	h	h	h	h	h	b	h	b	a	h	b	b	b	h	h	h	h	h	h	a	a	h	h	b	h	h	b	h	b
148	5	B5018a-7	57.14	b	b	h	h	h	h	h	h	b	h	b	a	h	b	b	b	h	h	h	h	h	h	a	a	h	h	b	h	h	b	h	b
149	5	B5018c-4	60.22	b	b	h	h	h	h	h	h	b	h	b	a	h	b	b	b	h	h	h	h	h	h	a	a	h	h	b	h	h	b	h	b
150	5	B5014a-4	61.42	b	b	h	h	h	h	h	h	b	h	b	a	h	b	b	b	a	h	h	h	h	h	a	a	h	h	b	h	h	b	h	b
151	5	B5014b-6	63.93	b	b	h	h	h	h	h	h	b	h	b	a	h	b	b	b	a	h	h	h	h	h	a	a	h	h	b	h	h	b	h	b
152	5	B5016-2	65.15	b	b	h	h	h	h	h	a	b	h	b	a	h	b	b	b	a	h	h	h	h	h	a	a	h	b	b	h	h	b	h	b
153	5	B5022b-4	65.74	b	b	h	h	h	h	h	a	b	h	b	a	h	b	b	b	a	a	h	h	h	h	a	a	h	b	b	h	h	b	h	b
154	5	B5022a-2	66.34	b	b	h	h	h	h	h	a	b	h	b	a	h	b	b	b	a	a	h	h	h	h	a	a	h	b	b	h	b	b	h	b
155	5	B5029-32	67.53	b	b	h	b	h	h	h	a	b	h	a	a	h	b	b	b	a	a	h	h	h	h	a	a	h	b	b	h	b	b	h	b
156	6	B6011b-1	0.00	b	a	b	a	a	a	h	h	a	a	h	h	b	h	b	b	a	a	a	b	b	b	h	a	h	b	b	h	a	b	h	a
157	6	B6011a-1	2.44	b	a	b	a	a	a	h	h	a	a	h	h	b	h	b	b	a	a	a	b	b	h	h	a	h	b	h	h	a	b	h	a
158	6	B6002a-2	6.85	b	a	b	a	a	a	a	h	a	a	h	h	b	h	b	b	a	a	a	b	b	h	h	a	h	b	h	h	a	b	h	a
159	6	B6002b-1	8.66	b	a	b	a	a	a	a	h	a	a	h	h	b	h	b	b	a	a	a	b	b	h	h	a	h	b	h	h	a	b	h	h
160	6	B6017-3	12.39	b	a	b	a	a	a	a	h	a	a	h	h	b	h	h	b	a	a	a	b	h	h	h	a	h	b	h	h	a	b	h	h
161	6	B6019-1	21.01	b	h	b	a	a	h	a	h	a	a	b	b	b	h	h	b	h	a	a	b	h	a	h	a	h	b	h	h	a	b	h	h
162	6	B6004-3	29.61	b	h	b	h	a	h	a	h	a	a	b	b	b	h	h	b	h	h	a	b	h	a	h	a	a	b	h	h	h	b	a	h
163	6	B6005-4	33.31	b	h	b	h	a	h	a	h	a	a	b	b	b	h	h	h	h	h	a	b	h	a	b	a	a	b	h	h	h	h	a	h
164	6	B6007-1	37.03	b	h	h	h	a	h	a	h	a	a	b	h	b	h	h	h	h	h	a	b	h	a	b	a	a	b	h	h	h	h	a	h
165	6	B6006a-2	40.09	h	h	h	h	a	h	a	h	a	a	b	h	h	h	h	h	h	h	a	b	h	a	b	a	a	b	h	h	h	h	a	h
166	6	B6006b-20	42.53	h	h	h	h	a	h	a	h	a	a	b	h	h	h	h	h	h	h	a	b	h	a	b	a	a	b	h	h	h	h	a	h
167	6	B6009c-46	44.34	h	h	h	h	a	h	a	h	a	a	b	h	h	h	h	h	h	h	h	b	h	a	b	b	a	b	h	h	h	h	a	h
168	6	B6009b-32	45.54	h	h	h	h	a	h	a	h	a	a	b	h	h	h	h	h	h	h	h	b	h	a	b	b	a	b	h	h	h	h	a	h
169	6	B6009a-3	46.73	h	h	h	h	a	h	a	h	a	a	b	h	h	h	h	h	h	h	h	b	h	a	b	b	a	b	h	h	h	h	a	h
170	6	B6020-1	47.92	h	h	h	h	a	h	a	h	a	a	b	h	h	b	h	h	h	h	h	b	h	a	b	b	a	b	h	h	h	h	a	h
171	6	B6014a-25	48.51	h	h	h	h	a	h	a	h	h	a	b	h	h	b	h	h	h	h	h	b	h	a	b	b	a	b	h	h	h	h	a	h
172	6	B6014b-1	49.70	h	h	h	h	a	h	a	h	h	a	b	h	h	b	h	h	h	h	h	b	h	a	b	b	a	b	h	h	h	h	a	h
173	6	B6014c-2	50.89	h	h	h	h	a	h	a	h	h	a	b	h	h	b	h	h	h	h	h	b	h	a	b	b	a	b	h	h	h	h	a	h
174	6	B6016-1	52.09	h	h	h	h	a	h	a	h	b	a	b	h	h	b	h	h	h	h	h	b	h	a	b	b	a	b	h	h	h	h	a	h
175	6	B6021-4	52.68	h	h	h	h	a	a	a	h	b	a	b	h	h	b	h	h	h	h	h	b	h	a	b	b	a	b	h	h	h	h	a	h
176	6	B6022-2	54.48	h	h	h	h	a	a	h	h	b	a	b	h	h	b	a	h	h	h	h	b	h	a	b	b	a	b	h	h	h	h	a	h
177	6	B6010a-5	57.52	h	h	h	h	a	a	h	h	b	a	b	h	h	b	a	a	h	h	h	b	h	a	b	b	a	b	h	h	h	b	a	h
178	6	B6010b-2	58.71	h	h	h	h	a	a	h	h	b	a	b	h	h	b	a	a	h	h	h	b	h	a	b	b	a	b	h	h	h	b	a	h
179	6	B6010c-2	59.30	h	h	h	h	a	a	h	h	b	a	b	h	h	b	a	a	h	h	h	b	h	h	b	b	a	b	h	h	h	b	a	h
180	6	B6010d-3	61.10	h	h	h	h	a	a	h	h	b	a	b	h	h	b	a	a	h	h	h	b	h	h	b	h	a	b	h	h	h	b	a	h

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	1	5	9	13	21	25	29	33	37	41	45	49	53	57	61	65	69	73	77	81	17	2	3	4	6	7	8	10	11	12	14	15
181	6	B6018a-3	62.29	h	h	h	h	a	a	h	a	b	a	b	h	h	b	a	a	h	h	h	b	h	h	b	h	a	b	h	h	h	b	a	h
182	6	B6018b-1	64.71	h	h	h	h	a	a	h	a	b	a	b	h	h	b	a	a	h	h	h	b	h	h	b	h	a	b	h	h	h	b	h	h
183	6	B6013-3	65.90	h	h	h	h	a	a	h	a	b	a	b	h	h	b	a	a	h	a	a	b	h	h	b	h	a	b	h	h	h	b	h	h
184	6	B6012a-3	68.98	h	b	h	h	a	a	h	a	b	a	b	h	a	b	a	a	h	a	a	b	h	h	b	h	a	b	h	h	h	b	h	h
185	6	B6012b-2	72.06	h	b	h	h	a	a	h	a	b	a	b	h	a	b	a	a	h	a	a	b	h	h	b	h	b	b	h	h	h	b	h	h
186	6	B6008-2	85.48	h	b	h	h	h	a	h	a	b	a	b	h	a	b	a	h	a	h	h	b	h	h	b	h	b	b	a	h	h	b	h	h
187	6	B6015-7	90.53	h	b	h	h	h	a	h	a	b	a	b	h	a	h	h	h	a	h	h	h	b	h	b	h	b	b	a	h	h	b	h	h
188	7	B7001e-3	0.00	h	h	h	h	b	b	b	h	h	h	h	a	b	b	b	a	a	h	h	b	b	a	h	h	h	h	b	a	h	h	b	a
189	7	B7001d-2	0.59	h	h	h	h	b	b	b	h	h	h	h	a	b	b	b	a	a	h	h	b	b	a	h	h	a	h	b	a	h	h	b	a
190	7	B7001c-8	1.18	h	h	h	h	b	b	b	h	h	h	h	a	b	b	b	a	a	h	h	b	b	a	h	h	a	h	b	a	h	h	b	a
191	7	B7001b-4	1.78	h	h	h	h	b	b	b	h	h	h	h	a	b	b	b	a	a	h	h	b	b	a	h	h	a	h	b	a	h	h	b	a
192	7	B7001a-7	2.98	h	h	h	h	b	b	b	h	h	h	h	a	b	b	b	a	a	h	h	b	b	a	h	h	a	h	b	h	h	h	b	a
193	7	B7018-2	4.78	h	h	h	h	b	b	b	b	h	h	h	a	b	b	b	a	a	h	h	b	b	a	h	h	a	h	b	h	h	h	b	a
194	7	B7002a-1	6.58	h	h	h	h	b	b	b	b	h	h	h	a	b	b	b	a	a	h	h	h	b	a	h	h	a	h	b	h	h	h	b	a
195	7	B7002b-1	7.77	h	h	h	h	b	b	b	b	h	h	h	a	b	b	b	a	a	h	h	h	b	a	h	h	a	h	b	h	h	h	b	a
196	7	B7002c-1	8.36	h	h	h	h	b	b	b	b	h	h	h	a	b	b	b	a	a	h	h	h	b	a	h	h	a	h	b	h	h	h	b	a
197	7	B7003-4	11.39	h	h	h	b	b	b	b	b	h	h	h	a	b	b	b	a	a	h	h	h	b	a	h	h	a	h	b	h	b	h	b	a
198	7	B7004-2	11.98	h	h	h	b	b	b	b	b	h	h	h	a	b	b	b	a	a	h	b	h	b	a	h	h	a	h	b	h	b	h	b	a
199	7	B7005-2	13.79	h	h	h	b	b	b	b	b	h	h	h	a	b	b	b	a	a	h	h	b	b	a	h	h	a	h	b	h	b	h	b	a
200	7	B7006a-1	14.38	h	h	h	b	b	b	b	b	h	b	h	a	b	b	b	a	a	h	h	b	b	a	h	h	a	h	b	h	b	h	b	a
201	7	B7006b-2	16.79	h	h	h	b	b	b	b	b	h	b	h	a	b	b	b	a	a	h	h	b	b	a	h	h	a	h	b	h	b	h	b	a
202	7	B7007a-1	17.38	a	h	h	b	b	b	b	b	h	b	h	a	b	b	b	a	a	h	h	b	b	a	h	h	a	h	b	h	b	h	b	a
203	7	B7007b-1	17.97	a	h	h	b	b	b	b	b	h	b	h	a	b	b	b	a	a	h	h	b	b	a	h	h	a	h	b	h	b	h	b	h
204	7	B7008a-2	22.28	a	h	h	b	b	b	b	b	h	b	h	a	b	b	h	a	a	h	h	b	b	a	a	h	a	h	b	h	b	h	b	h
205	7	B7008b-3	22.87	a	h	h	b	b	b	b	b	h	b	h	a	b	b	h	a	a	h	h	b	b	a	a	h	a	h	b	h	b	h	b	h
206	7	B7009a-1	24.08	a	h	h	b	b	b	b	b	h	b	h	a	b	b	a	a	a	h	h	b	b	h	a	h	a	h	b	h	b	h	b	h
207	7	B7009b-6	28.38	a	h	h	b	b	b	b	b	h	b	h	a	b	b	a	a	a	h	h	b	b	h	a	h	a	h	b	h	b	b	h	h
208	7	B7017a-1	30.80	a	h	b	b	b	b	b	b	h	b	h	a	b	b	a	a	a	h	h	b	b	h	a	h	a	h	h	h	b	b	h	h
209	7	B7017b-3	31.99	a	h	b	b	b	b	b	b	h	b	h	a	b	b	a	a	a	h	h	b	b	h	a	h	a	h	h	h	b	b	h	h
210	7	B7016-1	34.41	a	h	b	b	b	h	b	b	b	b	h	a	b	b	a	a	a	h	h	b	b	h	a	h	a	h	h	h	b	b	h	h
211	7	B7015-3	35.61	a	h	b	b	b	h	b	h	b	b	h	a	b	b	a	a	a	h	h	b	b	h	a	h	a	h	h	b	b	b	h	h
212	7	B7013a-1	48.25	a	h	b	b	b	h	b	h	b	b	h	a	h	h	a	a	a	h	h	b	b	h	a	h	a	h	h	b	b	b	h	h
213	7	B7013b-2	48.84	a	h	b	b	b	h	b	h	b	b	h	a	h	h	a	a	a	h	h	b	b	h	a	h	a	h	h	b	b	b	h	h
214	7	B7012b-1	50.04	a	h	b	b	b	h	b	h	b	b	h	h	h	h	a	a	a	h	h	b	b	h	a	h	a	h	h	b	b	b	h	h
215	7	B7012a-2	51.23	a	h	b	b	b	h	b	h	b	b	h	h	h	h	a	a	a	h	h	b	b	h	a	h	a	h	h	b	b	b	h	h
216	7	B7011-1	52.43	a	h	b	b	b	h	b	h	b	b	h	h	h	h	a	a	a	b	h	b	b	h	a	h	a	h	a	b	b	b	h	h
217	7	B7010-2	55.50	a	h	b	b	b	h	b	h	b	b	h	h	h	a	a	a	a	b	h	h	h	h	a	h	a	h	a	b	b	b	h	h

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	16	19	20	22	24	26	27	28	30	31	34	35	36	39	40	42	43	44	46	47	48	50	51	52	54	55	56	58	59	60	62	64
1	1	B1015-3	0.00	h	a	h	b	h	a	h	b	h	a	h	h	h	h	h	h	a	b	b	h	b	h	h	h	h	h	h	b	h	h	h	a
2	1	B1017-2	2.43	h	a	h	b	h	a	h	b	h	a	h	h	h	h	h	h	a	b	b	h	b	h	h	h	h	h	h	b	h	h	h	a
3	1	B1014-3	5.49	h	h	h	b	h	a	h	b	h	a	h	h	h	h	h	h	a	b	b	h	b	h	h	h	h	h	h	b	h	h	h	a
4	1	B1018-1	9.18	h	h	h	b	h	a	h	b	h	a	h	h	h	h	h	h	a	b	b	h	b	h	h	h	h	h	h	b	h	h	h	a
5	1	B1013b-1	11.61	h	b	h	b	h	a	h	b	h	a	h	h	h	h	h	h	a	b	b	h	b	h	h	h	h	h	h	b	h	h	h	a
6	1	B1013a-2	12.21	h	b	h	b	h	a	h	b	h	a	h	h	h	h	h	h	a	b	b	h	b	h	h	h	h	h	h	b	h	h	h	a
7	1	B1012c-4	19.51	h	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	b	b	b	h	h	h	h	h	h	b	b	a	h	a
8	1	B1012b-1	20.11	h	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	b	b	b	h	h	h	h	h	h	b	b	a	h	a
9	1	B1012a-1	20.70	h	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	b	b	b	h	h	h	h	h	h	b	b	a	h	a
10	1	B1019-1	21.29	h	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	b	b	b	h	h	h	h	h	h	b	b	a	h	a
11	1	B1020b-2	21.88	h	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	b	b	b	h	h	h	h	h	h	b	b	a	h	a
12	1	B1020a-4	23.98	h	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	b	b	b	h	h	h	h	h	h	b	b	a	h	a
13	1	B1001-1	26.09	a	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	h	h	b	h	h	h	h	h	h	b	b	a	h	a
14	1	B1002-1	26.68	a	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	h	h	b	h	h	h	h	h	h	b	b	a	h	a
15	1	B1003-3	27.87	a	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	h	h	b	h	h	h	h	h	h	h	b	a	h	a
16	1	B1004-1	28.46	a	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	h	h	b	h	h	h	h	h	h	h	b	a	h	a
17	1	B1005a-1	29.06	a	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	h	h	b	h	h	h	h	h	h	h	b	a	h	a
18	1	B1005b-1	29.65	a	b	h	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	h	h	b	h	h	h	h	h	h	h	b	a	h	a
19	1	B1005c-2	30.24	a	b	b	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	h	h	b	h	h	h	h	h	h	h	b	a	h	a
20	1	B1005d-5	30.83	a	b	b	h	h	a	h	h	h	a	h	h	h	h	h	h	a	b	h	h	b	h	h	h	h	h	h	h	b	a	h	a
21	1	B1006a-1	32.63	a	b	b	h	h	a	h	h	h	a	h	h	h	h	h	h	h	b	h	h	b	h	h	h	h	h	h	h	b	a	h	a
22	1	B1006b-1	34.43	a	b	b	h	h	a	h	h	h	a	h	a	h	h	h	h	h	b	h	h	b	h	h	h	h	h	h	h	b	a	h	a
23	1	B1006c-2	36.84	a	b	b	h	a	a	b	h	h	a	h	a	h	h	a	h	h	b	h	h	b	h	h	h	h	h	h	h	b	a	h	a
24	1	B1006d-6	38.03	a	b	b	h	a	a	b	h	h	a	h	a	h	h	a	h	h	b	h	h	b	h	b	a	h	h	h	h	b	a	h	a
25	1	B1007a-4	38.62	a	b	b	h	a	a	b	h	h	a	h	a	h	h	a	h	h	b	h	h	b	h	b	a	h	h	h	h	b	a	h	a
26	1	B1007b-16	39.21	a	b	b	h	a	a	b	h	h	h	h	a	h	h	a	h	h	b	h	h	b	h	b	a	h	h	h	h	b	a	h	a
27	1	B1008a-2	41.01	a	b	b	h	a	a	h	h	h	h	h	a	h	h	a	h	h	b	h	h	b	h	b	a	h	h	h	h	b	a	h	a
28	1	B1008b-4	42.84	h	b	b	h	a	a	h	h	h	h	h	a	h	h	a	h	b	b	h	h	b	h	b	a	h	h	h	h	b	a	a	a
29	1	B1009-3	43.44	h	b	b	h	a	a	h	h	h	h	h	a	h	h	a	h	b	b	h	h	b	h	b	a	h	h	h	h	b	a	a	a
30	1	B1010-4	44.63	h	b	b	h	a	a	h	h	h	h	h	a	h	h	a	h	b	b	h	h	b	h	b	a	h	h	h	h	b	a	a	a
31	1	B1011b-16	45.83	h	b	b	h	a	a	h	h	h	h	h	a	h	h	a	h	b	b	h	h	b	h	b	a	h	h	h	h	b	a	a	a
32	1	B1011a-15	46.42	h	b	b	h	a	a	h	h	h	h	h	a	h	h	a	h	b	b	h	h	b	h	b	a	h	h	h	h	b	h	a	a
33	2	B2013-3	0.00	a	a	b	b	h	h	h	b	a	a	a	a	a	h	a	a	h	b	a	h	h	b	h	h	h	h	b	b	b	a	h	b
34	2	B2008-22	1.20	a	a	b	b	h	h	h	b	a	a	a	a	a	h	a	a	h	b	h	h	h	b	h	h	h	h	b	b	b	a	h	b
35	2	B2001-11	2.39	a	a	b	b	h	h	h	b	a	a	a	a	a	h	a	a	h	b	a	h	h	b	h	h	h	h	b	b	b	a	h	b
36	2	B2012-27	2.99	a	a	b	b	h	h	h	b	a	a	a	a	a	h	a	a	h	b	a	h	h	b	h	h	h	h	b	b	b	a	h	b
37	2	B2010a-12	3.58	a	a	b	b	h	h	h	b	a	a	a	a	a	h	a	a	h	b	a	h	h	b	h	h	h	h	b	b	b	a	h	b
38	2	B2010b-4	5.40	a	a	b	b	h	h	h	b	a	a	a	a	a	h	a	a	h	b	a	a	h	b	h	h	b	h	b	b	b	a	h	b
39	2	B2014-4	6.01	a	a	b	b	h	h	h	b	a	a	a	a	a	h	a	a	h	b	a	a	h	b	h	h	b	h	b	b	b	a	h	b
40	2	B2009a-7	7.85	a	a	b	b	h	h	h	b	a	a	a	a	a	h	a	a	h	b	a	a	h	b	h	h	b	h	b	b	b	a	h	b
41	2	B2009b-3	9.06	a	h	b	b	h	h	a	b	a	a	a	a	a	h	a	a	h	b	a	a	h	b	h	h	b	h	b	b	b	a	h	b
42	2	B2009c-2	9.65	a	h	b	b	h	h	a	b	a	a	a	a	a	h	a	a	h	b	a	a	a	b	h	h	b	h	b	b	b	a	h	b
43	2	B2011-3	10.25	a	h	b	b	h	h	a	b	a	a	a	a	a	h	a	a	h	b	a	a	a	b	h	h	b	h	b	b	b	a	h	b
44	2	B2004a-4	12.73	a	h	b	b	h	h	a	b	a	a	a	a	a	h	a	a	h	b	a	a	a	h	h	h	b	h	h	b	b	a	h	b
45	2	B2004b-2	13.92	a	h	b	b	h	h	a	b	a	a	a	a	a	h	a	a	h	b	a	a	a	h	h	h	b	h	h	b	b	a	h	h
46	2	B2004c-4	15.11	a	h	b	b	h	h	a	h	a	a	a	a	a	h	a	a	h	b	a	a	a	h	h	h	b	h	h	b	b	a	h	b
47	2	B2007c-1	22.88	a	h	h	h	h	b	a	h	a	a	a	a	a	h	a	a	h	b	h	a	a	h	h	h	b	h	a	b	b	h	h	h
48	2	B2007b-1	23.47	a	h	h	h	h	b	a	h	a	a	a	a	a	h	a	a	h	b	h	a	a	h	h	h	h	h	a	b	b	h	h	h
49	2	B2007a-1	24.06	a	h	h	h	h	b	a	h	a	a	a	a	a	h	a	a	h	b	h	a	a	h	h	h	h	h	a	h	b	h	h	h
50	2	B2006-5	28.36	a	h	h	h	h	b	a	h	a	h	a	a	a	h	a	a	h	b	h	a	a	h	h	h	h	h	a	h	b	h	h	h
51	2	B2005b-3	35.99	h	h	h	a	h	b	a	h	a	h	a	a	a	h	a	a	b	b	h	a	a	h	h	a	h	h	a	h	b	h	h	h
52	2	B2005a-2	36.59	h	h	h	a	h	b	a	h	a	h	a	a	a	h	a	a	b	b	h	a	a	h	h	a	h	h	a	h	b	h	h	h
53	2	B2017b-2	37.78	h	h	h	a	h	b	a	h	a	h	a	a	a	h	a	a	b	b	h	a	a	h	h	a	h	h	a	h	b	h	h	h
54	2	B2017a-2	38.37	h	h	h	a	h	b	a	h	a	h	a	a	a	h	a	a	b	b	h	a	a	h	h	a	h	h	a	h	b	b	h	h
55	2	B2016b-2	39.57	h	h	h	a	h	b	a	h	a	h	a	a	a	h	a	a	b	b	h	a	a	h	h	a	h	h	a	h	b	b	h	h
56	2	B2016a-1	40.16	h	h	h	a	h	b	a	h	a	h	a	a	a	h	a	a	b	b	h	a	a	h	h	a	h	h	a	h	b	b	h	h
57	2	B2002-3	46.58	h	h	h	a	h	b	a	h	a	h	h	a	a	h	a	a	b	b	h	a	a	h	h	h	h	b	a	h	b	b	h	h
58	2	B2003-3	54.54	h	h	h	a	h	b	a	h	h	b	h	h	a	h	a	a	b	b	b	a	a	h	h	h	h	b	a	h	h	b	h	a
59	3	B3007-3	0.00	b	a	a	h	h	a	h	h	h	h	h	a	h	h	h	h	h	h	b	b	b	a	a	a	h	b	b	h	h	b	h	b
60	3	TP6279	1.82	b	a	a	h	h	a	h	h	h	h	h	a	h	h	h	h	h	h	b	b	b	a	a	a	h	b	b	h	h	b	h	b

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	16	19	20	22	24	26	27	28	30	31	34	35	36	39	40	42	43	44	46	47	48	50	51	52	54	55	56	58	59	60	62	64
61	3	B3014b-1	5.54	h	a	a	h	h	a	h	h	h	h	h	a	h	h	h	h	h	h	b	b	b	a	a	a	h	b	b	h	h	b	h	b
62	3	B3014a-1	7.35	h	a	a	b	h	a	h	h	h	h	h	a	h	h	h	h	h	b	b	b	b	a	h	a	h	b	b	h	h	b	h	b
63	3	B3013-1	10.41	h	a	a	b	h	a	h	h	h	h	h	a	h	h	h	h	h	b	b	b	b	a	b	a	h	b	b	h	h	b	h	b
64	3	B3006-2	13.54	h	a	a	b	h	a	h	h	h	h	h	a	h	h	h	h	h	b	b	b	h	a	b	a	h	b	b	h	h	b	h	b
65	3	B3008b-2	21.59	h	h	a	b	h	h	h	h	h	a	h	a	h	h	h	h	h	b	b	h	a	a	b	a	h	b	b	h	h	b	h	b
66	3	B3008a-5	22.79	h	h	a	b	h	h	h	h	h	a	h	a	h	h	h	h	h	b	b	h	a	h	b	a	h	b	b	h	h	b	h	b
67	3	TP3055	27.85	h	h	a	b	h	h	h	h	h	a	h	a	h	h	h	a	h	h	b	h	a	h	b	h	h	b	b	h	h	b	h	h
68	3	1_1627828	28.45	h	h	a	b	h	h	h	h	h	a	h	a	h	h	h	a	h	h	b	h	a	h	b	h	h	b	b	h	h	b	h	h
69	3	B3009b-3	30.26	h	h	a	b	h	h	h	h	h	a	h	a	h	h	h	a	h	h	b	h	a	h	b	h	h	b	b	h	h	b	h	h
70	3	B3009a-1	30.85	h	h	a	b	h	h	h	h	h	a	h	a	h	h	h	a	h	h	b	h	a	h	b	h	h	b	b	h	h	b	h	h
71	3	B3010b-1	36.70	h	b	a	b	h	h	h	h	h	a	h	a	h	h	h	a	h	h	b	h	a	h	b	h	a	b	b	h	a	b	a	h
72	3	B3010a-2	39.15	h	b	a	b	b	h	h	h	h	a	h	a	b	h	h	a	h	h	b	h	a	h	b	h	a	h	b	h	a	b	a	h
73	3	B3019-1	40.35	h	b	a	b	b	h	h	h	h	a	h	a	b	h	h	a	h	h	b	h	a	h	b	h	h	h	b	h	a	b	a	h
74	3	B3001a-3	41.56	h	b	a	b	b	h	h	h	h	a	h	a	b	h	h	a	h	h	h	h	a	h	b	h	h	h	b	h	a	b	a	h
75	3	B3001b-3	43.40	h	b	a	b	b	h	h	h	h	a	h	a	b	h	h	a	h	h	h	h	a	h	b	h	h	h	b	h	a	b	a	h
76	3	B3018-2	45.23	h	b	a	b	b	h	h	h	h	a	h	a	b	h	h	a	h	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
77	3	B3017-1	46.44	h	b	a	b	b	h	h	b	h	a	h	a	b	h	h	a	h	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
78	3	B3015d-5	47.05	h	b	a	b	b	h	h	b	h	a	h	a	b	h	h	a	h	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
79	3	B3015c-1	47.65	h	b	a	b	b	h	h	b	h	a	h	a	b	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
80	3	B3015b-2	48.85	h	b	a	b	b	h	h	b	h	a	h	a	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
81	3	B3016-4	50.06	h	b	a	b	b	h	h	b	h	a	h	a	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
82	3	B3002a-6	51.26	h	b	a	b	b	h	h	b	h	a	h	a	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
83	3	B3002c-1	51.85	h	b	a	b	b	h	h	b	h	a	h	a	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
84	3	B3002b-4	53.04	h	b	a	b	b	h	h	b	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
85	3	B3003d-3	53.63	h	b	a	b	b	h	h	b	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
86	3	B3003c-2	54.23	h	b	a	b	b	h	h	b	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
87	3	B3003b-6	54.83	h	b	a	b	b	h	h	b	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
88	3	B3003f-5	55.43	h	b	a	b	b	h	h	h	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	h	b	a	h
89	3	B3003e-22	56.63	h	b	h	b	b	h	h	h	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	a	b	a	b
90	3	B3003a-23	58.47	h	b	a	b	b	h	h	h	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	a	b	a	b
91	3	B3004b-5	60.93	h	b	h	b	b	h	h	h	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	a	b	a	b
92	3	B3004a-1	61.52	h	b	h	b	b	h	h	h	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	a	b	a	b
93	3	B3004c-1	65.34	h	b	h	h	h	h	h	b	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	a	b	a	b
94	3	B3004d-1	65.94	h	b	h	h	h	h	h	b	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	a	b	a	b
95	3	B3005a-7	67.14	h	b	h	h	h	h	h	b	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	a	b	h	b
96	3	B3005b-2	67.73	h	b	h	h	h	h	h	b	h	a	h	h	h	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	a	b	h	b
97	3	B3005c-7	69.53	h	b	h	h	h	h	h	b	h	a	h	h	a	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	a	b	h	b
98	3	B3012-1	71.98	h	b	h	h	h	h	h	b	h	a	h	h	a	h	h	a	b	h	h	h	a	h	b	h	h	h	b	h	a	b	h	h
99	3	B3011-3	73.78	h	b	h	h	h	h	h	b	h	a	h	h	a	h	h	a	b	h	h	h	a	h	b	h	h	a	b	h	a	b	h	h
100	3	B3020-1	74.97	h	b	h	h	h	h	h	b	h	a	h	h	a	h	h	a	b	h	h	h	a	h	b	h	h	a	b	h	a	b	h	h
101	4	B4001-29	0.00	b	h	b	h	a	a	h	h	h	b	h	h	h	h	h	b	h	b	h	h	h	h	h	b	b	b	b	a	h	b	a	h
102	4	B4002b-21	0.59	b	h	b	h	a	a	h	h	h	b	h	h	h	h	h	b	h	b	h	h	h	h	h	b	b	b	b	a	h	b	a	h
103	4	B4002a-3	1.78	b	h	b	a	a	a	h	h	h	b	h	h	h	h	h	b	h	b	h	h	h	h	h	b	b	b	b	a	h	b	h	h
104	4	B4004b-12	4.81	b	h	b	h	a	a	h	h	h	b	h	h	h	h	h	b	h	b	h	h	h	h	h	b	b	b	b	a	h	b	h	h
105	4	B4004a-10	5.41	b	h	b	h	a	a	h	h	h	b	h	h	h	h	h	b	h	b	h	h	a	h	h	b	b	b	b	a	h	b	h	h
106	4	B4007a-4	6.00	b	h	b	h	a	a	h	h	h	b	h	h	h	h	h	b	h	b	h	h	a	h	h	b	b	b	b	a	h	b	h	h
107	4	B4007b-5	7.19	b	h	b	h	a	a	h	h	h	b	h	h	h	h	h	b	h	b	h	h	a	h	h	h	b	b	b	a	h	b	h	h
108	4	B4007c-1	7.78	b	h	b	h	a	a	h	h	h	h	h	h	h	h	h	b	h	b	h	h	a	h	h	h	b	b	b	a	h	b	h	h
109	4	B4007d-1	8.37	b	h	b	h	a	a	h	h	h	h	h	h	h	h	h	b	h	b	h	h	a	h	h	h	b	b	b	a	h	b	h	h
110	4	B4007e-5	8.96	b	h	b	h	a	a	h	h	h	h	h	h	h	h	h	b	h	b	h	h	a	h	h	h	b	b	b	a	h	b	h	h
111	4	B4023-4	12.62	b	b	b	b	a	a	h	h	h	h	h	h	h	h	h	b	h	b	b	h	a	h	h	h	b	b	b	a	h	b	h	h
112	4	B4012-3	13.81	b	b	b	b	a	a	h	h	h	h	h	h	h	h	h	b	h	h	b	h	a	h	h	h	b	b	b	a	h	b	h	h
113	4	B4019-3	19.50	b	b	b	b	a	a	a	h	h	h	h	h	h	h	h	b	h	h	b	h	a	h	h	h	b	b	b	a	h	b	h	h
114	4	B4021-2	21.30	b	b	b	b	a	a	a	h	h	h	h	h	h	h	h	b	h	h	b	h	a	h	h	h	b	b	b	a	h	b	h	h
115	4	B4011-1	26.29	b	b	b	b	a	a	a	h	h	h	h	a	a	h	h	b	h	h	b	h	a	h	a	h	b	b	b	a	b	b	h	a
116	4	B4008a-5	28.70	b	b	b	b	a	a	a	h	h	h	h	a	a	h	h	b	h	a	b	h	a	h	a	h	b	h	b	a	b	b	h	a
117	4	B4008b-1	30.51	b	b	b	b	a	a	a	h	b	h	h	a	a	h	h	b	h	a	b	h	a	h	a	h	b	h	b	a	b	b	h	a
118	4	B4010-1	35.59	b	h	h	b	a	a	a	h	b	h	h	a	a	h	h	b	h	a	b	h	a	a	a	h	b	h	b	a	b	b	h	a
119	4	B4018-3	39.32	b	h	a	b	a	a	a	h	b	h	h	a	a	h	h	b	h	a	b	h	a	a	a	h	b	h	b	a	b	b	h	a
120	4	B4006b-1	46.11	b	h	a	b	h	h	a	h	h	h	h	a	a	h	a	b	h	a	b	h	a	a	a	h	b	a	h	a	b	h	h	a

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	16	19	20	22	24	26	27	28	30	31	34	35	36	39	40	42	43	44	46	47	48	50	51	52	54	55	56	58	59	60	62	64
121	4	B4006a-2	48.54	b	h	a	b	h	h	a	h	h	h	h	a	a	h	a	h	h	a	b	h	a	a	a	h	b	a	h	a	b	h	h	a
122	4	B4013-1	54.85	b	h	a	b	h	b	a	h	h	h	h	a	a	h	a	a	h	a	b	h	a	h	a	h	b	a	h	a	b	h	h	a
123	4	B4003b-2	57.26	h	h	a	b	h	b	a	h	h	h	h	a	a	h	a	a	h	a	b	h	a	h	a	h	b	a	h	h	h	h	h	a
124	4	B4003a-1	58.46	h	h	a	b	h	b	a	h	h	a	h	a	a	h	a	a	h	a	b	h	a	h	a	h	b	a	h	h	h	h	h	a
125	5	B5030-3	0.00	h	a	h	h	a	h	b	h	h	h	b	h	h	h	a	a	a	h	a	h	a	a	a	b	b	h	b	a	h	a	h	a
126	5	B5031-1	0.59	h	a	h	h	a	h	b	h	h	h	b	h	h	h	a	a	a	h	a	h	a	a	a	b	b	h	b	a	h	a	h	a
127	5	B5032a-1	1.18	h	a	h	h	a	h	b	h	h	h	b	h	h	h	a	a	a	h	a	h	a	a	a	b	b	h	b	a	h	a	h	a
128	5	B5032b-1	3.00	h	a	h	h	a	h	b	h	h	h	b	h	h	h	a	a	a	h	a	h	a	a	a	b	b	h	b	h	h	a	h	a
129	5	B5032c-1	7.37	h	a	h	h	a	h	b	h	h	h	b	h	h	h	a	a	h	h	a	a	a	a	a	b	h	h	b	h	h	a	h	h
130	5	B5011-2	14.53	h	a	h	h	a	h	b	h	h	a	b	h	b	h	a	a	h	h	a	a	a	a	a	b	h	h	b	h	b	a	h	h
131	5	B5033-1	17.25	a	a	h	h	a	h	b	h	h	a	h	h	b	h	a	a	h	h	a	a	a	a	a	b	h	h	b	h	b	a	h	h
132	5	B5001-1	20.01	a	a	h	h	a	h	b	h	h	a	h	h	b	h	a	a	h	h	h	a	a	a	a	b	h	h	b	h	b	a	h	h
133	5	B5002a-2	22.44	a	a	h	h	a	h	b	h	h	a	h	h	b	h	a	a	h	h	h	a	a	a	a	b	h	h	b	h	b	a	h	h
134	5	B5002b-1	29.66	a	a	h	b	a	a	b	h	h	a	h	h	b	h	a	a	h	h	h	a	a	h	h	b	h	b	b	h	h	a	h	h
135	5	B5003a-1	33.40	a	a	h	b	a	a	b	h	h	a	a	b	b	h	a	a	h	h	h	a	a	h	h	b	h	b	b	h	h	a	h	h
136	5	B5003b-3	34.60	a	a	h	b	a	a	b	h	h	a	a	b	b	b	a	a	h	h	h	a	a	h	h	b	h	b	b	h	h	a	a	h
137	5	B5004-5	37.03	a	a	h	b	a	a	b	h	h	a	a	b	h	b	a	a	h	h	h	a	a	h	h	b	a	b	b	h	h	a	a	h
138	5	B5005a-3	38.83	a	a	h	b	a	a	b	h	h	a	a	b	h	b	a	a	h	h	h	a	a	h	h	b	a	b	b	h	h	a	a	b
139	5	B5005b-1	41.28	a	a	h	b	a	a	b	h	h	a	a	b	h	b	a	a	h	h	h	a	a	h	h	b	a	b	b	h	h	h	a	b
140	5	B5005c-5	45.64	a	a	h	b	a	a	b	h	h	a	a	b	h	b	a	a	h	h	h	h	h	h	h	b	a	b	b	h	h	h	a	b
141	5	B5006-3	47.44	a	a	h	b	a	a	b	h	h	a	a	b	h	h	a	a	h	h	h	h	h	h	h	b	a	b	b	h	h	h	a	b
142	5	B5007b-1	48.63	a	a	h	b	a	a	b	h	h	a	a	b	h	h	a	a	h	h	h	h	h	h	h	h	a	b	b	h	h	h	a	b
143	5	B5007a-1	49.22	a	a	h	b	a	a	b	h	h	a	a	b	h	h	a	a	h	h	b	h	h	h	h	h	a	b	b	h	h	h	a	b
144	5	B5034d-4	50.42	a	a	h	h	a	a	b	h	h	a	a	b	h	h	a	a	h	h	b	h	h	h	h	h	a	b	b	h	h	h	a	b
145	5	B5034b-5	52.92	a	h	h	h	a	a	b	h	h	a	a	b	h	b	a	a	h	h	b	h	h	h	h	h	a	b	h	h	h	h	a	b
146	5	B5034a-1	54.11	a	h	h	h	a	h	b	h	h	a	a	b	h	b	a	a	h	h	b	h	h	h	h	h	a	b	h	h	h	h	a	b
147	5	B5018b-11	56.55	a	h	h	h	a	h	b	a	h	a	a	b	h	b	a	a	h	h	b	h	h	h	h	h	a	b	h	h	h	h	a	b
148	5	B5018a-7	57.14	a	h	h	h	a	h	b	a	h	a	a	b	h	h	a	a	h	h	b	h	h	h	h	h	a	b	h	h	h	h	a	b
149	5	B5018c-4	60.22	h	h	h	h	a	h	b	a	h	a	h	b	h	b	a	a	h	h	b	h	h	h	h	h	a	b	h	h	h	h	a	b
150	5	B5014a-4	61.42	h	h	h	h	a	h	b	a	h	a	h	b	h	b	a	a	h	h	b	h	h	h	h	h	a	b	h	h	h	h	h	b
151	5	B5014b-6	63.93	h	h	h	h	a	h	b	a	h	a	h	b	h	b	a	a	h	a	b	h	h	h	h	h	a	b	h	h	h	h	h	b
152	5	B5016-2	65.15	h	h	h	h	a	h	b	a	h	a	h	b	h	b	a	a	h	a	b	h	h	h	h	h	a	b	h	h	h	h	h	b
153	5	B5022b-4	65.74	h	h	h	h	a	h	b	a	h	a	h	b	h	b	a	a	h	a	b	h	h	h	h	h	a	b	h	h	h	h	h	b
154	5	B5022a-2	66.34	h	a	h	h	a	h	b	a	h	a	h	b	h	b	a	a	h	a	b	h	h	h	h	h	a	b	h	h	h	h	h	b
155	5	B5029-32	67.53	h	h	h	h	a	h	b	a	h	a	h	b	h	b	a	a	h	a	b	h	h	h	h	h	a	b	h	h	h	h	h	b
156	6	B6011b-1	0.00	a	b	h	b	a	b	h	a	a	h	a	a	b	h	b	b	b	a	h	b	b	h	h	h	b	h	h	h	a	h	b	h
157	6	B6011a-1	2.44	a	b	h	b	a	b	h	a	a	h	a	a	b	h	b	b	b	h	h	b	b	h	h	h	b	h	h	h	a	h	b	h
158	6	B6002a-2	6.85	a	b	h	b	a	b	h	a	a	h	a	a	b	h	h	b	b	h	h	b	b	h	h	h	b	h	h	h	a	h	h	h
159	6	B6002b-1	8.66	a	b	h	b	a	b	h	a	a	h	a	a	b	h	h	b	b	h	h	b	b	h	h	h	b	h	h	h	a	h	h	h
160	6	B6017-3	12.39	a	b	h	b	a	b	h	a	a	h	a	a	b	h	h	b	b	h	h	b	b	a	h	h	b	h	h	h	h	b	h	h
161	6	B6019-1	21.01	a	b	h	b	a	b	a	h	h	h	a	a	h	h	h	b	b	h	b	b	b	a	h	h	b	h	h	b	h	b	h	h
162	6	B6004-3	29.61	a	b	h	b	a	b	a	h	h	h	a	a	h	h	h	b	b	h	b	h	b	a	h	b	b	h	a	b	h	b	h	a
163	6	B6005-4	33.31	a	b	b	b	a	b	a	h	h	a	a	a	h	h	h	b	b	h	b	h	b	a	h	b	b	h	a	b	h	b	h	a
164	6	B6007-1	37.03	a	b	b	b	a	b	a	h	h	a	a	a	a	h	h	b	b	h	b	h	b	a	h	b	b	h	a	b	h	b	h	a
165	6	B6006a-2	40.09	a	b	b	b	h	b	a	h	h	a	a	a	a	h	h	b	b	h	b	h	b	a	a	b	b	h	a	b	h	b	h	a
166	6	B6006b-20	42.53	a	b	b	b	h	b	a	h	h	a	a	a	a	h	h	b	b	h	b	h	b	a	a	b	b	h	a	b	h	h	h	a
167	6	B6009c-46	44.34	a	b	b	b	h	b	a	h	h	a	a	a	a	h	h	b	b	h	b	h	b	a	a	b	b	h	a	b	h	h	h	a
168	6	B6009b-32	45.54	a	b	b	b	h	b	a	h	h	h	a	a	a	h	h	b	b	h	b	h	b	a	a	b	b	h	a	b	h	h	h	a
169	6	B6009a-3	46.73	a	b	b	b	h	b	a	h	h	h	h	a	a	h	b	b	b	h	b	h	b	a	a	b	b	h	a	b	h	h	h	a
170	6	B6020-1	47.92	a	b	b	b	h	b	a	h	h	h	h	a	a	h	b	b	b	h	b	h	b	a	a	b	b	h	a	b	h	h	h	a
171	6	B6014a-25	48.51	a	b	b	b	h	b	a	h	h	h	h	a	a	h	b	b	b	h	b	h	b	a	a	b	b	h	a	b	h	h	h	a
172	6	B6014b-1	49.70	a	b	b	b	h	b	a	h	h	h	h	a	a	h	h	b	b	h	b	h	b	a	a	b	b	h	a	b	h	h	h	a
173	6	B6014c-2	50.89	a	b	b	b	h	b	a	h	h	h	h	a	a	h	h	b	b	h	b	h	b	a	a	b	b	h	a	b	h	h	h	a
174	6	B6016-1	52.09	a	b	b	b	h	b	a	h	h	h	h	a	a	h	h	b	b	h	b	h	b	a	a	b	b	h	a	b	b	h	h	a
175	6	B6021-4	52.68	a	b	b	b	h	b	a	h	h	h	h	a	a	h	h	b	b	h	b	h	b	a	a	b	b	h	a	b	b	h	h	a
176	6	B6022-2	54.48	a	b	b	b	h	b	a	h	h	h	h	a	a	h	h	b	b	h	b	h	b	a	a	b	b	h	a	b	b	h	h	h
177	6	B6010a-5	57.52	a	b	b	b	h	a	a	h	h	h	h	a	a	h	h	b	b	h	b	h	b	a	a	b	b	h	a	b	b	h	h	h
178	6	B6010b-2	58.71	a	b	b	b	h	a	a	h	h	h	h	a	a	h	h	b	b	h	b	h	b	a	a	b	h	h	a	b	b	h	h	h
179	6	B6010c-2	59.30	a	b	b	b	h	a	a	h	h	h	h	a	a	h	h	b	b	h	b	h	b	a	a	b	h	h	a	b	b	h	h	h
180	6	B6010d-3	61.10	a	b	b	b	h	a	a	h	h	h	h	a	a	h	h	b	b	h	b	h	b	a	h	b	h	h	h	b	b	h	h	h

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	16	19	20	22	24	26	27	28	30	31	34	35	36	39	40	42	43	44	46	47	48	50	51	52	54	55	56	58	59	60	62	64
181	6	B6018a-3	62.29	a	b	b	b	h	a	a	h	h	h	h	a	a	h	h	b	h	h	b	h	b	a	h	b	h	h	h	b	b	h	h	h
182	6	B6018b-1	64.71	a	b	b	b	h	a	a	h	h	a	h	a	a	h	h	b	h	h	b	h	b	a	h	b	h	h	h	b	b	b	h	h
183	6	B6013-3	65.90	a	b	b	b	h	a	a	h	h	a	h	a	a	h	h	b	h	h	b	h	b	a	h	b	h	h	h	b	b	b	h	h
184	6	B6012a-3	68.98	a	b	b	b	b	a	a	h	h	a	h	a	a	b	h	b	h	h	b	h	b	a	h	b	h	h	h	b	b	b	h	h
185	6	B6012b-2	72.06	a	b	b	b	b	a	a	h	h	a	h	a	a	b	h	b	h	h	b	h	b	a	h	b	h	h	h	h	h	b	h	h
186	6	B6008-2	85.48	a	h	a	h	b	a	h	b	h	a	h	h	a	h	h	b	h	h	b	h	b	h	h	h	h	h	h	h	h	h	h	h
187	6	B6015-7	90.53	h	h	a	h	h	a	h	b	h	a	h	h	h	h	h	b	h	h	b	b	b	h	h	h	h	h	h	h	h	h	h	h
188	7	B7001e-3	0.00	b	a	a	b	a	h	h	a	h	b	h	h	h	h	h	h	h	h	h	h	h	h	a	h	a	a	h	h	h	h	a	h
189	7	B7001d-2	0.59	b	a	a	b	a	h	h	a	h	b	h	h	h	h	h	h	h	h	h	h	h	h	a	h	a	a	h	h	h	h	a	h
190	7	B7001c-8	1.18	b	a	a	b	a	h	h	a	h	b	h	h	h	a	h	h	h	h	h	h	h	h	a	h	a	a	h	h	h	h	a	h
191	7	B7001b-4	1.78	b	a	a	b	a	h	h	a	h	b	h	h	h	a	h	h	h	h	h	h	h	h	a	h	a	a	h	h	h	h	a	h
192	7	B7001a-7	2.98	b	a	a	b	a	h	h	a	h	b	h	h	h	a	h	h	h	h	h	h	h	h	a	h	a	a	h	h	h	h	a	h
193	7	B7018-2	4.78	b	a	a	b	a	h	h	a	h	b	h	h	h	h	h	h	h	h	h	h	h	h	a	h	a	a	h	h	h	h	a	h
194	7	B7002a-1	6.58	b	a	a	b	a	h	b	a	h	b	h	h	h	h	h	h	h	h	h	b	h	h	a	h	a	a	h	h	h	h	a	h
195	7	B7002b-1	7.77	b	a	a	b	a	h	b	a	h	b	h	h	h	h	h	h	h	b	h	b	h	h	a	a	a	a	h	h	h	h	a	h
196	7	B7002c-1	8.36	b	a	a	b	a	h	b	a	h	b	h	h	h	h	h	h	h	b	h	b	h	h	h	a	a	a	h	h	h	h	a	h
197	7	B7003-4	11.39	b	h	a	b	a	a	b	a	h	b	h	h	h	h	h	h	h	b	h	b	h	h	h	a	a	a	h	h	h	h	a	h
198	7	B7004-2	11.98	b	h	a	b	a	a	b	a	h	b	h	h	h	h	h	h	h	b	h	b	h	h	h	a	a	a	h	h	h	h	a	h
199	7	B7005-2	13.79	b	h	a	b	a	a	b	a	h	b	h	h	h	h	b	h	h	b	h	b	h	h	h	a	a	a	h	h	h	h	a	h
200	7	B7006a-1	14.38	b	h	a	b	a	a	b	a	h	b	h	h	h	h	b	h	h	b	h	b	h	h	h	a	a	a	h	h	h	h	a	h
201	7	B7006b-2	16.79	b	h	a	b	a	a	b	a	h	b	h	a	h	h	b	h	h	b	h	h	h	h	h	a	a	a	h	h	h	h	a	b
202	7	B7007a-1	17.38	b	h	a	b	a	a	b	a	h	b	h	a	h	h	b	h	h	b	h	h	h	h	h	a	a	a	h	h	h	h	a	b
203	7	B7007b-1	17.97	b	h	a	b	a	a	b	a	h	b	h	a	h	h	b	h	h	b	h	h	h	h	h	a	a	a	h	h	h	h	a	b
204	7	B7008a-2	22.28	b	h	a	b	a	a	b	a	h	b	h	a	h	h	b	h	h	h	h	h	a	h	h	a	a	a	h	h	h	h	a	b
205	7	B7008b-3	22.87	b	h	a	b	a	a	b	a	h	b	h	a	h	h	b	h	h	h	h	h	a	h	b	a	a	a	h	h	h	h	a	b
206	7	B7009a-1	24.08	b	h	a	b	a	a	b	a	h	b	h	a	h	h	b	h	h	h	h	h	a	h	b	a	a	a	h	h	h	h	a	b
207	7	B7009b-6	28.38	b	h	a	b	a	a	b	a	h	b	h	a	h	h	b	h	a	h	h	h	a	a	b	a	a	a	h	h	b	h	a	b
208	7	B7017a-1	30.80	b	h	a	b	a	a	b	a	h	b	h	a	h	h	b	h	a	h	h	h	h	a	b	a	a	a	h	h	b	h	a	b
209	7	B7017b-3	31.99	b	h	a	b	a	a	b	a	a	b	h	a	h	h	b	h	a	h	h	h	h	a	b	a	a	a	h	h	b	h	a	b
210	7	B7016-1	34.41	b	h	a	b	a	a	b	a	a	h	h	a	h	h	b	h	a	h	h	h	h	a	b	a	a	a	h	h	b	h	a	b
211	7	B7015-3	35.61	b	h	a	b	a	a	b	a	a	h	h	a	h	h	b	h	a	h	h	h	h	a	b	a	a	a	h	h	b	h	a	b
212	7	B7013a-1	48.25	b	b	a	b	h	a	h	a	a	a	a	a	b	h	b	a	a	h	h	h	h	a	b	h	a	h	b	h	b	b	a	b
213	7	B7013b-2	48.84	b	b	h	b	h	a	h	a	a	a	a	a	b	h	b	a	a	h	h	h	h	a	b	h	a	h	b	h	b	b	a	b
214	7	B7012b-1	50.04	b	h	h	b	h	a	h	a	a	a	a	a	b	h	b	a	a	h	h	h	h	a	b	h	a	h	b	h	b	b	a	b
215	7	B7012a-2	51.23	b	h	h	b	h	a	h	a	a	a	a	a	b	h	b	h	a	h	h	h	h	a	b	h	a	h	b	h	b	b	a	b
216	7	B7011-1	52.43	b	h	h	b	h	a	h	a	a	a	a	a	b	h	b	h	a	h	h	h	h	a	b	h	a	h	b	h	b	b	a	b
217	7	B7010-2	55.50	b	h	h	b	h	a	h	a	a	a	a	a	h	h	b	h	a	h	h	h	h	a	b	h	a	h	b	h	b	b	a	b

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	66	67	68	70	71	72	74	75	76	78	79	80	82	83	84	85	86	87	88	89	90
1	1	B1015-3	0.00	b	b	a	a	h	b	b	a	h	b	b	a	a	h	b	b	h	a	b	h	a
2	1	B1017-2	2.43	b	b	a	a	h	b	b	h	h	h	b	a	a	h	b	b	h	a	b	h	a
3	1	B1014-3	5.49	b	b	a	a	h	b	b	h	h	h	b	a	a	h	b	b	h	h	b	h	a
4	1	B1018-1	9.18	b	b	a	a	b	b	b	h	h	h	b	a	a	h	b	b	h	h	b	h	a
5	1	B1013b-1	11.61	b	h	a	a	b	b	b	h	h	h	b	a	a	a	b	b	h	h	b	h	a
6	1	B1013a-2	12.21	b	h	a	a	b	b	b	h	h	a	b	a	a	a	b	b	h	h	b	h	a
7	1	B1012c-4	19.51	b	h	a	a	b	b	b	h	a	a	b	a	a	a	h	b	h	h	h	h	a
8	1	B1012b-1	20.11	b	h	a	a	b	b	h	h	a	a	b	a	a	a	h	b	h	h	h	h	a
9	1	B1012a-1	20.70	b	h	a	a	b	b	h	h	a	a	h	a	a	a	h	b	h	h	h	h	a
10	1	B1019-1	21.29	b	h	a	a	b	b	h	h	a	a	h	a	a	a	h	b	h	h	h	h	a
11	1	B1020b-2	21.88	b	h	a	a	b	b	h	h	a	a	h	a	a	a	h	b	h	h	h	h	a
12	1	B1020a-4	23.98	b	h	a	a	b	b	h	h	h	a	h	a	a	a	h	b	h	h	h	h	a
13	1	B1001-1	26.09	b	h	a	a	b	b	h	h	h	a	h	a	a	a	h	b	h	h	h	h	a
14	1	B1002-1	26.68	b	h	a	a	b	b	h	h	h	a	h	a	a	a	h	b	h	h	h	h	a
15	1	B1003-3	27.87	b	h	a	a	b	b	h	h	h	a	h	a	a	a	h	b	h	h	h	h	a
16	1	B1004-1	28.46	b	h	a	a	b	b	h	h	h	a	h	a	a	a	h	b	h	h	h	h	a
17	1	B1005a-1	29.06	b	h	a	a	b	b	h	h	h	a	h	a	a	a	h	b	h	h	h	h	a
18	1	B1005b-1	29.65	b	h	a	a	b	b	h	h	h	a	h	a	a	a	h	b	h	h	h	h	a
19	1	B1005c-2	30.24	b	h	a	a	b	b	h	h	h	a	h	a	a	a	h	b	h	h	h	h	a
20	1	B1005d-5	30.83	b	h	a	a	b	b	h	h	h	a	h	a	a	a	h	b	h	h	a	h	a
21	1	B1006a-1	32.63	b	h	a	a	b	b	h	h	h	a	h	a	a	a	h	b	h	h	a	h	a
22	1	B1006b-1	34.43	b	h	a	a	b	h	h	b	h	a	h	a	a	a	h	b	h	h	a	h	a
23	1	B1006c-2	36.84	b	h	a	a	b	h	h	b	h	a	h	h	a	a	h	b	h	h	a	h	a
24	1	B1006d-6	38.03	b	h	a	a	b	h	h	b	h	a	h	h	a	a	h	b	h	h	a	h	a
25	1	B1007a-4	38.62	b	h	a	a	b	h	h	b	h	a	h	h	a	a	h	b	h	h	a	h	a
26	1	B1007b-16	39.21	b	h	a	a	b	h	h	b	h	a	h	h	a	a	h	b	h	h	a	h	a
27	1	B1008a-2	41.01	b	h	a	a	b	h	h	b	h	h	h	h	a	a	h	b	h	h	a	h	a
28	1	B1008b-4	42.84	b	h	a	a	b	h	h	b	h	h	h	h	a	a	h	b	h	h	a	h	a
29	1	B1009-3	43.44	b	h	a	a	b	h	h	b	h	h	h	h	a	a	h	b	h	h	a	h	a
30	1	B1010-4	44.63	b	h	a	a	b	h	h	b	h	b	a	h	a	a	h	b	h	h	a	h	a
31	1	B1011b-16	45.83	b	h	a	a	b	h	h	b	h	b	a	h	a	a	h	b	h	h	a	h	a
32	1	B1011a-15	46.42	b	h	a	a	b	h	h	b	h	b	a	h	a	a	h	b	h	h	a	h	a
33	2	B2013-3	0.00	h	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	h	b	b
34	2	B2008-22	1.20	h	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	h	b	b
35	2	B2001-11	2.39	h	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	h	b	b
36	2	B2012-27	2.99	h	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	h	b	b
37	2	B2010a-12	3.58	h	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	h	b	b
38	2	B2010b-4	5.40	h	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	h	b	b
39	2	B2014-4	6.01	h	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	h	b	b
40	2	B2009a-7	7.85	h	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	a	b	b
41	2	B2009b-3	9.06	h	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	a	b	b
42	2	B2009c-2	9.65	h	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	a	b	b
43	2	B2011-3	10.25	h	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	a	b	b
44	2	B2004a-4	12.73	b	b	b	b	a	h	h	h	h	h	b	b	h	h	h	h	a	b	a	b	b
45	2	B2004b-2	13.92	b	b	b	b	a	h	h	h	h	b	b	b	h	h	h	h	a	b	a	b	b
46	2	B2004c-4	15.11	b	b	b	b	a	h	h	h	h	b	b	b	h	h	h	h	a	b	a	b	b
47	2	B2007c-1	22.88	b	b	b	b	h	a	h	h	h	b	b	b	h	h	h	h	a	b	a	b	b
48	2	B2007b-1	23.47	b	b	b	b	h	a	h	h	h	b	b	b	h	h	h	h	a	b	a	b	b
49	2	B2007a-1	24.06	b	b	b	b	h	a	h	h	h	b	b	b	h	h	h	h	a	b	a	b	b
50	2	B2006-5	28.36	b	b	h	b	h	a	h	h	b	b	b	b	h	a	h	h	a	b	a	b	b
51	2	B2005b-3	35.99	b	b	h	h	h	a	h	h	h	b	b	b	h	a	h	h	a	h	a	b	h
52	2	B2005a-2	36.59	b	b	h	h	h	a	h	h	h	b	b	b	h	a	h	h	a	h	a	b	h
53	2	B2017b-2	37.78	b	b	h	h	h	a	h	h	h	b	b	b	h	a	h	h	a	h	a	b	h
54	2	B2017a-2	38.37	b	b	h	h	h	a	h	h	h	b	b	b	h	a	h	h	a	h	a	b	h
55	2	B2016b-2	39.57	b	b	h	h	h	a	b	h	h	b	b	b	h	a	h	h	a	h	a	b	h
56	2	B2016a-1	40.16	b	b	h	h	h	a	b	h	h	b	b	b	h	a	h	a	a	h	a	b	h
57	2	B2002-3	46.58	b	b	a	h	h	a	b	h	h	b	h	b	h	h	h	a	a	h	a	h	h
58	2	B2003-3	54.54	b	h	a	h	h	a	b	h	h	b	h	b	h	h	h	a	h	h	a	h	h
59	3	B3007-3	0.00	h	h	h	b	a	h	h	a	a	b	b	a	h	a	a	h	h	h	h	h	b
60	3	TP6279	1.82	h	h	h	b	a	h	h	a	a	b	b	a	h	a	a	h	h	h	h	h	b

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	66	67	68	70	71	72	74	75	76	78	79	80	82	83	84	85	86	87	88	89	90
61	3	B3014b-1	5.54	h	h	h	b	a	h	h	a	a	b	b	a	h	h	a	a	h	h	h	h	b
62	3	B3014a-1	7.35	h	h	h	b	a	h	h	a	a	b	b	a	h	h	a	a	h	h	h	h	b
63	3	B3013-1	10.41	h	h	h	b	a	h	h	a	a	b	b	a	b	h	a	a	h	h	h	h	b
64	3	B3006-2	13.54	h	h	h	b	a	h	a	a	a	b	b	a	b	h	h	a	h	h	h	h	b
65	3	B3008b-2	21.59	h	h	h	b	a	h	a	a	a	b	b	a	b	h	h	a	h	h	h	h	b
66	3	B3008a-5	22.79	h	h	h	b	a	h	a	a	a	b	b	a	b	h	h	a	h	h	h	h	b
67	3	TP3055	27.85	h	h	h	b	a	h	a	a	h	b	b	a	b	h	h	a	h	h	h	a	b
68	3	1_1627828	28.45	h	h	h	b	a	h	a	a	h	b	b	a	b	h	h	a	h	h	h	a	b
69	3	B3009b-3	30.26	h	h	h	b	a	b	a	a	h	b	b	a	b	h	h	a	h	h	h	a	b
70	3	B3009a-1	30.85	h	h	h	b	a	b	a	a	h	b	b	a	b	h	h	a	h	h	h	a	b
71	3	B3010b-1	36.70	h	a	h	b	a	b	a	a	h	b	h	a	b	h	h	a	h	h	h	h	b
72	3	B3010a-2	39.15	h	a	a	b	a	b	a	a	h	b	h	a	b	h	h	a	h	h	h	h	b
73	3	B3019-1	40.35	h	a	a	b	a	b	a	a	h	b	h	a	b	h	h	a	h	h	h	h	b
74	3	B3001a-3	41.56	h	a	a	b	a	b	a	a	h	b	h	a	b	h	h	a	h	h	h	h	b
75	3	B3001b-3	43.40	h	a	h	b	a	b	a	a	h	b	h	a	b	h	b	a	h	h	h	h	b
76	3	B3018-2	45.23	h	a	h	b	a	b	a	a	h	b	h	a	b	h	b	a	h	h	h	h	b
77	3	B3017-1	46.44	h	a	h	b	a	b	a	a	h	b	h	a	b	h	b	a	h	h	h	h	b
78	3	B3015d-5	47.05	h	a	h	b	a	b	a	a	h	b	h	a	b	h	b	a	h	h	h	h	b
79	3	B3015c-1	47.65	h	a	h	b	a	b	a	a	h	b	h	a	b	h	b	a	h	h	h	h	b
80	3	B3015b-2	48.85	a	a	h	b	a	b	a	a	h	b	h	a	b	h	b	a	h	h	h	h	b
81	3	B3016-4	50.06	a	a	h	b	a	b	a	a	h	b	h	a	b	h	b	a	h	h	h	h	b
82	3	B3002a-6	51.26	a	a	h	b	a	b	a	a	h	h	h	a	b	h	b	a	h	h	h	h	b
83	3	B3002c-1	51.85	a	a	h	b	a	b	a	a	h	h	h	a	b	h	b	a	h	h	h	h	b
84	3	B3002b-4	53.04	a	a	h	b	a	b	a	a	h	h	a	a	b	h	b	a	h	h	h	h	b
85	3	B3003d-3	53.63	a	a	h	b	a	b	a	a	h	h	a	a	b	h	b	a	h	h	h	h	b
86	3	B3003c-2	54.23	a	a	h	b	a	b	a	a	h	h	a	a	b	h	b	a	h	h	h	h	b
87	3	B3003b-6	54.83	h	a	h	b	a	b	a	a	h	h	a	a	b	h	b	a	h	h	h	h	b
88	3	B3003f-5	55.43	h	a	h	b	a	b	a	a	h	h	a	a	b	h	b	a	h	h	h	h	b
89	3	B3003e-22	56.63	h	a	h	b	a	b	a	a	h	h	a	a	b	h	b	a	h	h	h	h	b
90	3	B3003a-23	58.47	h	a	h	h	a	b	a	a	h	h	a	a	b	h	b	a	h	h	h	h	h
91	3	B3004b-5	60.93	h	a	h	b	a	b	a	a	h	h	a	a	b	h	b	a	h	h	h	h	b
92	3	B3004a-1	61.52	h	a	h	b	a	b	a	a	h	h	a	h	b	h	b	a	h	h	h	h	b
93	3	B3004c-1	65.34	h	a	h	h	a	b	a	a	h	h	a	h	b	h	b	h	h	h	h	h	h
94	3	B3004d-1	65.94	h	a	h	h	a	b	a	a	h	h	a	h	b	h	b	h	h	h	b	h	h
95	3	B3005a-7	67.14	h	a	h	h	a	b	a	a	h	h	a	h	b	h	b	h	h	h	b	h	h
96	3	B3005b-2	67.73	h	a	b	h	a	b	a	a	h	h	a	h	b	h	b	h	h	h	b	h	h
97	3	B3005c-7	69.53	a	a	b	h	a	b	a	a	h	h	a	h	b	a	b	h	h	h	b	h	h
98	3	B3012-1	71.98	a	a	b	h	a	b	a	a	h	h	a	h	b	a	b	h	h	h	b	h	h
99	3	B3011-3	73.78	a	a	b	h	a	b	a	a	h	h	a	h	b	a	b	h	h	h	b	h	h
100	3	B3020-1	74.97	a	a	b	h	a	b	a	a	h	h	a	h	b	a	b	h	h	h	b	h	h
101	4	B4001-29	0.00	h	b	b	h	b	h	b	b	b	b	h	b	h	a	a	a	b	b	h	a	h
102	4	B4002b-21	0.59	h	b	b	h	b	h	b	b	b	b	h	b	h	a	a	a	b	b	h	a	h
103	4	B4002a-3	1.78	h	b	b	h	b	h	b	b	b	b	h	b	h	a	a	a	b	b	h	a	h
104	4	B4004b-12	4.81	h	b	b	h	b	h	b	b	h	b	h	h	h	a	a	a	b	b	h	a	h
105	4	B4004a-10	5.41	h	b	b	h	b	h	b	b	h	b	h	h	h	a	a	a	b	b	h	a	h
106	4	B4007a-4	6.00	h	b	b	h	b	h	b	b	h	b	h	h	h	a	a	a	b	b	h	a	h
107	4	B4007b-5	7.19	h	b	b	h	b	h	b	b	h	b	b	h	h	a	a	a	b	b	h	a	h
108	4	B4007c-1	7.78	h	b	b	h	b	h	b	b	h	b	b	h	h	a	a	a	b	b	h	a	h
109	4	B4007d-1	8.37	h	b	b	h	b	h	b	b	h	b	b	h	h	a	a	a	b	b	h	a	h
110	4	B4007e-5	8.96	h	b	b	h	b	h	b	b	a	b	b	h	h	a	a	a	b	b	h	a	h
111	4	B4023-4	12.62	h	b	b	h	b	h	b	b	a	b	b	h	h	a	a	a	b	b	h	a	h
112	4	B4012-3	13.81	h	b	b	h	b	h	b	b	a	b	b	h	h	a	a	a	b	b	h	a	h
113	4	B4019-3	19.50	h	h	b	h	b	h	b	b	a	h	b	h	h	a	h	a	b	b	a	a	h
114	4	B4021-2	21.30	h	h	b	h	b	h	b	b	a	h	b	h	h	a	h	a	b	b	a	a	h
115	4	B4011-1	26.29	h	a	b	h	h	h	b	b	a	h	b	h	h	a	h	a	b	b	a	a	h
116	4	B4008a-5	28.70	h	a	b	h	h	h	b	b	a	h	b	h	h	a	h	a	b	b	a	a	h
117	4	B4008b-1	30.51	h	a	b	h	h	h	b	h	a	h	b	h	h	a	h	a	b	b	a	a	h
118	4	B4010-1	35.59	h	a	b	h	h	h	b	h	a	h	b	h	h	a	h	a	b	h	a	a	h
119	4	B4018-3	39.32	b	a	b	h	h	b	b	h	a	h	b	a	h	a	h	a	b	h	a	a	h
120	4	B4006b-1	46.11	b	a	b	h	a	b	h	h	a	h	b	a	h	a	h	a	b	h	h	a	h

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	66	67	68	70	71	72	74	75	76	78	79	80	82	83	84	85	86	87	88	89	90
121	4	B4006a-2	48.54	b	a	b	h	a	b	h	h	a	h	b	a	h	a	h	a	b	h	a	a	h
122	4	B4013-1	54.85	b	a	b	h	a	h	h	h	a	a	b	a	h	b	h	a	b	h	a	a	h
123	4	B4003b-2	57.26	b	a	b	h	a	h	h	h	a	a	b	a	h	b	h	a	b	h	a	a	h
124	4	B4003a-1	58.46	h	a	b	h	a	h	h	h	a	a	b	a	h	b	h	a	b	h	a	a	h
125	5	B5030-3	0.00	h	b	h	h	a	a	a	h	h	a	h	b	h	h	h	h	h	h	a	b	h
126	5	B5031-1	0.59	h	b	h	h	a	a	a	h	h	a	h	b	h	h	h	h	h	h	a	b	h
127	5	B5032a-1	1.18	h	b	h	h	a	a	a	h	h	a	h	b	h	h	h	h	h	h	a	b	h
128	5	B5032b-1	3.00	h	b	h	h	a	a	a	h	h	a	b	b	h	h	h	h	h	h	a	b	h
129	5	B5032c-1	7.37	h	b	h	h	a	a	a	h	h	a	h	b	h	h	h	h	h	b	a	b	h
130	5	B5011-2	14.53	h	b	h	h	a	a	h	b	h	a	h	b	h	h	h	h	h	b	h	b	h
131	5	B5033-1	17.25	h	b	h	h	a	a	h	b	h	a	h	b	h	h	h	h	h	b	-	b	h
132	5	B5001-1	20.01	h	b	h	h	a	a	h	b	h	a	h	b	h	h	h	h	h	b	b	b	h
133	5	B5002a-2	22.44	h	b	h	h	a	a	h	b	h	a	h	b	h	h	h	h	h	h	b	b	h
134	5	B5002b-1	29.66	h	b	h	h	a	a	h	b	h	a	h	b	h	b	b	h	h	h	b	b	h
135	5	B5003a-1	33.40	h	b	h	b	a	a	h	b	h	a	h	b	h	b	b	a	h	h	b	b	b
136	5	B5003b-3	34.60	h	b	h	b	a	a	h	b	h	a	h	b	h	b	b	a	h	h	b	b	b
137	5	B5004-5	37.03	h	b	h	b	a	a	h	b	h	a	h	b	h	b	b	a	h	h	b	b	b
138	5	B5005a-3	38.83	h	b	h	b	a	a	h	b	h	a	h	b	h	b	b	a	h	h	b	b	b
139	5	B5005b-1	41.28	h	b	h	b	h	a	h	b	h	a	h	b	h	b	b	a	a	h	b	b	b
140	5	B5005c-5	45.64	a	b	h	b	h	h	b	b	b	h	h	b	h	b	b	a	a	h	b	b	b
141	5	B5006-3	47.44	a	b	h	b	h	h	b	b	b	h	h	b	h	b	b	a	a	h	b	b	b
142	5	B5007b-1	48.63	a	b	h	b	h	h	b	b	b	h	h	b	h	b	b	a	a	h	b	b	b
143	5	B5007a-1	49.22	a	b	h	b	h	h	b	b	b	h	h	b	h	b	b	a	a	h	b	b	b
144	5	B5034d-4	50.42	a	b	h	b	h	h	b	b	b	h	h	b	h	b	b	a	a	h	b	b	b
145	5	B5034b-5	52.92	a	h	h	b	h	h	b	b	b	h	h	b	h	b	b	a	a	h	b	b	b
146	5	B5034a-1	54.11	a	h	h	b	h	h	b	b	b	h	h	b	h	b	b	a	a	h	b	b	b
147	5	B5018b-11	56.55	a	h	h	b	h	h	b	b	b	h	h	b	h	b	b	a	a	h	b	b	b
148	5	B5018a-7	57.14	a	h	h	b	h	h	b	b	b	h	h	b	h	b	b	a	a	h	b	b	b
149	5	B5018c-4	60.22	a	h	h	b	h	b	b	b	b	h	h	b	h	b	b	a	a	h	b	h	b
150	5	B5014a-4	61.42	a	h	h	b	h	b	b	b	b	h	h	b	h	b	b	a	a	h	b	h	b
151	5	B5014b-6	63.93	a	h	h	h	h	b	b	b	b	b	h	b	h	b	b	a	a	h	b	h	h
152	5	B5016-2	65.15	a	h	h	h	h	b	b	b	b	b	h	b	h	b	b	a	a	h	b	h	h
153	5	B5022b-4	65.74	a	h	h	h	h	b	b	b	b	b	h	b	h	b	b	a	a	h	b	h	h
154	5	B5022a-2	66.34	a	h	h	h	h	b	b	h	b	b	h	b	h	b	b	a	a	h	b	h	h
155	5	B5029-32	67.53	a	h	h	h	h	b	b	h	b	b	h	b	h	b	b	a	a	h	b	h	h
156	6	B6011b-1	0.00	h	h	h	h	h	b	a	b	a	h	h	h	h	h	b	h	h	h	b	h	h
157	6	B6011a-1	2.44	h	h	h	h	h	b	a	b	a	h	h	h	h	b	b	h	h	h	b	h	h
158	6	B6002a-2	6.85	h	a	h	h	h	b	a	b	a	h	b	h	h	b	b	h	a	h	h	h	h
159	6	B6002b-1	8.66	h	a	h	h	h	b	a	h	a	h	b	h	h	h	b	h	a	h	h	h	h
160	6	B6017-3	12.39	h	a	h	h	b	b	a	h	a	h	b	h	h	h	b	h	a	h	h	h	h
161	6	B6019-1	21.01	h	a	h	h	b	b	a	h	a	h	b	h	a	h	b	h	a	h	h	h	h
162	6	B6004-3	29.61	h	a	h	b	b	b	a	h	a	h	b	a	a	h	b	h	a	h	a	h	b
163	6	B6005-4	33.31	h	a	h	b	b	b	a	h	a	b	b	a	a	h	b	h	a	h	a	h	b
164	6	B6007-1	37.03	h	a	h	b	b	b	a	a	a	b	b	a	a	h	b	h	a	a	a	a	b
165	6	B6006a-2	40.09	h	a	h	b	h	b	a	a	a	b	h	a	a	h	b	h	a	a	a	a	b
166	6	B6006b-20	42.53	h	a	b	b	b	b	a	a	a	b	h	a	a	h	b	h	a	a	a	a	b
167	6	B6009c-46	44.34	h	a	b	b	b	b	a	a	a	b	h	a	a	h	b	h	a	a	a	a	b
168	6	B6009b-32	45.54	h	a	b	b	b	b	a	a	a	b	h	a	a	a	b	h	a	a	a	a	b
169	6	B6009a-3	46.73	h	a	b	b	b	b	a	a	a	b	h	a	a	a	b	h	a	a	a	a	b
170	6	B6020-1	47.92	h	a	b	b	b	b	a	h	a	b	h	a	a	a	b	h	a	a	a	a	b
171	6	B6014a-25	48.51	h	a	b	b	b	b	a	h	a	b	h	a	a	a	b	h	a	a	a	a	b
172	6	B6014b-1	49.70	h	a	b	b	b	b	a	h	a	b	h	a	a	a	b	b	a	a	a	a	b
173	6	B6014c-2	50.89	h	a	b	b	b	b	a	h	h	b	h	h	a	a	b	b	a	a	a	a	b
174	6	B6016-1	52.09	h	a	b	b	b	b	a	h	h	b	h	h	a	a	b	b	a	a	a	a	b
175	6	B6021-4	52.68	h	a	b	b	b	b	a	h	h	b	h	h	a	a	b	b	a	a	a	a	b
176	6	B6022-2	54.48	h	a	b	b	b	b	a	h	h	b	h	h	a	a	b	b	a	a	a	a	b
177	6	B6010a-5	57.52	h	a	b	b	b	b	a	h	h	b	h	h	a	a	b	b	a	a	h	a	b
178	6	B6010b-2	58.71	h	a	b	b	b	b	a	h	h	b	a	h	a	a	b	b	a	a	h	a	b
179	6	B6010c-2	59.30	h	a	b	b	b	b	a	h	h	b	a	h	a	a	b	b	a	a	h	a	b
180	6	B6010d-3	61.10	h	a	b	b	b	b	a	h	h	b	a	h	a	a	b	b	a	a	h	a	b

Table C: *F. iinumae* F1D segregation data for the 85F2D map.

Sort	LG	Bin	cM	66	67	68	70	71	72	74	75	76	78	79	80	82	83	84	85	86	87	88	89	90
181	6	B6018a-3	62.29	h	a	b	b	b	b	a	h	h	b	a	h	a	a	b	b	a	a	h	a	b
182	6	B6018b-1	64.71	h	a	b	b	b	h	a	h	h	b	a	h	a	a	b	b	a	a	h	a	b
183	6	B6013-3	65.90	h	a	b	b	b	h	a	h	h	b	a	h	a	a	b	b	a	a	h	a	b
184	6	B6012a-3	68.98	b	a	b	b	b	h	a	h	h	b	a	h	a	a	b	b	a	a	h	a	b
185	6	B6012b-2	72.06	b	h	b	b	b	h	a	h	h	b	a	h	a	a	b	b	a	a	h	a	b
186	6	B6008-2	85.48	b	h	h	b	b	h	h	h	h	b	a	h	a	a	b	b	a	a	h	a	b
187	6	B6015-7	90.53	b	h	h	b	b	h	h	h	h	b	a	h	a	a	b	b	a	a	h	a	b
188	7	B7001e-3	0.00	h	h	h	h	b	h	h	h	b	h	h	h	h	a	b	a	b	h	h	h	h
189	7	B7001d-2	0.59	h	h	h	h	b	h	h	h	b	h	h	h	h	a	b	a	b	h	h	h	h
190	7	B7001c-8	1.18	h	h	h	h	b	h	h	h	b	h	h	h	h	a	b	a	b	h	h	h	h
191	7	B7001b-4	1.78	h	h	h	h	b	h	h	h	b	h	h	h	h	a	b	a	b	h	b	h	h
192	7	B7001a-7	2.98	h	h	h	h	b	h	h	a	b	h	h	h	h	a	b	a	b	h	b	h	h
193	7	B7018-2	4.78	h	h	h	h	b	h	h	a	b	h	h	h	b	a	b	a	b	h	b	h	h
194	7	B7002a-1	6.58	h	h	h	h	b	h	h	a	b	h	h	h	b	a	b	a	b	h	b	h	h
195	7	B7002b-1	7.77	h	h	h	h	b	h	h	a	b	h	h	h	b	a	b	a	b	h	b	h	h
196	7	B7002c-1	8.36	h	h	h	h	b	h	h	a	b	h	h	h	b	a	b	a	b	h	b	h	h
197	7	B7003-4	11.39	h	h	h	h	b	h	h	a	b	h	b	h	b	a	b	a	b	h	b	h	h
198	7	B7004-2	11.98	h	h	h	h	b	h	h	a	b	h	b	h	b	a	b	a	b	h	b	h	h
199	7	B7005-2	13.79	h	h	h	h	b	h	h	a	b	h	b	h	b	a	b	a	b	h	b	h	h
200	7	B7006a-1	14.38	h	h	h	h	b	h	h	a	b	h	b	h	b	a	b	a	b	h	b	h	h
201	7	B7006b-2	16.79	h	b	h	h	b	h	h	a	b	h	b	h	b	a	b	a	b	h	b	h	h
202	7	B7007a-1	17.38	h	b	h	h	b	h	h	a	b	h	b	h	b	a	b	a	b	h	b	h	h
203	7	B7007b-1	17.97	h	b	h	h	b	h	h	a	b	h	b	h	b	a	b	a	b	h	b	h	h
204	7	B7008a-2	22.28	h	b	h	b	b	h	h	a	b	h	b	h	b	a	b	a	b	h	h	h	b
205	7	B7008b-3	22.87	h	b	h	b	b	h	h	a	b	h	b	h	b	a	b	a	b	h	h	h	b
206	7	B7009a-1	24.08	h	b	h	b	b	h	h	a	b	h	b	h	b	a	b	a	b	h	h	h	b
207	7	B7009b-6	28.38	b	b	h	b	b	h	h	a	h	h	b	h	b	a	b	a	b	h	h	h	b
208	7	B7017a-1	30.80	b	b	h	b	b	h	h	a	h	h	b	h	b	a	b	h	b	h	h	h	b
209	7	B7017b-3	31.99	b	b	h	b	b	h	h	a	h	h	b	h	b	h	b	h	b	h	h	h	b
210	7	B7016-1	34.41	b	h	h	b	b	h	h	a	h	h	b	h	b	h	b	h	b	h	h	h	b
211	7	B7015-3	35.61	b	h	h	b	b	h	h	a	h	h	b	h	b	h	b	h	b	h	h	h	b
212	7	B7013a-1	48.25	b	a	h	b	b	h	h	a	h	h	b	h	h	h	h	h	b	h	a	h	b
213	7	B7013b-2	48.84	b	a	h	b	b	h	h	a	h	h	b	h	h	h	h	h	b	h	a	h	b
214	7	B7012b-1	50.04	b	a	h	b	b	h	h	a	h	h	b	h	h	h	h	h	b	h	a	h	b
215	7	B7012a-2	51.23	b	a	h	b	b	h	h	a	h	h	b	h	h	h	h	h	b	a	a	h	b
216	7	B7011-1	52.43	b	a	h	b	b	h	h	a	h	h	b	h	h	h	h	h	b	a	a	h	b
217	7	B7010-2	55.50	b	a	h	b	b	h	h	a	h	h	b	h	a	h	h	h	b	a	a	h	b